

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 1, 2002, 16:17:34 ; Search time 35.93 Seconds
(without alignments)
44.781 Million cell updates/sec

Title: US-09-988-792-1
Perfect score: 61
Sequence: 1 RPKQGFGLM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 556

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 50%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: SPREMBL_17:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mhc:*
8: sp.phage:*
9: sp.plant:*
10: sp.porcine:*
11: sp.virus:*
12: sp.virulent:*
13: sp.verticillate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	72	4	09Y494 homo sapien
2	61	100.0	114	6	09Y947 tupia bela
3	61	100.0	128	4	09Y6V5 homo sapien
4	61	100.0	129	6	09Y948 tupia bela
5	53	86.9	97	11	09Z0K2 cavia porce
6	53	86.9	130	11	09Z0K1 cavia porce
7	53	86.9	135	11	09Z0K0 cavia porce
8	41	67.2	207	1	09HLY7 thermoplas
9	39	63.9	786	5	024014 dictyostell
10	39	63.9	803	5	024012 dictyostell
11	38	62.3	205	5	020174 caenorhabd
12	38	62.3	235	5	09YBWA4 drosophila
13	38	62.3	257	10	09SUN5 arabidopsis
14	38	62.3	293	10	049561 arabidopsis
15	38	62.3	496	13	09PVE8 fundulus he
16	38	62.3	500	13	09DE99 oryzias lat
17	38	62.3	3722	2	098T91 lysobacter
18	38	62.3	3722	2	094873 lysobacter
19	37	60.7	138	2	084949 salmonella

20	37	60.7	249	1	09V2N2 pyrococcus
21	36	59.0	177	5	09BPN9 caenorhabd
22	36	59.0	236	5	09BPN8 caenorhabd
23	36	59.0	352	12	09B283 unidentified
24	36	59.0	373	10	023876 oryza sativ
25	36	59.0	477	3	09UM05 clavispora
26	36	59.0	550	5	094130 caenorhabd
27	36	59.0	629	5	045273 caenorhabd
28	36	59.0	869	2	09F634 stigmarella
29	35	57.4	128	11	099N14 mus musculu
30	35	57.4	206	5	061761 caenorhabd
31	35	57.4	218	10	09L5Y0 streptomyce
32	35	57.4	296	10	09LWZ6 arabidopsis
33	35	57.4	297	2	09HV29 pseudomonas
34	35	57.4	347	10	040055 hordium vul
35	35	57.4	424	10	048648 adiantum ca
36	35	57.4	494	2	09C117 lactococc
37	35	57.4	497	2	09A0V7 streptococc
38	35	57.4	509	12	065191 african swi
39	35	57.4	521	5	018014 caenorhabd
40	35	57.4	681	5	09GUT4 leishmania
41	35	57.4	682	11	09ESL2 cavia porce
42	35	57.4	832	2	P74619 synchocyst
43	35	57.4	1043	5	09XRT20 caenorhabd
44	35	57.4	1278	4	09UPP5 homo sapien
45	35	57.4	1611	10	09SDB6 arabidopsis
46	35	57.4	1736	10	023025 arabidopsis
47	35	56.6	216	10	09CAM3 arabidopsis
48	34	55.7	154	11	09JK11 mus pahari
49	34	55.7	162	13	P70014 xenopus lae
50	34	55.7	167	2	09X8G5 streptomyce
51	34	55.7	216	10	09ZSX5 zea mays (m
52	34	55.7	253	2	054788 streptococ
53	34	55.7	266	12	056868 gallia herp
54	34	55.7	270	5	09GUG0 caenorhabd
55	34	55.7	304	6	09GXM6 macaca fasc
56	34	55.7	306	2	09JXY6 neisseria m
57	34	55.7	316	5	076902 drosophila
58	34	55.7	318	2	09JYV5 neisseria m
59	34	55.7	355	8	09MW81 physarum po
60	34	55.7	359	10	082469 mesembryant
61	34	55.7	393	10	049132 diospyros k
62	34	55.7	405	2	09Z5W4 pseudomonas
63	34	55.7	410	8	021172 galapagnus
64	34	55.7	415	3	013352 magnaporthe
65	34	55.7	502	11	006884 rattus norv
66	34	55.7	583	10	041486 solanum tub
67	34	55.7	628	10	09XIC7 arabidopsis
68	34	55.7	646	10	09C792 arabidopsis
69	34	55.7	737	2	09A926 caulobacter
70	34	55.7	738	5	09WSX2 drosophila
71	34	55.7	1487	5	09Y062 drosophila
72	34	55.7	1487	5	09V6I8 drosophila
73	34	55.7	1970	5	09VQU8 drosophila
74	34	55.7	71	2	09JUN9 neisseria m
75	34	55.7	101	1	058860 pyrococcus
76	34	55.7	102	11	09B6D2 mus musculu
77	34	55.7	103	10	09XJ71 cucumis sat
78	34	55.7	130	8	080033 exoneurella
79	34	55.7	131	8	080034 brunasappia
80	34	55.7	131	8	079125 brevineura
81	34	55.7	131	8	079126 exoneurella
82	34	55.7	151	8	099834 ophraella c
83	34	55.7	156	4	09G462 diadasia co
84	34	55.7	159	4	09HBQ6 homo sapien
85	34	55.7	161	11	09C9Y1 mus musculu
86	34	55.7	192	8	0967A3 brevineura
87	34	55.7	192	8	096798 xylocopa bo
88	34	55.7	197	8	096782 xylocopa va
89	34	55.7	198	8	0967A2 xylocopa mi
90	34	55.7	198	8	0967A1 xylocopa tr
91	34	55.7	198	8	096799 xylocopa vi
92	34	55.7	198	8	096799

93	33	54.1	198	8	09G797	09G797 xylocopa ta	166	33	54.1	413	8	09TC14	09TC14 lasioglossu
94	33	54.1	198	8	09G796	09G796 xylocopa si	167	33	54.1	413	8	09TC13	09TC13 lasioglossu
95	33	54.1	198	8	09G795	09G795 xylocopa vi	168	33	54.1	413	8	09TC12	09TC12 lasioglossu
96	33	54.1	198	8	09G793	09G793 xylocopa ar	169	33	54.1	413	8	09TC11	09TC11 lasioglossu
97	33	54.1	198	8	09G792	09G792 xylocopa li	170	33	54.1	413	8	09TC10	09TC10 lasioglossu
98	33	54.1	198	8	09G791	09G791 xylocopa pu	171	33	54.1	413	8	09TC09	09TC09 lasioglossu
99	33	54.1	198	8	09G790	09G790 xylocopa sc	172	33	54.1	413	8	09TC08	09TC08 lasioglossu
100	33	54.1	198	8	09G789	09G789 xylocopa ni	173	33	54.1	413	8	09TC07	09TC07 lasioglossu
101	33	54.1	198	8	09G788	09G788 xylocopa fl	174	33	54.1	413	8	09TC06	09TC06 lasioglossu
102	33	54.1	198	8	09G787	09G787 xylocopa ol	175	33	54.1	413	8	09TC05	09TC05 lasioglossu
103	33	54.1	198	8	09G786	09G786 xylocopa la	176	33	54.1	413	8	09TC04	09TC04 lasioglossu
104	33	54.1	198	8	09G785	09G785 xylocopa ac	177	33	54.1	413	8	09TC03	09TC03 lasioglossu
105	33	54.1	198	8	09G784	09G784 xylocopa ap	178	33	54.1	413	8	09TC02	09TC02 lasioglossu
106	33	54.1	198	8	09G783	09G783 xylocopa mi	179	33	54.1	413	8	09TC01	09TC01 lasioglossu
107	33	54.1	198	8	09G781	09G781 xylocopa gu	180	33	54.1	413	8	09TC00	09TC00 lasioglossu
108	33	54.1	198	8	09G780	09G780 xylocopa fr	181	33	54.1	413	8	09TC09	09TC09 lasioglossu
109	33	54.1	207	2	09A0J6	09A0J6 acinetobact	182	33	54.1	413	8	09TC08	09TC08 lasioglossu
110	33	54.1	211	2	09XDK9	09XDK9 bacteroides	183	33	54.1	413	8	09TC07	09TC07 lasioglossu
111	33	54.1	234	2	09KRA9	09KRA9 deinococcus	184	33	54.1	413	8	09TC06	09TC06 lasioglossu
112	33	54.1	240	11	09CR69	09CR69 mus musculu	185	33	54.1	413	8	09TC05	09TC05 lasioglossu
113	33	54.1	265	8	09RG67	09RG67 halictus fa	186	33	54.1	413	8	09TC04	09TC04 lasioglossu
114	33	54.1	265	8	09RG66	09RG66 halictus ru	187	33	54.1	413	8	09TC03	09TC03 lasioglossu
115	33	54.1	266	8	09RG65	09RG65 halictus po	188	33	54.1	413	8	09TC02	09TC02 lasioglossu
116	33	54.1	266	8	09RG64	09RG64 halictus po	189	33	54.1	413	8	09TC01	09TC01 lasioglossu
117	33	54.1	266	8	09T2W6	09T2W6 halictus li	190	33	54.1	413	8	09TC00	09TC00 lasioglossu
118	33	54.1	299	2	09J361	09J361 mycobacteri	191	33	54.1	413	8	09TC09	09TC09 lasioglossu
119	33	54.1	299	5	09NE15	09NE15 leishmania	192	33	54.1	413	8	09TC08	09TC08 lasioglossu
120	33	54.1	301	2	09E462	09E462 rhizobium p	193	33	54.1	413	8	09TC07	09TC07 lasioglossu
121	33	54.1	320	2	08J931	08J931 treponema r	194	33	54.1	413	8	09TC06	09TC06 lasioglossu
122	33	54.1	327	2	09RZU3	09RZU3 deinococcus	195	33	54.1	413	8	09TC05	09TC05 lasioglossu
123	33	54.1	327	2	09RZRI	09RZRI deinococcus	196	33	54.1	413	8	09TC04	09TC04 lasioglossu
124	33	54.1	327	2	09RZJ3	09RZJ3 deinococcus	197	33	54.1	413	8	09TC03	09TC03 lasioglossu
125	33	54.1	327	2	09RY10	09RY10 deinococcus	198	33	54.1	413	8	09TC02	09TC02 lasioglossu
126	33	54.1	327	2	09R314	09R314 deinococcus	199	33	54.1	413	8	09TC01	09TC01 lasioglossu
127	33	54.1	334	2	09CP29	09CP29 pasteurilla	200	33	54.1	413	8	09TC00	09TC00 lasioglossu
128	33	54.1	390	4	09B210	09B210 homo sapien	201	33	54.1	413	8	09TC09	09TC09 lasioglossu
129	33	54.1	399	4	09S684	09S684 homo sapien	202	33	54.1	413	8	09TC08	09TC08 lasioglossu
130	33	54.1	405	8	09TCF5	09TCF5 lasioglossu	203	33	54.1	413	8	09TC07	09TC07 lasioglossu
131	33	54.1	407	8	09B4P4	09B4P4 diadasia au	204	33	54.1	413	8	09TC06	09TC06 lasioglossu
132	33	54.1	409	8	09XP15	09XP15 apanteles c	205	33	54.1	413	8	09TC05	09TC05 lasioglossu
133	33	54.1	411	8	09B4P2	09B4P2 diadasia ba	206	33	54.1	413	8	09TC04	09TC04 lasioglossu
134	33	54.1	412	8	09G464	09G464 diadasia la	207	33	54.1	413	8	09TC03	09TC03 lasioglossu
135	33	54.1	412	8	09B4M3	09B4M3 melliphilops	208	33	54.1	413	8	09TC02	09TC02 lasioglossu
136	33	54.1	412	8	09B4K0	09B4K0 diadasia tu	209	33	54.1	413	8	09TC01	09TC01 lasioglossu
137	33	54.1	413	8	09TEC4	09TEC4 lasioglossu	210	33	54.1	413	8	09TC00	09TC00 lasioglossu
138	33	54.1	413	8	09TEC2	09TEC2 agapostemon	211	33	54.1	413	8	09TC09	09TC09 lasioglossu
139	33	54.1	413	8	09TEC1	09TEC1 agapostemon	212	33	54.1	413	8	09TC08	09TC08 lasioglossu
140	33	54.1	413	8	09TEC0	09TEC0 agapostemon	213	33	54.1	413	8	09TC07	09TC07 lasioglossu
141	33	54.1	413	8	09TEC9	09TEC9 agapostemon	214	33	54.1	413	8	09TC06	09TC06 lasioglossu
142	33	54.1	413	8	09TEC8	09TEC8 halictus co	215	33	54.1	413	8	09B4Q5	09B4Q5 diadasia af
143	33	54.1	413	8	09TEC7	09TEC7 halictus fa	216	33	54.1	413	8	09B4Q3	09B4Q3 diadasia af
144	33	54.1	413	8	09TEC6	09TEC6 halictus po	217	33	54.1	413	8	09B4P9	09B4P9 diadasia an
145	33	54.1	413	8	09TEC5	09TEC5 halictus li	218	33	54.1	413	8	09B4P7	09B4P7 diadasia an
146	33	54.1	413	8	09TEC4	09TEC4 halictus po	219	33	54.1	413	8	09B4P5	09B4P5 diadasia au
147	33	54.1	413	8	09TEC3	09TEC3 halictus ru	220	33	54.1	413	8	09B4P0	09B4P0 diadasia bl
148	33	54.1	413	8	09TEC2	09TEC2 mexalictus	221	33	54.1	413	8	09B4N9	09B4N9 diadasia bl
149	33	54.1	413	8	09TEC1	09TEC1 sphecodes m	222	33	54.1	413	8	09B4N8	09B4N8 diadasia ch
150	33	54.1	413	8	09TEC0	09TEC0 lasioglossu	223	33	54.1	413	8	09B4N6	09B4N6 diadasia co
151	33	54.1	413	8	09TCJ9	09TCJ9 lasioglossu	224	33	54.1	413	8	09B4N4	09B4N4 diadasia di
152	33	54.1	413	8	09TCJ8	09TCJ8 lasioglossu	225	33	54.1	413	8	09B4N1	09B4N1 diadasia hi
153	33	54.1	413	8	09TCJ7	09TCJ7 lasioglossu	226	33	54.1	413	8	09B4M9	09B4M9 diadasia kn
154	33	54.1	413	8	09TCJ6	09TCJ6 lasioglossu	227	33	54.1	413	8	09B4M7	09B4M7 diadasia lu
155	33	54.1	413	8	09TCJ5	09TCJ5 lasioglossu	228	33	54.1	413	8	09B4M6	09B4M6 diadasia lu
156	33	54.1	413	8	09TCJ4	09TCJ4 lasioglossu	229	33	54.1	413	8	09B4M5	09B4M5 diadasia ma
157	33	54.1	413	8	09TCJ3	09TCJ3 lasioglossu	230	33	54.1	413	8	09B4M4	09B4M4 diadasia ma
158	33	54.1	413	8	09TCJ2	09TCJ2 lasioglossu	231	33	54.1	413	8	09B4M1	09B4M1 melitoma ma
159	33	54.1	413	8	09TCJ1	09TCJ1 lasioglossu	232	33	54.1	413	8	09B4L7	09B4L7 diadasia oc
160	33	54.1	413	8	09TCJ0	09TCJ0 lasioglossu	233	33	54.1	413	8	09B4L5	09B4L5 diadasia oc
161	33	54.1	413	8	09TCI9	09TCI9 lasioglossu	234	33	54.1	413	8	09B4L3	09B4L3 diadasia op
162	33	54.1	413	8	09TCI8	09TCI8 lasioglossu	235	33	54.1	413	8	09B4K9	09B4K9 diadasia pe
163	33	54.1	413	8	09TCI7	09TCI7 lasioglossu	236	33	54.1	413	8	09B4K7	09B4K7 diadasia pi
164	33	54.1	413	8	09TCI6	09TCI6 lasioglossu	237	33	54.1	413	8	09B4K5	09B4K5 pilochirix
165	33	54.1	413	8	09TCI5	09TCI5 lasioglossu	238	33	54.1	413	8	09B4K3	09B4K3 loromelissa

239	33	54.1	413	8	09B4K1	09b4k1 diadastia tu	312	32	52.5	299	1	028568	028568 archaeoglob
240	33	54.1	413	8	09B4J9	09b4j9 diadastia ri	313	32	52.5	299	1	028888	028888 archaeoglob
241	33	54.1	413	8	09B4J7	09b4j7 diadastia au	314	32	52.5	299	1	028895	028895 archaeoglob
242	33	54.1	413	8	09B4J6	09b4j6 diadastia ri	315	32	52.5	299	1	028935	028935 archaeoglob
243	33	54.1	413	8	09B4J4	09b4j4 diadastia pi	316	32	52.5	305	10	09C6A2	09c6a2 arabidopsi
244	33	54.1	413	8	09B4J0	09b4j0 diadastia va	317	32	52.5	313	2	09ANA2	09ana2 bradyrhizob
245	33	54.1	413	8	09B1L9	09b1l9 diadastia ma	318	32	52.5	313	10	09LNU23	09lnu23 arabidopsi
246	33	54.1	413	8	09B1L2	09b1l2 diadastia nl	319	32	52.5	323	5	076920	076920 drosophila
247	33	54.1	413	8	09B1G0	09b1g0 diadastia nl	320	32	52.5	327	2	09PRK9	09prk9 delnoco
248	33	54.1	413	8	09B1D0	09b1d0 diadastia dl	321	32	52.5	331	2	087922	087922 yersinia in
249	33	54.1	413	8	09B0V7	09b0v7 diadastia pa	322	32	52.5	338	2	09AHG0	09ahg0 fusobacteri
250	33	54.1	413	8	09B0N8	09b0n8 diadastia me	323	32	52.5	345	2	09I1S0	09i1s0 pseudomonas
251	33	54.1	413	8	09B0M6	09b0m6 diadastia sp	324	32	52.5	357	1	028862	028862 archaeoglob
252	33	54.1	414	8	09B4Q1	09b4q1 alepidoscel	325	32	52.5	361	1	057936	057936 pyrococcus
253	33	54.1	416	2	09RVA2	09rva2 delnoco	326	32	52.5	368	5	017992	017992 caenorhabd
254	33	54.1	418	2	054651	054651 streptococ	327	32	52.5	370	10	09SUR1	09sur1 arabidopsi
255	33	54.1	433	4	09BSU8	09bsu8 homo sapien	328	32	52.5	381	10	09FKW2	09fkw2 arabidopsi
256	33	54.1	439	8	09MEK9	09mek9 acalymma vl	329	32	52.5	384	2	09K3I1	09k3i1 streptomyce
257	33	54.1	440	8	09MEK8	09mek8 acalymma bl	330	32	52.5	400	2	09KXG1	09kxg1 streptomyce
258	33	54.1	440	8	09MEK7	09mek7 diabrotica	331	32	52.5	402	5	021056	021056 caenorhabd
259	33	54.1	440	8	09MEK6	09mek6 diabrotica	332	32	52.5	402	5	09NEQ0	09neq0 caenorhabd
260	33	54.1	440	8	09MEK5	09mek5 diabrotica	333	32	52.5	402	5	09NEQ0	09neq0 chlamydia m
261	33	54.1	440	8	09MEK4	09mek4 diabrotica	334	32	52.5	419	2	09PUQ0	09puq0 chlamydia m
262	33	54.1	440	8	09MEK3	09mek3 diabrotica	335	32	52.5	419	4	09H7H6	09h7h6 homo sapien
263	33	54.1	440	8	09MEK2	09mek2 diabrotica	336	32	52.5	426	2	09HXI4	09hxi4 pseudomonas
264	33	54.1	440	8	09MEK1	09mek1 diabrotica	337	32	52.5	432	2	09PND9	09pnd9 campylobact
265	33	54.1	440	8	09MEK0	09mek0 diabrotica	338	32	52.5	433	2	09ZSL0	09zsl0 leptospira
266	33	54.1	440	8	09MEJ9	09mej9 diabrotica	339	32	52.5	445	2	F74224	F74224 synechocyst
267	33	54.1	440	8	09MEJ8	09mej8 diabrotica	340	32	52.5	464	2	056885	056885 yersinia en
268	33	54.1	440	8	09MEJ7	09mej7 diabrotica	341	32	52.5	464	2	084498	084498 chlamydia t
269	33	54.1	440	8	09MEJ6	09mej6 diabrotica	342	32	52.5	464	2	09Z7U4	09z7u4 chlamydia p
270	33	54.1	440	8	09MEJ5	09mej5 diabrotica	343	32	52.5	478	2	P74978	P74978 yersinia en
271	33	54.1	444	12	P88924	P88924 keposi's sa	344	32	52.5	478	2	09KRX8	09krx8 vibrio chol
272	33	54.1	454	3	09UOK2	09uok2 schizosacch	345	32	52.5	484	10	09FEF6	09fef6 caenorhabd
273	33	54.1	495	2	099W86	099w86 staphylococ	346	32	52.5	508	13	013254	013254 gallus gall
274	33	54.1	512	11	061745	061745 mus musculu	347	32	52.5	513	4	09UPE1	09upe1 homo sapien
275	33	54.1	512	11	061364	061364 mus musculu	348	32	52.5	518	5	017616	017616 caenorhabd
276	33	54.1	528	10	09B9I3	09b9i3 waterstonie	349	32	52.5	522	12	09WHJ1	09whj1 walleye ept
277	33	54.1	546	4	09SKL1	09skl1 arabidopsi	350	32	52.5	539	2	09FAH8	09fah8 porphyromon
278	33	54.1	566	4	09H6A8	09h6a8 homo sapien	351	32	52.5	567	10	09SVL5	09svl5 arabidopsi
279	33	54.1	573	11	09QXW2	09qxw2 mus musculu	352	32	52.5	579	2	09K474	09k474 streptomyce
280	33	54.1	612	5	09VNR5	09vnr5 drosophila	353	32	52.5	612	2	09X7Y5	09x7y5 streptomyce
281	33	54.1	711	2	09S517	09s517 staphylococ	354	32	52.5	614	2	052516	052516 pseudomonas
282	33	54.1	712	10	080890	080890 arabidopsi	355	32	52.5	614	5	022708	022708 caenorhabd
283	33	54.1	734	5	09BHZ0	09bhz0 leishmania	356	32	52.5	617	2	09JZ26	09jz26 neisseria m
284	33	54.1	745	3	P79086	P79086 collettotric	357	32	52.5	628	2	09JUZ1	09ju21 neisseria m
285	33	54.1	755	10	09LXW7	09lxw7 arabidopsi	358	32	52.5	637	10	080625	080625 arabidopsi
286	33	54.1	1106	2	09EVO3	09ev03 erwina chr	359	32	52.5	667	5	09Y117	09y117 drosophila
287	33	54.1	1357	12	089328	089328 rice ragged	360	32	52.5	673	5	09VFM2	09vfm2 arabidopsi
288	33	54.1	1741	5	046095	046095 drosophila	361	32	52.5	700	10	09LFM2	09lfm2 arabidopsi
289	33	54.1	1741	5	09W517	09w517 drosophila	362	32	52.5	768	11	088797	088797 raltus norv
290	33	53.3	97	5	09V8C5	09v8c5 drosophila	363	32	52.5	841	5	09U6X3	09u6x3 drosophila
291	32	52.5	87	12	09B675	09b675 simlan cyto	364	32	52.5	922	11	09QXJ2	09qxj2 mus musculu
292	32	52.5	132	2	09EZM6	09ezm6 staphylococ	365	32	52.5	925	11	09QZEA	09qze4 mus musculu
293	32	52.5	133	2	099748	099748 staphylococ	366	32	52.5	1016	4	043147	043147 homo sapien
294	32	52.5	154	11	09R129	09r129 raltus norv	367	32	52.5	1039	5	023567	023567 caenorhabd
295	32	52.5	155	11	09R132	09r132 raltus norv	368	32	52.5	1197	11	09ZOR5	09zor5 mus musculu
296	32	52.5	155	11	09R131	09r131 raltus norv	369	32	52.5	1307	2	09MXR1	09mxr1 acetobacter
297	32	52.5	155	11	09R127	09r127 raltus norv	370	32	52.5	1415	2	09HVI8	09hvi8 pseudomonas
298	32	52.5	157	4	013092	013092 homo sapien	371	32	52.5	1503	3	09V6P4	09v6p4 drosophila
299	32	52.5	168	11	09DPD6	09dpd6 mus musculu	372	32	52.5	1658	11	045176	045176 caenorhabd
300	32	52.5	180	2	055966	055966 synechocyst	373	32	52.5	1658	11	09ZOR6	09zor6 mus musculu
301	32	52.5	198	12	09B674	09b674 simlan cyto	374	32	52.5	1718	5	062603	062603 trypanosoma
302	32	52.5	210	2	034947	034947 bacillus su	375	32	52.5	1817	11	019931	019931 caenorhabd
303	32	52.5	219	10	09AVT2	09avt2 picea abies	376	32	52.5	2157	11	09ZLRI	09zlr1 mus musculu
304	32	52.5	220	2	052941	052941 calochrix v	377	32	52.5	2161	12	09R1F1	09r1f1 meleagridd h
305	32	52.5	225	2	09RVM8	09rvm8 delnoco	378	32	52.5	2195	3	002822	002822 saccharomyc
306	32	52.5	255	4	09BZ16	09bzt16 homo sapien	379	32	52.5	2164	12	09DH52	09dh52 meleagridd h
307	32	52.5	264	12	085481	085481 tobacco mos	380	32	52.5	2204	12	099FV6	099fv6 porcine tes
308	32	52.5	286	10	09C738	09c738 arabidopsi	381	32	52.5	2502	12	099AVL6	099avl6 porcine rep
309	32	52.5	288	2	09R2F8	09r2f8 delnoco	382	32	52.5	2503	12	09YN02	09yn02 porcine rep
310	32	52.5	288	2	09RV34	09rv34 delnoco	383	32	52.5	2503	12	09WJb2	09wjb2 porcine rep
311	32	52.5	289	5	09VB79	09vb79 drosophila	384	32	52.5	2503	12	09WJb2	09wjb2 porcine rep

385	32	52.5	2503	12	Q9ENK6	Q9enK6 porcine rep	458	31	50.8	409	2	Q9x668	Q9x668 staphylococ
386	32	52.5	2503	12	Q9EBN0	Q9ebN0 porcine rep	459	31	50.8	409	5	Q9BK22	Q9BK22 caenorhabdi
387	32	52.5	2503	12	Q99136	Q99136 porcine rep	460	31	50.8	411	2	Q99BK2	Q99BK2 streptococc
388	32	52.5	2503	12	Q99B06	Q99B06 porcine rep	461	31	50.8	415	2	Q33471	Q33471 pseudomonas
389	32	52.5	3956	12	Q9DLM9	Q9dLm9 porcine rep	462	31	50.8	415	2	Q50214	Q50214 pseudomonas
390	32	52.5	3960	12	Q9DLE1	Q9dLE1 porcine rep	463	31	50.8	415	2	Q33494	Q33494 pseudomonas
391	32	52.5	3960	12	Q9DLE0	Q9dLE0 porcine rep	464	31	50.8	420	3	Q9C1B5	Q9C1B5 fusarium sp
392	32	52.5	3960	12	Q9DLN8	Q9dLN8 porcine rep	465	31	50.8	425	3	P95472	P95472 pseudomonas
393	31	50.8	77	10	Q41157	Q41157 rubus hispi	466	31	50.8	465	10	Q9LKR3	Q9LKR3 arabidopsis
394	31	50.8	79	2	Q32020	Q32020 bacillus su	467	31	50.8	465	10	Q9FV44	Q9FV44 arabidopsis
395	31	50.8	83	5	Q9U7Z9	Q9U7Z9 hesperocida	468	31	50.8	469	10	Q9ZMB4	Q9ZMB4 arabidopsis
396	31	50.8	112	6	Q9N1T9	Q9n1T9 canis fam11	469	31	50.8	472	13	Q9J342	Q9J342 gallus gall
397	31	50.8	126	1	Q92899	Q92899 archaeoglob	470	31	50.8	476	2	Q9JY27	Q9JY27 neisseria m
398	31	50.8	131	8	Q79123	Q79123 ceratina au	471	31	50.8	477	2	Q32354	Q32354 corynebacte
399	31	50.8	133	3	Q94586	Q94586 schizosacch	472	31	50.8	477	2	Q9Z474	Q9Z474 corynebacte
400	31	50.8	136	10	Q9SN73	Q9sn73 arabidopsis	473	31	50.8	479	5	Q17697	Q17697 caenorhabdi
401	31	50.8	138	10	Q04222	Q04222 helianthus	474	31	50.8	479	5	Q9MBD5	Q9MBD5 gentiana tr
402	31	50.8	159	2	Q9JYV2	Q9jYV2 neisseria m	475	31	50.8	481	13	Q9D633	Q9D633 brachydanio
403	31	50.8	163	2	Q9RL62	Q9RL62 streptomyce	476	31	50.8	488	12	Q9WT03	Q9WT03 human herpe
404	31	50.8	176	2	Q9RZR2	Q9rZR2 deinococcus	477	31	50.8	496	8	Q34175	Q34175 cepaea nemo
405	31	50.8	180	5	Q9U249	Q9u249 caenorhabdi	478	31	50.8	504	5	Q9VFM0	Q9VFM0 drosophila
406	31	50.8	186	5	Q9YAP7	Q9yaf7 drosophila	479	31	50.8	508	13	Q9PU44	Q9PU44 gallus gall
407	31	50.8	189	8	Q63003	Q63003 blindia acu	480	31	50.8	512	3	Q9UQZ1	Q9UQZ1 colletoctic
408	31	50.8	190	10	Q9MB83	Q9mb83 nepenthes a	481	31	50.8	517	13	Q9D634	Q9D634 brachydanio
409	31	50.8	191	10	Q9MB80	Q9mb80 nepenthes a	482	31	50.8	517	13	Q9B0C7	Q9B0C7 brachydanio
410	31	50.8	192	10	Q9FS59	Q9fs59 triticum ur	483	31	50.8	524	4	Q9BTT6	Q9BTT6 homo sapien
411	31	50.8	192	10	Q9FS58	Q9fs58 triticum ur	484	31	50.8	527	5	Q9VJK5	Q9VJK5 drosophila
412	31	50.8	193	10	Q9C9H1	Q9c9H1 arabidopsis	485	31	50.8	529	2	P74332	P74332 synchocyst
413	31	50.8	197	4	Q9HAC0	Q9hac0 homo sapien	486	31	50.8	532	5	Q23296	Q23296 caenorhabdi
414	31	50.8	198	8	Q9G7A0	Q9g7A0 xylocopa au	487	31	50.8	537	5	Q9VP64	Q9VP64 drosophila
415	31	50.8	198	10	Q9MB84	Q9mb84 nepenthes a	488	31	50.8	538	5	Q25416	Q25416 leishmania
416	31	50.8	201	10	Q9MB81	Q9mb81 nepenthes a	489	31	50.8	546	1	Q9HLE7	Q9HLE7 thermoplas
417	31	50.8	206	1	Q50104	Q50104 pyrococcus	490	31	50.8	547	4	Q9NVO9	Q9NVO9 homo sapien
418	31	50.8	206	9	Q9G0P6	Q9G0P6 roseophaga	491	31	50.8	547	4	Q9NVO9	Q9NVO9 homo sapien
419	31	50.8	216	5	Q20623	Q20623 caenorhabdi	492	31	50.8	547	4	Q9BTR2	Q9BTR2 homo sapien
420	31	50.8	218	12	Q9DHN1	Q9dhn1 yaba-like d	493	31	50.8	558	10	Q9C9H4	Q9C9H4 arabidopsis
421	31	50.8	219	2	Q9JXY9	Q9jxy9 neisseria m	494	31	50.8	566	10	Q9LXA3	Q9LXA3 saccharomyc
422	31	50.8	226	5	Q45753	Q45753 caenorhabdi	495	31	50.8	583	3	Q08961	Q08961 arabidopsis
423	31	50.8	226	10	Q22614	Q22614 kostelezky	496	31	50.8	593	10	Q9FLB0	Q9FLB0 arabidopsis
424	31	50.8	242	12	Q9WNC4	Q9wng4 tobacco mos	497	31	50.8	596	12	Q9YMT0	Q9YMT0 lymantria d
425	31	50.8	245	10	Q9AVQ7	Q9avq7 sesbania ro	498	31	50.8	607	13	Q9W715	Q9W715 oncorhynchus
426	31	50.8	245	10	Q9AVQ4	Q9avq4 sesbania ro	499	31	50.8	607	13	Q9PW89	Q9PW89 salvelinus
427	31	50.8	249	4	Q9H8W4	Q9h8W4 homo sapien	500	31	50.8	632	6	Q9N1P6	Q9N1P6 canis fam11
428	31	50.8	252	10	Q9M6N6	Q9m6N6 hordeum vul	501	31	50.8	649	4	Q9P215	Q9P215 homo sapien
429	31	50.8	258	5	Q9VHB3	Q9vhb3 drosophila	502	31	50.8	656	5	Q9N342	Q9N342 caenorhabdi
430	31	50.8	263	5	Q9U2T5	Q9u2T5 caenorhabdi	503	31	50.8	661	6	Q9GLE5	Q9GLE5 bos taurus
431	31	50.8	266	5	Q96202	Q96202 plasmodium	504	31	50.8	667	10	Q9ZS01	Q9ZS01 arabidopsis
432	31	50.8	266	10	Q9MAN2	Q9man2 medicago tr	505	31	50.8	678	2	P73509	P73509 synchocyst
433	31	50.8	271	2	Q9RXY2	Q9rxy2 deinococcus	506	31	50.8	678	10	Q9SG80	Q9SG80 arabidopsis
434	31	50.8	286	6	Q9GLZ3	Q9GLZ3 macaca fasc	507	31	50.8	679	10	Q9FG18	Q9FG18 arabidopsis
435	31	50.8	316	12	Q68400	Q68400 human cytom	508	31	50.8	687	11	Q9R0L8	Q9R0L8 mus musculu
436	31	50.8	320	10	Q9CAH5	Q9cah5 arabidopsis	509	31	50.8	687	11	Q9DRB0	Q9DRB0 mus musculu
437	31	50.8	330	10	Q9ZRX2	Q9zrx2 triticum ae	510	31	50.8	700	4	Q9P244	Q9P244 homo sapien
438	31	50.8	333	10	Q9ZS77	Q9zS77 hordeum vul	511	31	50.8	704	5	Q9N2U0	Q9N2U0 caenorhabdi
439	31	50.8	335	10	Q9SE65	Q9seg5 arabidopsis	512	31	50.8	735	3	Q9PSU8	Q9PSU8 neurospora
440	31	50.8	337	5	Q45279	Q45279 caenorhabdi	513	31	50.8	745	5	Q9U195	Q9U195 leishmania
441	31	50.8	338	2	P73085	P73085 synchocyst	514	31	50.8	762	6	Q9TUK0	Q9TUK0 sus scrofa
442	31	50.8	345	10	Q9LS32	Q9LS32 physcomitire	515	31	50.8	763	6	Q9TUK1	Q9TUK1 sus scrofa
443	31	50.8	348	5	Q9VWG7	Q9vWg7 drosophila	516	31	50.8	763	11	Q9R101	Q9R101 spermophilu
444	31	50.8	349	5	Q9RPM1	Q9rpm1 pseudomonas	517	31	50.8	775	2	Q9Z879	Q9Z879 chlamydia p
445	31	50.8	355	5	Q22383	Q22383 caenorhabdi	518	31	50.8	775	2	Q9ZS20	Q9ZS20 chlamydia p
446	31	50.8	358	4	Q9UG73	Q9UG73 homo sapien	519	31	50.8	797	5	Q9XU17	Q9XU17 caenorhabdi
447	31	50.8	371	2	Q9Z897	Q9z897 chlamydia p	520	31	50.8	807	2	Q9A950	Q9A950 caulobacter
448	31	50.8	372	4	Q9H9X4	Q9H9X4 homo sapien	521	31	50.8	808	2	Q87758	Q87758 klebsiella
449	31	50.8	377	3	Q74794	Q74794 schizosacch	522	31	50.8	865	5	Q18395	Q18395 drosophila
450	31	50.8	379	2	Q9KDI5	Q9KDI5 bacillus ha	523	31	50.8	865	5	Q9N998	Q9N998 leishmania
451	31	50.8	385	1	Q9YAV4	Q9YAV4 staphylococ	524	31	50.8	866	5	Q9BNW9	Q9BNW9 drosophila
452	31	50.8	391	2	Q9YAV4	Q9YAV4 aeropyrum p	525	31	50.8	925	4	Q95786	Q95786 homo sapien
453	31	50.8	391	2	Q9KVV2	Q9KVV2 vibrio chol	526	31	50.8	948	5	Q9U304	Q9U304 caenorhabdi
454	31	50.8	398	4	Q9NT04	Q9nt04 homo sapien	527	31	50.8	958	10	Q9AVP6	Q9AVP6 vicia faba
455	31	50.8	399	4	Q9HAH7	Q9hah7 homo sapien	528	31	50.8	997	5	Q01858	Q01858 caenorhabdi
456	31	50.8	400	4	Q9UDX4	Q9UDX4 homo sapien	529	31	50.8	1019	3	Q9P7T4	Q9P7T4 schizosacch
457	31	50.8	400	11	Q9Z1J8	Q9z1J8 rattus norv	530	31	50.8	1118	10	Q9LJS9	Q9LJS9 arabidopsis

531	31	50.8	1139	5	076601	076601 caenorhabd
532	31	50.8	1164	4	09H1S5	09H1S5 homo sapien
533	31	50.8	1170	2	09AJR8	09AJR8 erysipeloth
534	31	50.8	1222	10	09SVW6	09SVW6 arabidopsis
535	31	50.8	1265	5	09NCL9	09NCL9 culcx quing
536	31	50.8	1323	10	09MOM2	09MOM2 arabidopsis
537	31	50.8	1377	13	09DDN5	09DDN5 xenopus lae
538	31	50.8	1454	5	010463	010463 caenorhabd
539	31	50.8	1669	11	09QZS0	09QZS0 mus musculu
540	31	50.8	1765	11	088457	088457 rattus norv
541	31	50.8	1765	11	09R053	09R053 mus musculu
542	31	50.8	1765	11	09JMD4	09JMD4 mus musculu
543	31	50.8	1840	11	061818	061818 mus musculu
544	31	50.8	1963	5	09VSK5	09VSK5 drosophila
545	31	50.8	1964	10	09JLM2	09JLM2 arabidopsis
546	31	50.8	1966	5	09NMX6	09NMX6 drosophila
547	31	50.8	2051	5	09NWM9	09NWM9 anopheles g
548	31	50.8	2454	3	09UVP2	09UVP2 emericeila
549	31	50.8	2454	3	09UVS6	09UVS6 hepaticis c
550	31	50.8	3033	12	09Q9B0	09Q9B0 drosophila
551	31	50.8	6815	5	091704	091704 drosophila
552	31	50.8	16215	5	09NFS3	09NFS3 drosophila
553	30.5	50.0	445	2	09KPB7	09KPB7 vibrlo chol
554	30.5	50.0	574	2	09K9B5	09K9B5 bacillus ha
555	30.5	50.0	603	5	09N9A4	09N9A4 caenorhabd
556	30.5	50.0	1423	5	09W1A0	09W1A0 drosophila

ALIGNMENTS

RESULT	1					
ID	09Y494	PRELIMINARY:	PRT:	72	AA.	
AC	09Y494:					
DT	01-NOV-1999 (TReMBLrel. 12, Created)					
DT	01-NOV-1999 (TReMBLrel. 12, Last sequence update)					
DT	01-JUN-2001 (TReMBLrel. 17, Last annotation update)					
DE	GAMMA PREPROTACHYKININ (FRAGMENT).					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=BL00D, AND BRAIN;					
RA	Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;					
RT	"Identification of a Delta isoform of preprotachykinin mRNA in Human					
RT	Mononuclear Phagocytes and Lymphocytes";					
RL	Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.					
DR	EMBL: AF050657; AAC15703.1;					
DR	InterPro: IPR002040; Tachykinin.					
DR	InterPro: IPR003580; Protachykinin.					
DR	Pfam: PF02202; Tachykinin; 1					
DR	PROSITE: PS00267; TACHYKININ; UNKNOWN_2.					
DR	SMART: SM00203; TK; 2.					
FT	NON_TER	1				
FT	NON_TER	72				
FT	NON_TER	72				
SO	SEQUENCE	72	AA;	8274	MM;	2C02B2BA41EAD16 CRC64;

Query Match 100.0%; Score 61; DB 4; Length 72;
 Best Local Similarity 100.0%; Pred. No. 0.00031;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	RPKPOFFGLM 11	
Db	23	RPKPOFFGLM 33	
RESULT	2		
097947			
ID	097947	PRELIMINARY:	PRT: 114

AC	097947:					
DT	01-MAY-1999 (TReMBLrel. 10, Created)					
DT	01-MAY-1999 (TReMBLrel. 10, Last sequence update)					
DT	01-JUN-2001 (TReMBLrel. 17, Last annotation update)					
DE	GAMMA PREPROTACHYKININ 1.					
OS	Tupia belangeri (northern tree shrew).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Scandentia; Tupaiidae; Tupala.					
OX	NCBI_TaxID=37347;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=BRIN;					
RA	Heitland A., Meegert H.J., Krueffer M., Forssmann W.G.;					
RT	"Tachykinin precursors are highly conserved among different mammals.";					
RT	Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.					
RL	Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.					
DR	EMBL: Z50785; CAA90648.1;					
DR	InterPro: IPR002040; Tachykinin.					
DR	InterPro: IPR003580; Protachykinin.					
DR	Pfam: PF02202; Tachykinin; 1.					
DR	PRODOM: PD005598; Protachykinin; 1.					
DR	PROSITE: PS00267; TACHYKININ; UNKNOWN_2.					
DR	SMART: SM00203; TK; 2.					
FT	CHAIN	58				SUBSTANCE P.
FT	CHAIN	72				NEUROPEPTIDE GAMMA.
FT	CHAIN	83				NEUROKININ A.
SO	SEQUENCE	114	AA;	13281	MM;	B439C3D27FD47CAB CRC64;

Query Match 100.0%; Score 61; DB 6; Length 114;
 Best Local Similarity 100.0%; Pred. No. 0.00049;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	RPKPOFFGLM 11	
Db	58	RPKPOFFGLM 68	
RESULT	3		
ID	09Y6V5	PRELIMINARY:	PRT: 128
AC	09Y6V5:		
DT	01-NOV-1999 (TReMBLrel. 12, Created)		
DT	01-NOV-1999 (TReMBLrel. 12, Last sequence update)		
DT	01-JUN-2001 (TReMBLrel. 17, Last annotation update)		
DE	WOGSC:H_DJ0841B21.1 PROTEIN.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kalicki J., Angell S.;		
RT	"The sequence of Homo sapiens PAC clone DJ0841B21.";		
RT	Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RA	Waterston R.;		
DR	Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AC004140; AAC02754.1;		
DR	InterPro: IPR002040; Tachykinin.		
DR	InterPro: IPR003580; Protachykinin.		
DR	Pfam: PF02202; Tachykinin; 1.		
DR	PROSITE: PS00267; TACHYKININ; UNKNOWN_2.		
DR	SMART: SM00203; TK; 1.		
SO	SEQUENCE	128	AA;

Query Match 100.0%; Score 61; DB 4; Length 128;
 Best Local Similarity 100.0%; Pred. No. 0.00056;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	RPKPOFFGLM 11	

Db 58 RPKPOOFGLM 68

RESULT 4

097948 PRELIMINARY; PRT: 129 AA.

AC 097948;

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE BETA PREPROTACHYKININ I.

OS Tupia belangeri (northern tree shrew).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.

OX NCBI_TaxID=37347;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-BRAIN;

RA Heiland A., Maegert H.J., Kruboeffer M., Forssmann W.G.;

RT "Tachykinin precursors are highly conserved among different mammals.";

RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; 250786; CAA90649.1; -

DR InterPro: IPR003580; Tachykinin.

DR Pfam: PF02202; Tachykinin; 1.

DR ProDom: PD005598; Protachykinin; 1.

DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.

DR SMART; SM00203; TK; 2.

FT CHAIN 58 68 SUBSTANCE P.

FT CHAIN 72 107 NEUROPEPTIDE K.

FT CHAIN 98 107 NEUROKININ A.

SQ SEQUENCE 129 AA; 14941 MW; 5855E7ADC2D8674E CRC64;

Query Match 100.0%; Score 61; DB 6; Length 129;

Best Local Similarity 100.0%; Pred. No. 0.00056;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOOFGLM 11

Db 58 RPKPOOFGLM 68

RESULT 5

0920K2 PRELIMINARY; PRT: 97 AA.

AC 0920K2;

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE DELTA PREPROTACHYKININ I.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystriocognath; Cavidae; Cavia.

OX NCBI_TaxID=10141;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-PBRIDGE WHITE; TISSUE-BRAIN;

RA Heiland A., Maegert H.J., Kruboeffer M., Forssmann W.G.;

RT "Tachykinin precursors are highly conserved among different mammals.";

RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; 250782; CAA90645.1; -

DR InterPro: IPR003580; Protachykinin.

DR ProDom: PD005598; Protachykinin; 1.

FT CHAIN 58 68 SUBSTANCE P.

SQ SEQUENCE 97 AA; 11222 MW; FFD50C3297E3F7E3 CRC64;

Query Match 86.9%; Score 53; DB 11; Length 97;

Best Local Similarity 90.9%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOFGLM 11

Db 58 RPKPOOFGLM 68

RESULT 6

0920K1 PRELIMINARY; PRT: 115 AA.

AC 0920K1;

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE GAMMA PREPROTACHYKININ I.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystriocognath; Cavidae; Cavia.

OX NCBI_TaxID=10141;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-PBRIDGE WHITE; TISSUE-BRAIN;

RA Heiland A., Maegert H.J., Kruboeffer M., Forssmann W.G.;

RT "Tachykinin precursors are highly conserved among different mammals.";

RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; 250783; CAA90646.1; -

DR InterPro: IPR003580; Tachykinin.

DR ProDom: PD005598; Protachykinin; 1.

DR PROSITE; PS00267; TACHYKININ; UNKNOWN_1.

FT CHAIN 58 68 SUBSTANCE P.

FT CHAIN 72 92 NEUROPEPTIDE GAMMA.

FT CHAIN 98 92 NEUROKININ A.

SQ SEQUENCE 115 AA; 13190 MW; 39EFBE8CBBA7174 CRC64;

Query Match 86.9%; Score 53; DB 11; Length 115;

Best Local Similarity 90.9%; Pred. No. 0.016;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOFGLM 11

Db 58 RPKPOOFGLM 68

RESULT 7

0920K0 PRELIMINARY; PRT: 130 AA.

AC 0920K0;

DT 01-MAY-1999 (TREMBLrel. 10, Created)

DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE BETA PREPROTACHYKININ I.

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Hystriocognath; Cavidae; Cavia.

OX NCBI_TaxID=10141;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-PBRIDGE WHITE; TISSUE-BRAIN;

RA Heiland A., Maegert H.J., Kruboeffer M., Forssmann W.G.;

RT "Tachykinin precursors are highly conserved among different mammals.";

RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; 250784; CAA90647.1; -

DR InterPro: IPR003580; Tachykinin.

DR ProDom: PD005598; Protachykinin; 1.

FT CHAIN 58 68 SUBSTANCE P.

FT CHAIN 72 107 NEUROPEPTIDE K.

FT CHAIN 98 107 NEUROKININ A.

SQ SEQUENCE 130 AA; 14850 MW; CAB2F55B6A60A7C0 CRC64;

Query Match 86.9%; Score 53; DB 11; Length 130;

Best Local Similarity 90.9%; Pred. No. 0.018;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
1111111111

Db 58 RPKPOQFFGLM 68

RESULT 8

Q9HLV7 PRELIMINARY; PRT; 207 AA.

AC Q9HLV7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HYPOTHETICAL PROTEIN TA0086.
GN TA0086.
OS Thermoplasma acidophilum.
OC Archaea: Euryarchaeota; Thermoplasmatales; Thermoplasmataceae;
OC Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RA MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Granel W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Friseman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513(2000).
DR EMBL: AL445063; CAC11234.1; "-
DR InterPro: IPR001279; Beta_lactam_met.
DR Pfam: PF00753; lactamase_B.1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 207 AA; 22741 MW; 60136f482EB2A94D CRC64;

Query Match 67.2%; Score 41; DB 1; Length 207;
Best Local Similarity 70.0%; Pred. No. 5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPKPOQFFGLM 11
1111111111

Db 100 RPKRSFFGRM 109

RESULT 9

Q24014 PRELIMINARY; PRT; 786 AA.

AC Q24014;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE G1-LIKE ORF'S PRODUCT.
OS Dictyostelium mucoroides (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=31287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DMUC2;
RA MEDLINE=94302132; PubMed=8029320;
RA Kiyosawa H., Hughes J.E., Welker D.L.;
RT "Compatible Dictyostelium mucoroides nuclear plasmids Dmp1 and Dmp2
RT both belong to the Ddpl plasmid family.";
RL Plasmid 31:121-130(1994).
DR EMBL: U00176; AAC14374.1; "-
SQ SEQUENCE 786 AA; 90191 MW; 2167146E1F012003 CRC64;

Query Match 63.9%; Score 39; DB 5; Length 786;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGL 10

Db 717 RPKPIQFFGI 726

RESULT 10

Q24012 PRELIMINARY; PRT; 803 AA.

AC Q24012;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE G1-LIKE ORF'S PRODUCT.
OS Dictyostelium mucoroides (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=31287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DMUC2;
RA MEDLINE=94302132; PubMed=8029320;
RA Kiyosawa H., Hughes J.E., Welker D.L.;
RT "Compatible Dictyostelium mucoroides nuclear plasmids Dmp1 and Dmp2
RT both belong to the Ddpl plasmid family.";
RL Plasmid 31:121-130(1994).
DR EMBL: U00175; AAC14372.1; "-
SQ SEQUENCE 803 AA; 91385 MW; 219F8272FA16FACD CRC64;

Query Match 63.9%; Score 39; DB 5; Length 803;
Best Local Similarity 60.0%; Pred. No. 49;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGL 10
1111111111

Db 734 RPKPIQFFGI 743

RESULT 11

Q20174 PRELIMINARY; PRT; 205 AA.

AC Q20174;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE COSMID F38E9.
GN F38E9.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten T., Laister N., Latreille P.,
RA Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showmken R.,
RA Smailson N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterson R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Wu X., Gattung S.,
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: U46668; AAA93346.1; -
SQ SEQUENCE 205 AA; 23000 MW; B99FB37DB706ECOD CRC64;

Query Match 62.3%; Score 38; DB 5; Length 205;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RPKQOFG 8
1111111
Db 151 RPKQOFG 157

RESULT 12

Q9VBM4 PRELIMINARY; PRT; 235 AA.

AC Q9VBM4
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG13653 PROTEIN.
GN CG13653
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Banos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jaisli D., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sidani-Klimos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-Z., Zaveli J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2135-2195(2000).
DR EMBL: AE003751; AAF56413.1; -
DR FLYbase: FBgn039288; CG13653.
SQ SEQUENCE 235 AA; 27051 MW; F99BDB4555BA7A3E CRC64;

Query Match 62.3%; Score 38; DB 5; Length 235;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKQOFG 10
1111111
Db 85 RPKQOFG 94

RESULT 13

Q9SUN5 PRELIMINARY; PRT; 257 AA.

AC Q9SUN5
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PURATIVE SNRNP PROTEIN.
GN Pp13.90 OR AT4G20440.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RA Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Pohl T., Weizenegger T., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL080253; CAB45810.1; -
DR EMBL: AL161553; CAB79044.1; -
DR InterPro: IPR002965; P_tich_extensn.
DR InterPro: IPR001163; snRNP_Sm.
DR Pfam: PF01423; Sm; 1.
DR PRINTS: PR01217; PRICHEXTENS.
SQ SEQUENCE 257 AA; 27140 MW; D931178BCBC51B5 CRC64;

Query Match 62.3%; Score 38; DB 10; Length 257;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKQOFG 9
1111111
Db 189 RPKQOFG 197

RESULT 14

Q49561 PRELIMINARY; PRT; 293 AA.

AC Q49561

DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE GIBBERELIN 20-OXIDASE - LIKE PROTEIN (GIBBERELIN 20-OXIDASE-LIKE PROTEIN).

GN Pp13.140 OR AT4G21200.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Murphy G., Drost L., Hall C., Hudson S., Ridley P.,
 RA Bancroft I., Mewes H.W., Mayer K., Schueller C.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL021960; CAIL7539.1; -;
 DR EMBL; AL161554; CAB79120.1; -;
 DR Mendel; 27589; Arath; 2972; 27589.
 DR InterPro: IPR002419; Fe-asc-oxidored.
 DR Pfam: PF00671; Fe_Asc-oxidored; 1.
 SO SEQUENCE 293 AA; 34050 MW; 5138093F136DF66 CRC64;

Query Match 62.3%; Score 38; DB 10; Length 293;
 Best Local Similarity 60.0%; Pred. No. 26;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPQFFGLM 11
 111 : 111
 Db 159 PKPVEYGLM 168

RESULT 15
 Q9PVE8 PRELIMINARY; PRT; 496 AA.
 AC Q9PVE8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME P450 3A30.
 GN CYP3A30.
 OS Fundulus heteroclitus (Killifish) (Mummichog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Cyprinodontiformes; Fundulidae; Fundulus.
 OX NCBI_TaxID=8078;
 RN [1]
 RP SEQUENCE OF 313-436 FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE-97382427; PubMed-9240431;
 RA Celander M., Stegeman J.J.;
 RT "Isolation of a cytochrome P450 3A cDNA sequence (CYP3A30) from the
 RT marine teleost Fundulus heteroclitus and phylogenetic analyses of
 RT CYP3A genes.";
 RL Blochem. Biophys. Res. Commun. 236:306-312(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Celander M., Hegelund-Myrback T., Stegeman J.J.;
 RT "Cloning and sequencing of the complete coding region of cytochrome
 RT P450 3A30 (CYP3A30) from the marine teleost Fundulus heteroclitus.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
 CC OXIDIZED FLAVOPROTEIN + H(2)O.
 CC -1- SUBCELLULAR LOCATION: MEMBRANE-BOUND. ENDOPLASMIC RETICULUM (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR EMBL; AF105068; AAF14117.1; -;
 DR InterPro: IPR001128; Cyt_P450.
 DR Pfam: PF0067; P450; 1.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
 DR Ection transport; Endoplasmic reticulum; Heme; Membrane; Microsome;

KW Monooxygenase; Oxidoreductase.
 SQ SEQUENCE 496 AA; 57051 MW; 40CFB23D75F4A4EB CRC64;

Query Match 62.3%; Score 38; DB 13; Length 496;
 Best Local Similarity 70.0%; Pred. No. 45;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQFFGLM 11
 111 : 111
 Db 40 PKPVEFGTM 49

RESULT 16
 Q9DE99 PRELIMINARY; PRT; 500 AA.
 AC Q9DE99;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME P450 3A.
 GN CYP3A.
 OS Oryzias latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MEDAKA;
 RA Kullman S.W., Hamm J.T., Hinton D.E.;
 RT "Identification and Characterization of a cDNA Encoding Cytochrome
 RT P450 3A from the Fresh Water Teleost Oryzias latipes.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 DR EMBL; AF105018; AAG35209.1; -;
 DR InterPro: IPR001128; Cyt_P450.
 DR Pfam: PF0067; P450; 1.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
 KW Heme; Monooxygenase; Oxidoreductase.
 SQ SEQUENCE 500 AA; 57381 MW; EB0A8479601CE8C7 CRC64;

Query Match 62.3%; Score 38; DB 13; Length 500;
 Best Local Similarity 70.0%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPQFFGLM 11
 111 : 111
 Db 41 PKPVEFGTM 50

RESULT 17
 Q98T91 PRELIMINARY; PRT; 502 AA.
 AC Q98T91;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME P450 3A40.
 GN CYP3A40.
 OS Oryzias latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OX NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kullman S.W., Hinton D.E.;
 RT "Identification of multiple isozyms of cytochrome P450 3A from the

RT fresh water teleost medaka: Characterization and ontogeny."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF251272; AAK37960.1; -
SQ SEQUENCE 502 AA; 57707 MW; 1E9FE38B21CED1D8 CRC64;

Query Match 62.3%; Score 38; DB 13; Length 502;
Best Local Similarity 70.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKPOQFFGLM 11
|||:||||
DB 41 RKPVPFFGLM 50

RESULT 18
P94873 PRELIMINARY; PRT; 3722 AA.
ID P94873
AC P94873;
DT 01-MAY-1997 (TRIMBLrel. 03, Created)
DR 01-MAY-1997 (TRIMBLrel. 03, Last sequence update)
DE 01-JUN-2001 (TRIMBLrel. 17, Last annotation update)
DE ALPHA-AMINOADIPYL-CYSTEINYL-VALINE SYNTHETASE.
GN PCAB.
OS Lysobacter lactamgenus.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
CX Lysobacter.
RN NCBI_TaxID=39596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TK30;
RX MEDLINE=96275943; Pubmed=8737573;
RA Kimura H., Miyashita H., Sumino Y.;
RT "Organization and expression in *Pseudomonas putida* of the gene cluster
involved in cephalosporin biosynthesis from *Lysobacter lactamgenus*
RT TK30".
RL Appl. Microbiol. Biotechnol. 45:490-501(1996).
DR EMBL: D50308; BAA08846.1; -
DR HSSP: P14687; 1AMU.
DR InterPro: IPR002106; AA_trna_ligase_II.
DR InterPro: IPR000873; AMP-bind.
DR InterPro: IPR000977; DNA_ligase.
DR InterPro: IPR001242; DUF4.
DR InterPro: IPR000379; Est_III_thioest_actsite.
DR InterPro: IPR003880; Phosphopant_attach.
DR InterPro: IPR001031; Thioesterase.
DR Pfam: PF00501; AMP-binding; 3.
DR Pfam: PF00568; Condensation; 3.
DR Pfam: PF00550; PP-binding; 3.
DR Pfam: PF00975; Thioesterase; 1.
DR PROSITE: PS00179; AA-trna_ligase_II_1; UNKNOWN_1.
DR PROSITE: PS50075; ACP DOMAIN; 3.
DR PROSITE: PS00455; AMP BINDING; 1.
DR PROSITE: PS00657; DNA_LIGASE_A1; UNKNOWN_2.
DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_2.
KW Phosphopantetheine.
SQ SEQUENCE 3722 AA; 411611 MW; 3597B3483463809B CRC64;

Query Match 62.3%; Score 38; DB 2; Length 3722;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQFFGLM 11
|||:||||
DB 1412 RKPDEFGLV 1421

RESULT 19
084949 PRELIMINARY; PRT; 138 AA.
ID 084949
AC 084949;
DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE SSEE.
GN SSEE.
OS Salmomella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmomella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SL1344;
RA Cirillo D.M., Valdivia R.H., Monack D., Falkow S.;
RT "Macrophage-dependent induction of the *Salmomella* pathogenicity island
RT 2 type III secretion system and its role in intracellular survival."
RL Mol. Microbiol. 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=99000132; Pubmed=9786193;
RA Hensel M., Shea J.E., Waterman R., Mundy R., Nikolaus T., Banks G.,
RA Vazquez-Torres A., Gleeson C., Fang F.C., Holden D.W.;
RT "Genes encoding putative effector proteins of the type III secretion
RT system of *Salmomella* pathogenicity island 2 are required for bacterial
RT virulence and proliferation in macrophages."
RL Mol. Microbiol. 30:163-174(1998).
DR EMBL: AF020808; AAC28883.1; -
DR EMBL: AJ24892; CAA12189.1; -
SQ SEQUENCE 138 AA; 16266 MW; 4712D484CB8440E3 CRC64;

Query Match 60.7%; Score 37; DB 2; Length 138;
Best Local Similarity 54.5%; Pred. No. 18;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RKPQOEFGLM 11
:|:|||||
DB 60 OPRQOLFHL 70

RESULT 20
O9V2N2 PRELIMINARY; PRT; 249 AA.
ID O9V2N2
AC O9V2N2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DR 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 29.2 KDA PROTEIN.
GN PAB2321.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Hellig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution."
RT submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ248283; CAB48966.1; -
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 249 AA; 29212 MW; 392F2EC61C84D6FD CRC64;

Query Match 60.7%; Score 37; DB 1; Length 249;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RKPQOEFGL 10
|:|:||||
DB 124 RIKPEKFFGI 133

RESULT 21

09BPN9
ID 09BPN9 PRELIMINARY: PRT: 177 AA.
AC 09BPN9:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL PROTEIN Y92H12BR.2.
GN Y92H12BR.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC087232; AAK09077.1; -; A2B3104976B88E5E CRC64;
SQ SEQUENCE 177 AA: 21018 MW: A2B3104976B88E5E CRC64;

Query Match 59.0%; Score 36; DB 5; Length 177;
Best Local Similarity 85.7%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOOF 7
DB 68 RPKPROF 74

RESULT 22
ID 09NEW8 PRELIMINARY: PRT: 236 AA.
AC 09NEW8:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Y11B2A.16 PROTEIN.
GN Y11B2A.16.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Sulston J.E.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL: AL132904; CAC35845.1; -;
SQ SEQUENCE 236 AA: 26444 MW: 344BEE28A01C5431 CRC64;

Query Match 59.0%; Score 36; DB 5; Length 236;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RPKPOOF 8
DB 15 RPKPSF 21

RESULT 23
ID 086283 PRELIMINARY: PRT: 352 AA.
AC 086283:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE REOVIRUS SP. 1.24KB RNA SEGMENT.
OS unidentified.
OC unclassified.
OX NCBI_TaxID=32644;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95313344; PubMed=7793063;
RA Bigot Y., Drexler J.M., Sizaret P.Y., Rabouille A., Hamelin M.H.,
Periquet G.;
RT "The genome segments of DpRV, a commensal reovirus of the wasp
Diatromus pulchellus (Hymenoptera).";
RL Virology 210:109-119(1995).
DR EMBL: X82046; CAA57562.1; -;
SQ SEQUENCE 352 AA: 39977 MW: 79F3DF03F0FE8939 CRC64;

Query Match 59.0%; Score 36; DB 12; Length 352;
Best Local Similarity 60.0%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOOFGL 10
DB 35 RPAFRRLFGL 44

RESULT 24
ID 023876 PRELIMINARY: PRT: 373 AA.
AC 023876:
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE PCF2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE; TISSUE=MERISTEMATIC TISSUE;
RX MEDLINE=97480096; PubMed=9338963;
RA Kosugi S., Ohashi Y.;
RT "PCF1 and PCF2 specifically bind to cis elements in the rice
proliferating cell nuclear antigen gene.";
RL Plant Cell 9:1607-1619(1997).
DR EMBL: D87261; BAA23143.1; -;
DR Mendel; 24192; Oryza; 3166; 24192.
SQ SEQUENCE 373 AA: 38529 MW: 111C093A043F8B2E CRC64;

Query Match 59.0%; Score 36; DB 10; Length 373;
Best Local Similarity 54.5%; Pred. No. 79;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOOFFGLM 11
DB 55 KPEPVFFFGM 65

RESULT 25
ID 09UW05 PRELIMINARY: PRT: 477 AA.
AC 09UW05:

DT 01-MAY-2000 (TRIMBLREL. 13, Created)
 DT 01-MAY-2000 (TRIMBLREL. 13, Last sequence update)
 DT 01-JUN-2001 (TRIMBLREL. 17, Last annotation update)
 DE SPM12 TRANSCRIPTION FACTOR HOMOLOG.
 CN CLS12.
 OS Clavispora lusitanae.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Metchnikowiaceae; Clavispora.
 OX NCBI_Taxid=36911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 42720;
 RA Young L., Lorenz M., Heitman J.;
 RT "A STE12 homolog is required for mating but dispensable for
 filamentation in Candida lusitanae."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF1755524; AAD51741.1; -.
 DR InterPro: IPR003120; STE.
 DR Pfam: PF02200; STE; 1.
 DR SMART: SM00424; STE; 1.
 SO SEQUENCE 477 AA; 54716 MW; FFBCAF29FMAAB542 CRC64;

Query Match 59.0%; Score 36; DB 3; Length 477;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOOFFGL 10
 Db 384 PPPAOFYGL 392

RESULT 26
 ID 094130 PRELIMINARY; PRT; 550 AA.
 AC 094130;
 DT 01-FEB-1997 (TRIMBLREL. 02, Created)
 DT 01-FEB-1997 (TRIMBLREL. 02, Last sequence update)
 DT 01-JUN-2001 (TRIMBLREL. 17, Last annotation update)
 DE M89 PROTEIN PRECURSOR.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RL MEDLINE=96291396; PubMed=8689684;
 RA Porter J.A., Ekker S.C., Park W.-J., von Kessler D.P., Young K.E.,
 RA Chen C.-H., Ma Y., Woods A.S., Cotter R.J., Koonin E.V., Beachy P.A.;
 RT "Hedgehog patterning activity: role of a lipophilic modification
 mediated by the carboxy-terminal autoprocessing domain";
 RL Cell 86:21-34(1996).
 CC -1- PPM: THE C-TERMINAL DOMAIN DISPLAYS AN AUTOPROTEOLYSIS ACTIVITY
 (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEDGEHOG FAMILY.
 DR EMBL; U61237; AAB17542.1; -.
 DR InterPro: IPR001767; HIntC.
 DR InterPro: IPR003586; HIntC.
 DR InterPro: IPR003587; HIntN.
 DR Pfam; PF01079; HIntC; 1.
 DR SMART; SM00305; HIntC; 1.
 DR SMART; SM00306; HIntN; 1.
 KW Signal; Glycoprotein.
 FT SIGNAL 1 19
 FT CHAIN 2C 550
 FT CHAIN 2C 550
 FT CHAIN 341 550
 FT CHAIN 341 550
 FT DNA_BIND 333 403
 FT CARBOHYD 97 97
 FT CARBOHYD 164 164
 FT CARBOHYD 269 269
 FT CARBOHYD 450 450

SO SEQUENCE 550 AA; 62100 MW; 2CD8B1A0178E5B5B CRC64;

Query Match 59.0%; Score 36; DB 5; Length 550;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOFF 8
 Db 301 QPPPOOFF 308

RESULT 27
 ID 045273 PRELIMINARY; PRT; 629 AA.
 AC 045273;
 DT 01-JUN-1998 (TRIMBLREL. 06, Created)
 DT 01-NOV-1998 (TRIMBLREL. 08, Last sequence update)
 DT 01-JUN-2001 (TRIMBLREL. 17, Last annotation update)
 DE C29F3.2 PROTEIN.
 GN C29F3.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Matthews L.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Lalister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Tillery-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterson R.,
 RA Watson A., Weinstock L., Wilkinson-Spratt J., Wollman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans";
 RL Nature 368:32-38(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA White S.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z81043; CAB02804.1; -.
 DR EMBL; AL023813; CAB02804.1; JOINED.
 DR EMBL; AL023813; CAA19424.1; -.
 DR EMBL; Z81043; CAA19424.1; JOINED.
 DR InterPro: IPR001767; HIntC.
 DR InterPro: IPR003586; HIntC.
 DR InterPro: IPR003587; HIntN.
 DR Pfam; PF01079; HIntC; 1.
 DR SMART; SM00305; HIntC; 1.
 DR SMART; SM00306; HIntN; 1.
 SO SEQUENCE 629 AA; 71349 MW; 4D812B872AD5FE43 CRC64;

Query Match 59.0%; Score 36; DB 5; Length 629;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOFF 8
 Db 380 QPPPOOFF 387

RESULT 28
 Q9F634

ID Q9F634 PRELIMINARY; PRT; 869 AA.
 AC Q9F634;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MXCH.
 GN MXCH.
 OS Stigmatella aurantiaca.
 CC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
 CC Myxococcales; Cystobacterineae; Cystobacteraceae; Stigmatella.
 OX NCBI_TaxID=41;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SG A15;
 RX PubMed-11029592;
 RA Sliakowski B., Kunze B., Nordstiek G., Blocker H., Hoile G., Muller R.;
 RT "The myxochelin iron transport regulon of the myxobacterium
 Stigmatella aurantiaca Sg a15.";
 RL Eur. J. Biochem. 267:6476-6485(2000).
 DR EMBL: AF299336; AAC31132.1; -;
 SQ SEQUENCE 869 AA; 95371 MW; 34102ELAD6AD33E1 CRC64;

Query Match 59.0%; Score 36; DB 2; Length 869;
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 PRPQPF 9
 1:1:111
 DB 637 PRPDEF 644

RESULT 29
 Q99N14 PRELIMINARY; PRT; 128 AA.
 AC Q99N14;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PREPROTACHKININ C.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang Y., Lu L., Furlonger C., Gillian W., Paige C.J.;
 RT "Hemokinin is a hemopoietic-specific tachykinin that regulates B
 lymphopoiesis.";
 RL Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF235035; AAK15025.1; -;
 SQ SEQUENCE 128 AA; 13937 MW; FED91DCAB39CB444 CRC64;

Query Match 57.4%; Score 35; DB 11; Length 128;
 Best Local Similarity 54.5%; Pred. No. 40;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOFFGIM 11
 1:1:11111
 DB 56 RSRTRQFVGLM 66

RESULT 30
 O61761 PRELIMINARY; PRT; 206 AA.
 AC O61761;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE F56C3.9 PROTEIN.
 DR F56C3.9;
 GN Caenorhabditis elegans.
 OS

CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 CC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten N., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Stoneking T.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF067214; AAC17009.1; -;
 SQ SEQUENCE 206 AA; 24599 MW; 3F530D03A57CD7A9 CRC64;

Query Match 57.4%; Score 35; DB 5; Length 206;
 Best Local Similarity 62.5%; Pred. No. 66;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOFF 8
 1:1:1111
 DB 188 RPKPOFF 195

RESULT 31
 Q9LSY0 PRELIMINARY; PRT; 218 AA.
 AC Q9LSY0;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HYPOTHETICAL 24.3 KDA PROTEIN.
 OS Streptomyces verticillius.
 CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=29309;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC15003;
 RA Chen M., Edwards D.J., Sanchez C., Du L., Shen B.;
 RT "N-acetyl-glucosamine biosynthesis genes in Streptomyces verticillius
 ATCC15003.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF245690; AAF68966.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 218 AA; 24320 MW; 085A18C6E222459F CRC64;

Query Match 57.4%; Score 35; DB 2; Length 218;
 Best Local Similarity 66.7%; Pred. No. 70;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 RPKPOFFGIM 11
 1:1:11111

Db 104 KPSTFGLL 112

RESULT 32

Q9LVZ6 PRELIMINARY; PRT; 296 AA.

ID Q9LVZ6

AC Q9LVZ6; 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DE GENOMIC DNA, CHROMOSOME 3, p1 CLONE: MSJ11.

OS Arabidopsis thaliana (Mouse ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_Taxid=3702.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA.

RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA.

RA Nakamura Y.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence

RT features of the regions of 4,504,864 bp covered by sixty p1 and TAC

RT clones."

RL DNA Res. 7:131-135(2000).

DR EMBL: AB017071; BAB02314.1; -

SQ SEQUENCE 296 AA; 32690 MM; B5BCD83423353EPE CRC64;

Query Match 57.4%; Score 35; DB 10; Length 296;

Best Local Similarity 62.5%; Pred. No. 96;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPOOFFG 9

Db 185 PRPOFFLG 192

RESULT 33

Q9HVZ9 PRELIMINARY; PRT; 297 AA.

ID Q9HVZ9

AC Q9HVZ9; 01-MAR-2001 (TReMBLrel. 16, Created)

DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)

DE HYPOTHETICAL PROTEIN PA4779.

GN PA4779.

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;

OC Pseudomonas.

NCBI_Taxid=287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PA01;

RA MEDLINE=20437337; PubMed=10984043;

RA Stover C.K., Pham X.-Q.T., Ervin A.L., Mizoguchi S.D., Warrenner P.,

RA Hickey M.J., Burkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Iarbig K., Lim R.M.,

RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizler J., Salier M.H., Hancock R.E.W., Lory S., Olson M.V.;

RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an

RT opportunistic pathogen.";

RL Nature 406:959-964(2000).

DR EMBL: AE004891; AAC08165.1; -

DR InterPro: IPR000620; DUF6.

DR Pfam: PF00892; DUF6; 2.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 297 AA; 31656 MM; 55FF9F205C79B1DA CRC64;

Query Match 57.4%; Score 35; DB 2; Length 297;

Best Local Similarity 54.5%; Pred. No. 96;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 PKPOOFFG 11

Db 111 RPTPRGLFGL 121

RESULT 34

ID Q40055 PRELIMINARY; PRT; 347 AA.

AC Q40055;

DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)

DE C HORDEIN PRECURSOR.

OS Hordeum vulgare (barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Hordeum.

NCBI_Taxid=4513;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BOMI; TISSUE=IMMATURE ENDOSPERM;

RX MEDLINE=89351278; PubMed=3255313;

RA Entwistle J.;

RT "Primary structure of a C-hordein gene from barley."

RL Carlberg Res. Commun. 53:247-258(1988).

DR EMBL: M36941; AAA9233.1; -

DR Mendel; 16774; Horvu; 2592; 16774.

KW Signal; Seed storage protein.

FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 347 C HORDEIN.

SQ SEQUENCE 347 AA; 40546 MM; 1E48919B2BCBC9D CRC64;

Query Match 57.4%; Score 35; DB 10; Length 347;

Best Local Similarity 85.7%; Pred. No. 1.1e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPOOFF 8

Db 60 PTPPOFF 66

RESULT 35

ID Q48648 PRELIMINARY; PRT; 424 AA.

AC Q48648;

DT 01-JUN-1998 (TReMBLrel. 06, Created)

DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)

DE PHYTOCHROME (FRAGMENT).

GN PHY4.

OS Adiantum capillus-veneris (Fern).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Filicophyta; Filicopsida; Filicales; Adiantaceae; Adiantum.

NCBI_Taxid=1818;

RN [1]

RP SEQUENCE FROM N.A.

RC TRANSPOSON-ARET-1;

RA Nozue K., Kanegae T., Wada M.;

RL J. Plant Res. 110:495-499(1997).

DR EMBL: AB003364; BAA24885.1; -

DR Mendel; 24641; Adica; 2331; 24641.

DR InterPro: IPR000014; PAS.

DR InterPro: IPR001294; Phytochrome.

DR Pfam: PF003018; GAF.

KW Pfam; PF00360; phytochrome; 1.

DR pfam: PF00989; PAS; 1.
 DR PRINTS: PRO1033; PHYTOCHROME.
 DR PROSITE: PS00245; PHYTOCHROME_1; 1.
 DR PROSITE: PS50046; PHYTOCHROME_2; 1.
 DR SMART: SM00055; GAF; 1.
 DR SMART: SM00091; PAS; 1.
 KW Phytochrome.
 FT NON_TER 1 1
 FT 424 424
 SEQUENCE 424 AA; 47115 MW; 5510380FAD212E64 CRC64;

Query Match 57.4%; Score 35; DB 10; Length 424;
 Best Local Similarity 45.5%; Pred. No. 1.4e+02;
 Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOFFGLM 11
 DB 97 RPKPRKMGVLV 107

RESULT 36
 O9CII7 PRELIMINARY; PRT; 494 AA.
 AC O9CII7:
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE LYSYL-TRNA SYNTHETASE (EC 6.1.1.6).
 GN LYS5.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 CC Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IL403:
 RA Bojoltin A., Wincker P., Manger S., Jallion O., Malarme K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis.";
 RL Genome Res. 0:0-0(2001).
 CC -1- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + TRNA(AMINO ACID) = AMP +
 CC PYROPHOSPHATE + L-AMINOACYL-TRNA(AMINO ACID).
 CC -1- CATALYTIC ACTIVITY: ATP + L-ASPARTATE (OR L-ASPARAGINE) +
 CC TRNA(ASN) = AMP + PYROPHOSPHATE + L-ASPARTYL-TRNA(ASP) (OR L-
 CC ASPARAGINYL-TRNA(ASN)).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO AMINOACYL-TRANSFER RNA SYNTHETASES CLASS-II
 CC FAMILY.
 CC -1- SIMILARITY: BELONGS TO ASPARTYL-TRNA SYNTHETASE FAMILY.
 DR EMBL: AE006274; AK04471.1; -
 DR InterPro: IPR002106; AA_TRNA_ligase_II.
 DR InterPro: IPR002309; trna-synt.2.
 DR InterPro: IPR002312; trna-synt.2.
 DR InterPro: IPR002313; trna-synt.2.
 DR pfam: PF00152; trna-synt.2; 1.
 DR pfam: PF01336; trna-anti.1.
 DR PRINTS: PRO1042; TRNASYTHASP.
 DR PRINTS: PRO0982; TRNASYTHYS.
 DR PROSITE: PS00179; AA_TRNA_LIGASE_II_1; 1.
 DR ATP-binding; Aminoacyl-TRNA synthetase; Complete proteome; Ligase;
 KW Protein biosynthesis.
 SO SEQUENCE 494 AA; 56615 MW; 571CDA0F69ADB8 CRC64;

Query Match 57.4%; Score 35; DB 2; Length 494;
 Best Local Similarity 60.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 OY 1 RPKPOOFFGL 10
 |||:::|

DB 143 RPLPEKFHGL 152

RESULT 37
 O9A0V7 PRELIMINARY; PRT; 497 AA.
 AC O9A0V7:
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PUTATIVE LYSYL-TRNA SYNTHETASE (EC 6.1.1.6).
 GN LYS5 OR SPY0595.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 CC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SF370:
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 DR EMBL: AE006515; AK33574.1; -
 KW Aminoacyl-TRNA synthetase; Ligase; Complete proteome.
 SO SEQUENCE 497 AA; 56599 MW; EBFDA25D5DAF92C8 CRC64;

Query Match 57.4%; Score 35; DB 2; Length 497;
 Best Local Similarity 60.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOOFFGL 10
 DB 145 RPLPEKFHGL 154
 |||:::|

RESULT 38
 O65191 PRELIMINARY; PRT; 509 AA.
 AC O65191:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE HELICASE.
 GN OP509L.
 OS African swine fever virus (ASFV).
 OC Viruses; dsDNA viruses, no RNA stage; Asfarviridae;
 OC African swine fever-like viruses.
 OX NCBI_TaxID=10497;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BA71V:
 RX MEDLINE=96036500; PubMed=7483270;
 RA Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C.,
 RA Rodriguez J.F., Vinuela E.;
 RT "Immune protection conferred by the baculovirus-related glycoprotein
 RT of Thogoto virus (Orthomyxoviridae).";
 RL Virology 208:249-278(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BA71V:
 RX MEDLINE=94233765; PubMed=8178480;
 RA La Vega I., Gonzalez A., Blasco R., Calvo V., Vinuela E.;
 RT "Nucleotide sequence and variability of the inverted terminal
 RT repetitions of African swine fever virus DNA.";
 RL Virology 201:152-156(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BA71V:

RX MEDLINE=90219205; PubMed=2325203;
RA Gonzalez A., Celivo V., Almazan F., Almendral J.M., Ramirez J.C.,
La Vega I., Blasco R., Vinuela E.;
RT "Multigene families in African swine fever virus: family 360.";
RL J. Virol. 64:2073-2081(1990).
[14]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=90219204; PubMed=2325202;
RA Almendral J.M., Almazan F., Blasco R., Vinuela E.;
RT "Multigene families in African swine fever virus: family 110.";
RL J. Virol. 64:2064-2072(1990).
[15]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=91134988; PubMed=1994575;
RA Camacho A., Vinuela E.;
RT "Protein p22 of African swine fever virus: an early structural protein that is incorporated into the membrane of infected cells.";
RL J. Virol. 181:251-257(1991).
[16]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RA Almazan F., Murguía J.R., Rodriguez J.M., La Vega I., Vinuela E.;
RL J. Gen. Virol. 0:0-0(0).
[17]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=94187118; PubMed=8139051;
RA Rodriguez J.M., Yanez R.J., Pan R., Rodriguez J.F., Salas M.L.,
Vinuela E.;
RT "Multigene families in African swine fever virus: family 505.";
RL J. Virol. 68:2746-2751(1994).
[18]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93346971; PubMed=8393914;
RA Yanez R.J., Rodriguez J.M., Rodriguez J.F., Salas M.L., Vinuela E.;
RT "African swine fever virus thymidylate kinase gene: sequence and transcriptional mapping.";
RL J. Gen. Virol. 74:1633-1638(1993).
[19]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=94065656; PubMed=8245848;
RA Alcamí A., Angulo A., Vinuela E.;
RT "Mapping and sequence of the gene encoding the African swine fever virus protein of M(r) 11500.";
RL J. Gen. Virol. 74:2317-2324(1993).
[110]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93277388; PubMed=8503790;
RA Munoz M., Freije J.M., Salas M.L., Vinuela E., Lopez-Otin C.;
RT "Structure and expression in E. coli of the gene coding for protein p10 of African swine fever virus.";
RL Arch. Virol. 130:93-107(1993).
[111]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=90357780; PubMed=2389555;
RA Blasco R., Lopez-Otin C., Munoz M., Bockamp E.O., Simon-Mateo C.,
Vinuela E.;
RT "Sequence and evolutionary relationships of African swine fever virus thymidine kinase.";
RL Virology 178:301-304(1990).
[112]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93281350; PubMed=8506138;
RA Yanez R.J., Boursnell M., Nogal M.L., Yuste L., Vinuela E.;
RT "African swine fever virus encodes two genes which share significant homology with the two largest subunits of DNA-dependent RNA

RT polymerases.";
RL Nucleic Acids Res. 21:2423-2427(1993).
[113]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93353606; PubMed=8102411;
RA Rodriguez J.M., Yanez R.J., Almazan F., Vinuela E., Rodriguez J.F.;
RT "African swine fever virus encodes a CD2 homolog responsible for the adhesion of erythrocytes to infected cells.";
RL J. Virol. 67:5312-5320(1993).
[114]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=94085774; PubMed=8262374;
RA Yanez R.J., Rodriguez J.M., Boursnell M., Rodriguez J.F., Vinuela E.;
RT "Two putative African swine fever virus helicases similar to yeast 'DEAF' pre-mRNA processing proteins and vaccinia virus ATPases D1L and D6R.";
RL Gene 134:161-174(1993).
[115]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=90223993; PubMed=2327074;
RA Lopez-Otin C., Freije J.M., Parra F., Mendez E., Vinuela E.;
RT "Mapping and sequence of the gene coding for protein p12, the major capsid protein of African swine fever virus.";
RL Virology 175:477-484(1990).
[116]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=94123986; PubMed=8293992;
RA Rodriguez J.M., Yanez R.J., Rodriguez J.F., Vinuela E., Salas M.L.;
RT "The DNA polymerase-encoding gene of African swine fever virus: sequence and transcriptional analysis.";
RL Gene 136:103-110(1993).
[117]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93327788; PubMed=8335009;
RA Simon-Mateo C., Andres G., Vinuela E.;
RT "Polypeptide processing in African swine fever virus: a novel gene expression strategy for a DNA virus.";
RL EMBO J. 12:2977-2987(1993).
[118]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93233210; PubMed=8474154;
RA Prados F.J., Vinuela E., Alcamí A.;
RT "Sequence and characterization of the major early phosphoprotein p32 of African swine fever virus.";
RL J. Virol. 67:2475-2485(1993).
[119]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=92260660; PubMed=1583732;
RA Alcamí A., Angulo A., Lopez-Otin C., Munoz M., Freije J.M., Carrascosa A.L., Vinuela E.;
RT "Amino acid sequence and structural properties of protein p12, an African swine fever virus attachment protein.";
RL J. Virol. 66:3860-3868(1992).
[120]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93174976; PubMed=8438592;
RA Yanez R.J., Vinuela E.;
RT "African swine fever virus encodes a DNA ligase.";
RL Virology 193:531-536(1993).
[121]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE=93174941; PubMed=8382399;
RA Pena L., Yanez R.J., Revilla Y., Vinuela E., Salas M.L.;
RT "African swine fever virus guanylyltransferase.";

RL Virology 193:319-328(1993).
RN [22]
RP SEQUENCE FROM N.A.
RC STRAIN-BA71V;
RA MEDLINE-95159428; Pubmed-7856088;
RT Simon-Mateo C., Freije J.M., Andres G., Lopez-Otin C., Vinuela E.;
RT "Mapping and sequence of the gene encoding protein p17, a major
RT African swine fever virus structural protein.";
RL Virology 206:1140-1144(1995).
RN [23]
RP SEQUENCE FROM N.A.
RC STRAIN-BA71V;
RA MEDLINE-92263807; Pubmed-1316688;
RT Garcia-Beato R., Freije J.M., Lopez-Otin C., Blasco R., Vinuela E.,
RT Salas M.L.;
RT "A gene homologous to topoisomerase II in African swine fever virus.";
RL Virology 188:938-947(1992).
RN [24]
RP SEQUENCE FROM N.A.
RC STRAIN-BA71V;
RA MEDLINE-94091056; Pubmed-8266720;
RT Freije J.M., Lain S., Vinuela E., Lopez-Otin C.;
RT "Nucleotide sequence of a nucleoside triphosphate phosphohydrolase
Query Match 57.4%; Score 35; DB 12; Length 509;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOOFF 8
DB 199 RKPPOFF 206
RESULT 39
ID Q18014 PRELIMINARY; PRT; 521 AA.
AC Q18014;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHETICAL PROTEIN C15C7.1.
GN C15C7.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID-6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE-99069613; Pubmed-9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Leimbach D.;
RT "The sequence of C. elegans cosmid C15C7.";
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U41528; AAK3917.1.;
DR InterPro; IPR000727; T_SNARE.
DR SMART; SM00397; T_SNARE; 1.
SQ SEQUENCE 521 AA; 58924 MW; 7E52486E751D48F5 CRC64;

Query Match 57.4%; Score 35; DB 5; Length 521;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 RPKPOFFGL 10
DB 504 PRSAFFGI 512
RESULT 40
ID Q9GUT4 PRELIMINARY; PRT; 681 AA.
AC Q9GUT4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE L4270.4.
GN L4270.4.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID-5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Myler P.J., Sisk E., Cawthra J., Handley F., Vogt C., Robertson L.,
RA McDonagh P., Stuart K., Ivens A., Worthey E.A.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC012524; AAG16717.1.;
SQ SEQUENCE 681 AA; 71416 MW; 6074EAA755F16F1E CRC64;

Query Match 57.4%; Score 35; DB 5; Length 681;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 RPKPOFFG 9
DB 223 RPKPOFFG 231
RESULT 41
ID Q9ESL2 PRELIMINARY; PRT; 682 AA.
AC Q9ESL2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ACYL-COA SYNTHETASE 5.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
OX NCBI_TaxID-10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HARTLEY; TRISUE-SPLEEN;
RA Ohtani M., Watanabe N., Kobayashi Y.;
RT "Analysis of genes associated with the guinea pig skin delayed-type
RT hypersensitivity reaction.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049761; BAB1604.1.;
DR InterPro; IPR000873; AMP-bind.
DR PROSITE; PS00455; AMP_BINDING; 1.
SQ SEQUENCE 682 AA; 75875 MW; 0566F8CA70B016E7 CRC64;

Query Match 57.4%; Score 35; DB 11; Length 682;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

-QY 1 RPKPOFFGL 10
DB 127 KPSPOFFGI 136
RESULT 42

P74619 PRELIMINARY: PRT: 832 AA.
 AC P74619;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE HYPOTHETICAL 92.9 KDA PROTEIN.
 GN SL1477.
 OS Synchocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirosewa M., Sugiyura M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nario K., Okumura S.,
 RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synchocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL: D90916; BAA18727.1; -
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 832 AA; 92864 MW; CE02AA8DAFB2B9BE CRC64;

Query Match 57.4%; Score 35; DB 2; Length 832;
 Best Local Similarity 60.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 PRPQOFGFL 10
 Db 669 PRQDMQFECI 678

RESULT 43
 O9XT20 PRELIMINARY: PRT: 1043 AA.
 AC O9XT20;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE R03E1.1 PROTEIN.
 GN R03E1.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peleciderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA McMurtry A.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sprat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL: 292837; CAB07400.1; -
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 6.

DR PRINTS: PR00320; GPROTEINBRPT.
 DR SMART: SM00320; WD40; 6.
 DR PROSITE: PS50082; WD_REPEATS_2; 4.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 2.
 KW Repeat; WD repeat.
 SO SEQUENCE 1043 AA; 115073 MW; A2B6FCDDC07536DF CRC64;

Query Match 57.4%; Score 35; DB 5; Length 1043;
 Best Local Similarity 50.0%; Pred. No. 3.6e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRPQOFGFL 11
 Db 955 PRPQVFNNML 964

RESULT 44
 O9UPP5 PRELIMINARY: PRT: 1278 AA.
 AC O9UPP5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE KIA1107 PROTEIN (FRAGMENT).
 GN KIA1107.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=99397452; PubMed=10470851.
 RA Kikuno R., Nagase T., Ishikawa K., Hirosewa M., Miyajima N.,
 RA Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 6:197-205(1999).
 DR EMBL: AB029030; BAA83059.1; -
 FT NON-TER
 SO SEQUENCE 1278 AA; 140799 MW; DE032B2C4E1BDA29 CRC64;

Query Match 57.4%; Score 35; DB 4; Length 1278;
 Best Local Similarity 60.0%; Pred. No. 4.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRPQOFGFL 11
 Db 890 PAPQOFGFII 899

RESULT 45
 O9SDB6 PRELIMINARY: PRT: 1611 AA.
 AC O9SDB6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PUTATIVE MYOSIN HEAVY CHAIN.
 GN AT2G33240.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eustoids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV_COLUMBIA;
 RX MEDLINE=20083487; PubMed=10617197;
 RL Lin X., Kaul S., Rounsley S.D., Shena T.P., Benito M.-I., Town C.D.,

RESULT 48

09JUK11 PRELIMINARY; PRT; 154 AA.
AC 09JUK11;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE EOSINOPHIL-ASSOCIATED RIBONUCLEASE 2 PRECURSOR.
GN EAR2.
OS Mus pahari (shrew mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10093;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243759; PubMed=10758160;
RA Zhang J., Dyer R.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
family by rapid gene sorting and positive selection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238402; AAF67702.1;
DR InterPro: IPR001427; RNaseH.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SMO0092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN.1.
SQ SEQUENCE 154 AA; 17927 MW; 08F002D5B461D6 CRC64;

Query Match 55.7%; Score 34; DB 11; Length 154;
Best Local Similarity 60.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKQOQFGL 10
Db 27 RPTPSQRFGL 36

RESULT 49
P70014 PRELIMINARY; PRT; 162 AA.
AC P70014;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE OLFACTORY RECEPTOR (FRAGMENT).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96112032; PubMed=8845161;
RA Freitag J., Krieger J., Strotman J., Breer H.;
RT "Two classes of olfactory receptors in Xenopus laevis.";
RL Neuron 15:1383-1392(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Freitag J.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
DE EMBL; Y08203; CAA69385.1;
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_FL_2; 1.
FT NON_TER 1
FT 162 162
SQ SEQUENCE 162 AA; 18296 MW; 6F75BDFB58B34541 CRC64;

Query Match 55.7%; Score 34; DB 13; Length 162;
Best Local Similarity 60.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 RPKQOQFGLM 11
Db 145 PKDOFFALL 154

RESULT 50
09X8G5 PRELIMINARY; PRT; 167 AA.
AC 09X8G5;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE PUTATIVE INTEGRAL MEMBRANE PROTEIN.
GN SCF7.08C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kleiser H.M., Denapate D., Eichner A., Cullum J.,
RA Klinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL M.O.L. Microbiol. 21:77-96(1996).
DR EMBL; AL049819; CAB42667.1;
SQ SEQUENCE 167 AA; 18565 MW; 2A54F1F879D899E2 CRC64;

Query Match 55.7%; Score 34; DB 2; Length 167;
Best Local Similarity 55.6%; Pred. No. 81;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKQOQFGL 9
Db 18 RPEPLRFTG 26

RESULT 51
09ZSX5 PRELIMINARY; PRT; 216 AA.
AC 09ZSX5;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE HYPOTHETICAL 23.8 KDA PROTEIN.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Song R., Liaca V., Messing J.;
RT "Analysis of a 22-kDa alpha zein cluster in maize.";

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090446; AAD09013.1; -
KW Hypothetical protein.
SQ SEQUENCE 216 AA; 23774 MW; EA9E524C2B4E227B CRC64;

Query Match 55.7%; Score 34; DB 10; Length 216;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFGLM 11
||||| : |||
DB 69 RPKPSRTFALV 79

RESULT 52
O54788 PRELIMINARY; PRT; 253 AA.
AC O54788;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TRANSPOSASE.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95189099; PubMed=7883181;
RA Hui F.M., Zhou L., Morrison D.A.;
RT "Competence for genetic transformation in Streptococcus pneumoniae:
RT organization of a regulatory locus with homology to two lactococcal A
RT secretion genes.";
RL Gene 153:25-31(1995).
DR EMBL; M36180; AAA69508.1; -
DR InterPro: IPR002560; Transposase_12.
DR Pfam: PF01610; Transposase_12; A7832B3118D11749 CRC64;
SQ SEQUENCE 253 AA; 30676 MW; A7832B3118D11749 CRC64;

Query Match 55.7%; Score 34; DB 2; Length 253;
Best Local Similarity 55.6%; Pred. No. 1.3e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOQFGLM 11
||||| : |||
DB 162 EPEKFFGLI 170

RESULT 53
O56868 PRELIMINARY; PRT; 266 AA.
AC O56868;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE VIRAL TEGUMENT PROTEIN.
GN UL49.
OS gallid herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirinae;
OX NCBI_TaxID=10386;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98080487; PubMed=9420298;
RA Ziemann K., Mettenleiter T.C., Fuchs W.;
RT "Gene arrangement within the unique long genome region of infectious
RT taryngotracheitis virus is distinct from that of other
RT alphaherpesviruses.";
RL J. Virol. 72:847-852(1997).
DR EMBL; Y14300; CAA74678.1; -
DR InterPro: IPR001917; AminoTransf_2.

DR PROSITE; PS00599; AA_TRANSFER_CLASS_2; UNKNOWN_1.
SQ SEQUENCE 266 AA; 30358 MW; FF0459DAE1C6F4A9 CRC64;

Query Match 55.7%; Score 34; DB 12; Length 266;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOFF 7
||||| : |||
DB 28 RPKPOFF 34

RESULT 54
O9GUG0 PRELIMINARY; PRT; 270 AA.
AC O9GUG0;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HYPOTHETICAL PROTEIN Y73B6BL.M.
GN Y73B6BL.M.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC084197; AAG23472.1; -
SQ SEQUENCE 270 AA; 30321 MW; 08F5ABA5FEFC3446 CRC64;

Query Match 55.7%; Score 34; DB 5; Length 270;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 PKPOFF 8
||||| : |||
DB 151 PKPEFF 157

RESULT 55
O9GKX6 PRELIMINARY; PRT; 304 AA.
AC O9GKX6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE HYPOTHETICAL 34.0 KDA PROTEIN (FRAGMENT).
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN PARIENTAL LOBE;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DB 49 RPKSROFF 56

RESULT 58

Q9JYV5 PRELIMINARY; PRT; 318 AA.

AC Q9JYV5;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE PUTATIVE RIBOFLAVIN KINASE/PMN ADENYLYLTRANSFERASE (EC 2.7.1.26).

GN RIBF OR NMA0621.

OS Neisseria meningitidis (serogroup A).

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_Taxid=65699;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;

RX MEDLINE=20222556; PubMed=10761919;

RA Parhill J., Achman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holtroyd S., Jags K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;

RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491."

RL Nature 404:502-506(2000).

DR EMBL; AL162753; CAB83911.1; -.

DR InterPro: IPR002606; FAD_Synth.

DR InterPro: IPR001412; tRNA-Synt_L.

DR Pfam: PF01687; FAD_Synth; 1.

DR ProDom: PD003662; FAD_Synth; 1.

DR PROSITE: PS00178; AA-TRNA_LIGASE_I; UNKNOWN_1.

KW Transferase; Kinase; Nucleotidyltransferase; Complete proteome.

SQ SEQUENCE 318 AA; 35605 MW; 224286E1C6DA0528 CRC64;

Query Match 55.7%; Score 34; DB 2; Length 318;

Best Local Similarity 55.6%; Pred. No. 1.6e+02;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKPOOFFGL 10

DB 68 PPKPFALL 76

RESULT 59

O9MJ81 PRELIMINARY; PRT; 355 AA.

AC O9MJ81;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE MITOCHONDRIAL DNA, COMPLETE GENOME.

OS Physarum polycephalum (Slime mold).

OC Mitochondrion.

OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;

OX NCBI_Taxid=5791;

RN [1]

RP SEQUENCE FROM N.A.

RA Takano H., Abe T., Sakurai R., Moriyama Y., Miyazawa Y., Nozaki H., Kawano S., Sasaki N., Kuroiwa T.;

RT "The complete DNA sequence of the mitochondrial genome of Physarum polycephalum."

RT Mol. Gen. Genet. 0:0-0(2000).

DR EMBL; AB027295; BAB08081.1; -.

KW Mitochondrion.

SQ SEQUENCE 355 AA; 43335 MW; 5CE0AABD08D6E88F CRC64;

Query Match 55.7%; Score 34; DB 8; Length 355;

Best Local Similarity 50.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOOFFGL 10

DB 207 KRPDPNFSL 216

RESULT 60

O82469 PRELIMINARY; PRT; 359 AA.

AC O82469;

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE PROTEIN PHOSPHATASE-2C.

GN PP2C.

OS Mesembryanthemum crystallinum (Common ice plant).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.

OX NCBI_Taxid=3544;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LEAF;

RA Miyazaki S., Koga R., Bohnert H.J., Fukuhara T.;

RT "Cell-, tissue- and environmental response-specific expression of 10 members of the PP2C gene family in Mesembryanthemum crystallinum."

RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF075580; AAC36698.1; -.

DR HSSP; P35813; 1A6O.

DR InterPro: IPR000222; PP2C.

DR InterPro: IPR003589; PP2C catalytic.

DR InterPro: IPR001932; PP2C domain.

DR InterPro: IPR003588; PP2C_sig.

DR Pfam; PF00481; PP2C; 1.

DR SMART; SM00331; PP2C; 1.

DR SMART; SM00331; PP2C; 1.

DR PROSITE; PS01032; PP2C; 1.

SQ SEQUENCE 359 AA; 39565 MW; 42CCF7092742CD6C CRC64;

Query Match 55.7%; Score 34; DB 10; Length 359;

Best Local Similarity 55.6%; Pred. No. 1.8e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOOFFGL 10

DB 84 PKPSAFYGV 92

RESULT 61

O49132 PRELIMINARY; PRT; 393 AA.

AC O49132;

DT 01-JUN-1998 (TREMBLrel. 06, Created)

DT 01-JAN-1999 (TREMBLrel. 09, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE POLYPHENOL OXIDASE (FRAGMENT).

OS Diospyros kaki (kaki persimmon).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; Ericales; Ebenaceae; Diospyros.

OX NCBI_Taxid=35925;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FUJY;

RA Bahn S.C., Shin J.S.;

RT "Cloning and expression of PPO(Polyphenol Oxidase) cDNA in persimmon

RT (Diospyros kaki).";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF039165; AAC69365.1; -
 DR Mendel: 33386; DIOKA:1008;33386.
 DR InterPro: IPR002227; Tyrosinase.
 DR Pfam: PF00264; tyrosinase.1.
 DR PRINTS: PR00092; TYROSINASE.
 DR PROSITE: PS00497; TYROSINASE_1; 1.
 DR PROSITE: PS00498; TYROSINASE_2; 1.
 FT NON_TER 393 393
 SQ SEQUENCE 393 AA; 45559 MW; DBCCE42CB49B8E51 CRC64;

Query Match 55.7%; Score 34; DB 10; Length 393;
 Best Local Similarity 75.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQFG 9
 | | | | |
 DB 169 PCPSQFG 176

RESULT 62
 O9Z5W4 PRELIMINARY; PRT; 405 AA.
 AC O9Z5W4;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE TOPOISOMERASE.
 CS TOP.
 CN Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 CC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=142;
 RA Tsol T.V., Plotnikova E.G., Cole J.R., Guerin W.F., Bagdasarian M.,
 RA Tiedje J.M.;
 RT "Cloning, expression and nucleotide sequence of the Pseudomonas
 aeruginosa strain 142 ohb genes for oxygenolytic ortho-dehalogenation
 of halobenzoates.";
 RL Appl. Environ. Microbiol. 65:0-0(1999).
 DR EMBL: AF121970; AAD20003.1; -
 DR InterPro: IPR000380; Pro_topoisomerase.
 DR Pfam: PF01396; zf-C4_Topoisom; 2.
 KW Isomerase.
 SQ SEQUENCE 405 AA; 45242 MW; 76BDCBBE52812509 CRC64;

Query Match 55.7%; Score 34; DB 2; Length 405;
 Best Local Similarity 85.7%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQF 7
 | | | | |
 DB 189 RPDPOQF 195

RESULT 63
 O21172 PRELIMINARY; PRT; 410 AA.
 AC O21172;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 OS Galapagus galapagensis.
 CG Mitochondrion.
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 CC Cucujiformia; Phyllophaga; Curculionidae; Entiminae; Entimini;

OC Galapagus.
 OX NCBI_TaxID=63362;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sequence A.S., Farrell B., Salmore A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 DR EMBL: AF015914; AAB64294.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 410 410
 SQ SEQUENCE 410 AA; 45420 MW; B4C17F9E7A8C698F CRC64;

Query Match 55.7%; Score 34; DB 8; Length 410;
 Best Local Similarity 85.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQOFFGL 10
 | | | | |
 DB 346 PQHFFGL 352

RESULT 64
 O13352 PRELIMINARY; PRT; 415 AA.
 AC O13352;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE MAP KINASE MPK1.
 GN MPK1.
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.
 OX NCBI_TaxID=148305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GV11;
 RA Xu J.R., Hamer J.E.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF020316; AAC63682.1; -
 DR HSSP: O16539; IMFC.
 DR InterPro: IPR000719; Euk_Kinase.
 DR InterPro: IPR003527; MAP_Kin.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR Pfam: PF00069; kinase.1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 415 AA; 46992 MW; F149D728145E2EA CRC64;

Query Match 55.7%; Score 34; DB 3; Length 415;

Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOQFGLM 11
1:11::11
DB 391 PRPOEVGOM 400

RESULT 65
Q06884 PRELIMINARY; PRT; 502 AA.

AC Q06884;
DT 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE CYTOCHROME P450 11A (EC 1.14.14.1) (STEROID INDUCIBLE).
GN CYP3A1 OR CYP3A23.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SLC-WISTAR; TISSUE=LIVER;
RX MEDLINE=9409605; PubMed=8274011;
RA Kirita S., Matsubara T.;
RT "cDNA cloning and characterization of a novel member of steroid-
induced cytochrome P450 3A in rats."
RL Arch. Biochem. Biophys. 307:253-258(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=LIVER;
RX MEDLINE=95096005; PubMed=7528203;
RA Komori M., Oda Y.;
RT "A major glucocorticoid-inducible P450 in rat liver is not P450 3A1."
RL J. Biochem. 116:114-120(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Miyata M., Nagata K., Yamazoe Y., Kato R.;
RL Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strotkamp D., Roos P.H., Hanstein W.G.;
RL Submitted (Apr-1996) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE DAWLEY; TISSUE=LIVER;
RA Nagata K., Ogino M., Shimada M., Miyata M., Frank G.J., Yamazoe Y.;
RL Submitted (Nov-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLOASE
MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATTY
ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + REDUCED FLAVOPROTEIN + O(2) = ROH +
OXIDIZED FLAVOPROTEIN + H(2)O.
CC -1- SUBCELLULAR LOCATION: MEMBRANE BOUND.
CC -1- INDUCTION: P450 CAN BE INDUCED TO HIGH LEVELS IN LIVER AND OTHER
TISSUES BY VARIOUS FOREIGN COMPOUNDS, INCLUDING DRUGS, PESTICIDES,
AND CARCINOGENS.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

DR EMBL; AB008382; BAA23003.1; JOINED.
DR EMBL; AB008383; BAA23003.1; JOINED.
DR EMBL; AB008384; BAA23003.1; JOINED.
DR EMBL; AB008385; BAA23003.1; JOINED.
DR EMBL; D13912; BAA03008.1; -.
DR EMBL; D29967; BAA06233.1; -.
DR InterPro: IPR001128; Cyt_P450.
DR pfam: PF00067; p450.1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Electron transport; Heme; Membrane; Microsome; Monooxygenase;
KW Oxidoreductase.
FT BINDING 441 441 HEME (BY SIMILARITY).
FT CONFLICT 107 107 D->Y (IN REF. 2).
SQ SEQUENCE 502 AA; 57675 MW; B37837D1E180697D CRC64;

Query Match 55.7%; Score 34; DB 11; Length 502;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOQFPG 9
11111111
DB 41 PKPLPFG 48

RESULT 66
Q41486 PRELIMINARY; PRT; 583 AA.

AC Q41486;
DT 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE PROPOLYPHENOL OXIDASE PRECURSOR (FRAGMENT).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93144692; PubMed=7678763;
RA Hunt M., Eannetta N.T., Yu H., Newman S.M., Steffens J.C.;
RT "cDNA cloning and expression of potato polyphenol oxidase."
RL Plant Mol. Biol. 21:59-68(1993).
DR EMBL; M95196; AAA02877.1; -.
DR Mendel; 10542; Soltu;1008;10542.
DR InterPro: IPR002227; Tyrosinase.
DR pfam: PF00264; tyrosinase; 1.
DR PRINTS: PR00092; TYROSINASE.
DR PROSITE: PS00497; TYROSINASE_1; 1.
DR PROSITE: PS00498; TYROSINASE_2; 1.
KW Transit peptide.
FT NON_TER 1
FT TRANSIT <1 83 POTENTIAL.
FT CHAIN 84 583 POLYPHENOL OXIDASE.
SQ SEQUENCE 583 AA; 65742 MW; 6FB0E542B0B703ED CRC64;

Query Match 55.7%; Score 34; DB 10; Length 583;
Best Local Similarity 75.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOQFPG 9
11111111
DB 296 PCPSQFPG 303

RESULT 67
Q9XIC7 PRELIMINARY; PRT; 628 AA.
AC Q9XIC7;
DT 01-NOV-1999 (TREMBLREL. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DB HYPOTHEtical 69.4 KDA PROTEIN F23M19.11.
GN F23M19.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
RA Lee J., Liu A., Li J., Kremenetskaia I., Luros J., Gonzalez A.,
RA Alatafi H., Araujo R., Chao Q., Conn L., Conway A.B., Dunn P.,
RA Hansen N., Hultzer L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
RA Davis R.W., Ecker J.R., Federpiet N.A., Theologis A.,
RT "Arabidopsis thaliana chromosome 1 BAC F23M19 sequence."
RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AC007454; AAD39611.1; -.
DR HSSP; P09215; 1BDY.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam; PF00560; LRR; 4.
DR Pfam; PF00069; Jkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00370; LRR; 4.
DR SMART; SM00221; STYKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 628 AA: 69402 MW: 23F6C0DC3717C74F CRC64;

Query Match 55.7%; Score 34; DB 10; Length 628;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFF 8
DB 267 RRPQEFF 274

RESULT 68
OY 09C792 PRELIMINARY; PRT; 646 AA.
AC 09C792;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYPOTHEtical 73.9 KDA PROTEIN.
GN F10D13_27.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federpiet N.A., Kaul S.,
RA White O., Alonso J., Alatafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dekar K.,
RA Dunn P., Etyu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kuriz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maltl R., Matzali A.,
RA Milttscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana."
RL Nature 408:816-820(2000).
DR EMBL; AC073178; AAG60099.1; -.
DR InterPro: IPR003864; DUF221.
DR Pfam; PF02714; DUF221; 1.
KW Hypothetical protein.
SQ SEQUENCE 646 AA: 73897 MW: DB99E6D3D7E1D4F CRC64;

Query Match 55.7%; Score 34; DB 10; Length 646;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFF 7
DB 108 RRPQEFF 114

RESULT 69
OY 09A926 PRELIMINARY; PRT; 737 AA.
AC 09A926;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE TONB-DEPENDENT RECEPTOR, PUTATIVE.
GN CC0815.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21173696; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005758; AAK22800.1; -.
DR TIGR; CC0815; -.
KW Receptor; Complete proteome.
SQ SEQUENCE 737 AA: 80297 MW: F09B9EAFDE6A6328 CRC64;

Query Match 55.7%; Score 34; DB 2; Length 737;
Best Local Similarity 71.4%; Pred. No. 3.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFF 7
DB 723 RRPQEFF 729


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RESULT 70
09W5X2
ID 09W5X2 PRELIMINARY: PRT: 738 AA.
AC 09W5X2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CG15332 PROTEIN.
GN CG15332.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegam C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
RA Kimmel B.E., Kohira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE002611; AAF45377.1;
DR FlyBase; FBgn0031088; CG15332.
SQ SEQUENCE 738 AA; 78968 MW; 2ED221B8563B1639 CRC64;
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AC 09Y062;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE RECO HELICASE HOMOLOG.
GN BLM OR DMBIM OR CG6920.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99160561; PubMed=10049920;
RA Kusano K., Berres M.E., Engels W.R.;
RT "Evolution of the RCO family of helicases: A drosophila homolog,
RT Dmbim, is similar to the human bloom syndrome gene."
RL Genetics 151:1027-1039(1999).
CC -1- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.
CC -1- SIMILARITY: TO DEAD/DEAH C-TERMINAL DOMAIN.
DR EMBL; U92536; AAD4141.1; -.
DR FlyBase; FBgn0015800; blm.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR002464; DEAH_ATP_helicase.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR002121; HRDC.
DR Pfam; PF00270; DEAD_1.
DR Pfam; PF00271; helicase_C_1.
DR Pfam; PF00570; HRDC_1.
DR SMART; SM00487; DEXDC_1.
DR SMART; SM00490; HELICG_1.
DR SMART; SM00341; HRDC_1.
DR PROSITE; PS00690; DEAH_ATP_HELICASE; UNKNOWN_1.
DR ATP-binding; Helicase.
KW SEQUENCE 1487 AA; 165777 MW; 5233D770AB4A3E30 CRC64;
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Query Match 55.7%; Score 34; DB 5; Length 1487;
Best Local Similarity 54.5%; Pred. NO. 7.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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OY 1 RPKPOFFGIM 11
DB 953 RSKPOHFGIIT 963

RESULT 72
09VG18
ID 09VG18 PRELIMINARY: PRT: 1487 AA.
AC 09VG18;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BLM PROTEIN.
GN BLM OR CG6920.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshneff A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sider-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -1- SIMILARITY: TO DEAD/DEAH BOX HELICASE FAMILY.
 CC -1- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.
 DR EMBL: AEO03692; AAF54691.1; -
 DR FlyBase: FBgn0015800; b1m.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR002464; DEAH_ATP_helicase.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR001211; HRDC.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR Pfam: PF00570; HRDC; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC; 1.
 DR SMART: SM00341; HRDC; 1.
 DR PROSITE: PS00690; DEAH_ATP_HELICASE; UNKNOWN.1.
 DR AMP-binding; Helicase.
 KW AP-1-binding; Helicase.
 SQ SEQUENCE 1487 AA; 166077 MW; 07361B8005E29432 CRC64;

Query Match 55.7%; Score 34; DB 5; Length 1487;
 Best Local Similarity 54.5%; Pred. No. 7.9e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 RPKRQFFGLM 11
 Db 953 RSKRQHSGLI 963
 RESULT 73
 ID 09V0U8 PRELIMINARY; PRT; 1970 AA.
 AC 09V0U8;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CG10020 PROTEIN.
 GN CG10020.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; Pubmed=10731132;
 RA Adams M.D., Geniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.E., Aspray A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshneff A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sider-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AEO03578; AAF51066.2; -
 DR FlyBase: FBgn0031569; CG10020.
 DR InterPro: IPR001478; PDZ.
 DR InterPro: IPR001849; PH.
 DR Pfam: PF00595; PDZ; 1.
 DR Pfam: PF00169; PH; 2.
 DR SMART: SM00228; PDZ; 1.
 DR SMART: SM00233; PH; 2.
 DR PROSITE: PS50106; PDZ; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 1.
 SQ SEQUENCE 1970 AA; 220273 MW; 4D1C41FDF72E6E26 CRC64;

Query Match 55.7%; Score 34; DB 5; Length 1970;
 Best Local Similarity 45.5%; Pred. No. 1.1e+03;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 RPKRQFFGLM 11
 Db 54 RPRRFRFGCL 64
 RESULT 74
 ID 09JUN9 PRELIMINARY; PRT; 71 AA.
 AC 09JUN9;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE HYPOTHETICAL PROTEIN NMA1216.
 GN NMA1216.
 OS *Neisseria meningitidis* (serogroup A).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

Query Match 54.18; Score 33; DB 10; Length 103;
 Best Local Similarity 66.7%; Pred. No. 76;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOFFGL 10
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 Db 74 PKPSDFGL 82

RESULT 78
 080033 PRELIMINARY; PRT; 130 AA.

AC 080033;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 OS Exoneurella lawsoni.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Exoneurella.
 NCBI_TaxID=78187;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
 RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera: Apidae: Allodapini): evidence from molecular and morphological data sets."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF072661; AAC24880.1; -.
 DR InterPro: IPR000883; COX1. 1.
 DR Pfam: PF00115; COX1. 1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 130 130
 SQ SEQUENCE 130 AA; 15339 MW; 11CFAF1F1EAE22F2 CRC64;

Query Match 54.18; Score 33; DB 8; Length 130;
 Best Local Similarity 75.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
 || | |||
 Db 56 PQHFLGLM 63

RESULT 79
 080034 PRELIMINARY; PRT; 130 AA.

AC 080034;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 OS Exoneurella tridentata.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Exoneurella.
 NCBI_TaxID=78189;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
 RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera: Apidae: Allodapini): evidence from molecular and morphological data sets."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF072663; AAC24882.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1. 1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 130 130
 SQ SEQUENCE 130 AA; 15438 MW; 4B9444ABF5AC3F4F CRC64;

Query Match 54.18; Score 33; DB 8; Length 130;
 Best Local Similarity 75.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
 || | |||
 Db 56 PQHFLGLM 63

RESULT 80
 079124 PRELIMINARY; PRT; 131 AA.

AC 079124;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 OS Braunsapis unicolor.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Braunsapis.
 NCBI_TaxID=78183;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
 RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera: Apidae: Allodapini): evidence from molecular and morphological data sets."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF072659; AAC24878.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1, 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 131
FT NON_TER 1 131
SQ SEQUENCE 131 AA; 15603 MW; F1407925903C9FE8 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 131;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
DB 56 POFFGLM 63

RESULT 81
ID 079125 PRELIMINARY; PRT; 131 AA.
AC 079125;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
OS Brevineura xanthoclypeata.
OG Mitochondrion.
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Brevineura.
OX NCBI_TaxID=78184;
RN [1]
RP SEQUENCE FROM N.A.
RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
RT Apoidea: Allodapini): evidence from molecular and morphological data
RT sets.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF072660; AAC24879.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1, 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 131
FT NON_TER 1 131
SQ SEQUENCE 131 AA; 15508 MW; D5E0508AB020093F CRC64;

Query Match 54.1%; Score 33; DB 8; Length 131;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
DB 56 POFFGLM 63

RESULT 82
ID 079126 PRELIMINARY; PRT; 131 AA.
AC 079126;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
OS Exoneurella eremophila.
OG Mitochondrion.
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Exoneurella.
OX NCBI_TaxID=78186;
RN [1]
RP SEQUENCE FROM N.A.
RA Reyes S.G., Cooper S.J.B., Schwarz M.P.;
RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
RT Apoidea: Allodapini): evidence from molecular and morphological data
RT sets.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF072662; AAC24881.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1, 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 131
FT NON_TER 1 131
SQ SEQUENCE 131 AA; 15531 MW; 55B915590BDFCF85 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 131;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
DB 56 POFFGLM 63

RESULT 83
ID 099834 PRELIMINARY; PRT; 151 AA.
AC 099834;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
OS Ophraella communis.
OG Mitochondrion.
CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Phyltophaga; Chrysomeloidea; Chrysomelidae; Galerucinae;
OX Ophraella.
OX NCBI_TaxID=38162;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=99261638; PubMed=10331253;
RA Funk D.J.:
RT "Molecular systematics of cytochrome oxidase I and 16S from
RL Neochlamisus leaf beetles and the importance of sampling."
RL Mol. Biol. Evol. 16:67-82(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER E (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
CC FERROCYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF092679; AAD05540.1; -.
DR InterPro: IPR000883; COX1.
DR PRINTS: PF00115; COX1.1.
DR PIRNTS: PR01165; CYCOXIDASE1.
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT SEQUENCE 151 AA; 17205 MW; 0ED59F8A4C59B2DE CRC64;

Query Match 54.1%; Score 33; DB 8; Length 151;
Best Local Similarity 75.0%; Pred. NO. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
1111111
Db 99 PQHFLGLM 106

RESULT 84
Q9G462 PRELIMINARY; PRT; 156 AA.
AC Q9G462;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
OS Diadastia consociata.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Diadastia.
OX NCB1_TaxID=70982;
RN [1]
RP SEQUENCE FROM N.A.
RA Sipes S.D., Wolf P.G.:
RT "Phylogenetic relationships in Diadastia, a group of specialist bees."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
CC FERROCYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF300575; AAG48588.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.

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DR PRINTS: PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT SEQUENCE 156 AA; 18513 MW; 7F32509B13AD420B CRC64;

Query Match 54.1%; Score 33; DB 8; Length 156;
Best Local Similarity 75.0%; Pred. NO. 1.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
1111111
Db 75 PQHFLGLM 82

RESULT 85
Q9HB06 PRELIMINARY; PRT; 159 AA.
AC Q9HB06;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 18.5 KDA PROTEIN (SIMILAR TO F-BOX AND WD-40 DOMAIN
DE PROTEIN 5).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.:
RT "Novel human cDNA clones with function of inhibiting cancer cell
RT growth."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=CERVIX CARCINOMA;
RA Strausberg R.:
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF217998; AAC17240.1; -.
DR EMBL: BC000850; AAH00850.1; -.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40.2.
DR SMART: SM00320; WD40.2.
DR PROSITE: PSS0082; WD_REPEATS.2; 1.
DR PROSITE: PSS0294; WD_REPEATS_REGION.1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 159 AA; 18545 MW; 2DDBBF5544D00E68 CRC64;

Query Match 54.1%; Score 33; DB 4; Length 159;
Best Local Similarity 62.5%; Pred. NO. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOOFF 8
1111111
Db 144 RPKPRTF 151

RESULT 86
Q9CV91 PRELIMINARY; PRT; 161 AA.
AC Q9CV91;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 2300004H16RIK PROTEIN (FRAGMENT).
GN 2300004H16RIK.
OS Mus musculus (Mouse).

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CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TONGUE;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Koshida H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Sessa T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection.";
 RT Nature 409:685-690(2001).
 RL EMBL: AK009028; BAB26036.1; -;
 DR MGD: MGI:1913752; 2300004H6GR1K.
 FT NON_TER 161 161
 SO SEQUENCE 161 AA; 18414 MW; 54C67BF91F6E0B17 CRC64;

Query Match 54.1%; Score 33; DB 11; Length 161;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOOFF 8
 111111
 Db 38 RPKPOOFF 45

RESULT 87
 09G7A3 PRELIMINARY; PRT; 192 AA.
 AC 09G7A3;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Brevineura rufitarsis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Brevineura.
 CC NCBI_TaxID=135662;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRUP143.2;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xylocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERRICYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005222; AAG24230.1; -;
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 192 192
 SO SEQUENCE 192 AA; 22364 MW; 54C417614E83D918 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 192;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
 111111
 Db 116 POOFFGLM 123

RESULT 88
 09G798 PRELIMINARY; PRT; 192 AA.
 AC 09G798;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xylocopa bombylans.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 CC Apoidea; Apidae; Xylocopa.
 CC NCBI_TaxID=135667;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DES.BOM;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xylocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005222; AAG24235.1; -;
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 192 192
 SO SEQUENCE 192 AA; 22133 MW; F25AF0200986BC0 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 192;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 |||
 DB 117 PQHFLGLM 124

RESULT 89

09G782 PRELIMINARY; PRT: 197 AA.
 AC 09G782;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xyllocopa varipuncta.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apidae; Apidae; Xyllocopa.
 OX NCBI_TaxID=135685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEO.VAR.
 RA Lays R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005245; AAG24231.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1.1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 197
 FT NON_TER 1 197
 SO SEQUENCE 197 AA; 22799 MW; 524729587C51DEB7 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 197;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 |||
 DB 116 PQHFLGLM 123

RESULT 90

09G7A2 PRELIMINARY; PRT: 198 AA.
 AC 09G7A2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xyllocopa micans (southern carpenter bee).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apidae; Apidae; Xyllocopa.
 OX NCBI_TaxID=135663;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SCH.MI2;
 RA Lays R., Cooper S.J.B., Schwarz M.B.;

RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005223; AAG24231.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1.1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 198
 FT NON_TER 1 198
 SO SEQUENCE 198 AA; 22749 MW; 1C18C71053A23E07 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 |||
 DB 117 PQHFLGLM 124

RESULT 91

09G7A1 PRELIMINARY; PRT: 198 AA.
 AC 09G7A1;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xyllocopa tranquebarica.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apidae; Apidae; Xyllocopa.
 OX NCBI_TaxID=135664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NYCTOI;
 RA Lays R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERRICYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AY005224; AAG24232.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
KM Copper: Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 198 AA; 22876 MW; B87C26FA7B716B78 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
DB 117 POFFGLM 124

RESULT 92
ID 09G799 PRELIMINARY; PRT; 198 AA.
AC 09G799;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Xylcopa violacea.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Xylcopa.
OX NCBI_TaxID=135666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X.VIOL3;
RA Leys R., Cooper S.J.B., Schwarz M.B.;
RT "Molecular phylogeny of the large carpenter bees, genus Xylcopa (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AY005226; AAG24234.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 198 AA; 22909 MW; 7B5511PCD129FE82 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
DB 117 POFFGLM 124

RESULT 93
ID 09G797 PRELIMINARY; PRT; 198 AA.
AC 09G797;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Xylcopa tabaniformis tabaniformis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Xylcopa.
OX NCBI_TaxID=135668;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOT01;
RA Leys R., Cooper S.J.B., Schwarz M.B.;
RT "Molecular phylogeny of the large carpenter bees, genus Xylcopa (Hymenoptera: Apidae) based on mitochondrial DNA sequences.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AY005228; AAG24236.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 198 AA; 22941 MW; 517DE2848CD0A53A CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
DB 117 POFFGLM 124

RESULT 94
ID 09G796 PRELIMINARY; PRT; 198 AA.
AC 09G796;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Xylcopa sicheli.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Xyllocopa.
OX NCBI_TaxID=135670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GENA.SIC2;
RA Lays R., Cooper S.J.B., Schwarz M.B.;
RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
(Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AY005230; AAG24237.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 198
SQ SEQUENCE 198 AA; 22911 MW; 3BB7A2DDDA4CC3BC CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 POEFGLM 11
|||
Db 117 PQHFLGLM 124

RESULT 95
09G795 PRELIMINARY; PRT; 198 AA.
AC 09G795;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Xyllocopa virginica virginica (common carpenter bee).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Xyllocopa.
OX NCBI_TaxID=135671;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=XO1D;
RA Lays R., Cooper S.J.B., Schwarz M.B.;
RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
(Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AY005234; AAG24240.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 198
SQ SEQUENCE 198 AA; 22932 MW; 9E20D0DF4109493C CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AY005231; AAG24238.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 198
SQ SEQUENCE 198 AA; 22892 MW; F48FB16F6A913010 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 POEFGLM 11
|||
Db 117 PQHFLGLM 124

RESULT 96
09G793 PRELIMINARY; PRT; 198 AA.
AC 09G793;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Xyllocopa aruana.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Xyllocopa.
OX NCBI_TaxID=135674;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KOP.TV2;
RA Lays R., Cooper S.J.B., Schwarz M.B.;
RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
(Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AY005234; AAG24240.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 198
SQ SEQUENCE 198 AA; 22932 MW; 9E20D0DF4109493C CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 POOFFGLM 11
 DB 117 PQHFLGLM 124

RESULT 97
 09G792 PRELIMINARY; PRT: 198 AA.

AC 09G792;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xyllocopa liefinckl.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Xyllocopa.
 NC NCBL_Taxid=135675;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KOP.AP1;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences."
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERRICYTOCHROME C.
 CC -1- CORFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005235; AAG24241.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1
 FT NON_TER 198
 FT SEQUENCE 198 AA; 22857 MW; EFE3E2ABA4FDE49B CRC64;
 SQ

Query Match 54.1%; Score 33; DB 8; Length 198;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 POOFFGLM 11
 DB 117 PQHFLGLM 124

RESULT 98
 09G791 PRELIMINARY; PRT: 198 AA.

AC 09G791;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xyllocopa pubescens.
 OG Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Xyllocopa.
 NC NCBL_Taxid=135676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KOP.IS1;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences."
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERRICYTOCHROME C.
 CC -1- CORFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005236; AAG24242.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1
 FT NON_TER 198
 FT SEQUENCE 198 AA; 22924 MW; 77DD3631F592908D CRC64;
 SQ

Query Match 54.1%; Score 33; DB 8; Length 198;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 POOFFGLM 11
 DB 117 PQHFLGLM 124

RESULT 99
 09G790 PRELIMINARY; PRT: 198 AA.

AC 09G790;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xyllocopa sciocensis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Xyllocopa.
 NC NCBL_Taxid=135677;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KOP.SA1;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences."
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AY005237; AAC24243.1; -.
DR InterPro: IPR000383; COX1.
DR Pfam: PF00115; COX1.
DR PRINTS: PR01165; CYCOXIDASE1.
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT 198
SQ SEQUENCE 198 AA; 22950 MW; FA187D7A98E3CEBD CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFGLM 11
1111111
DB 117 POHFGLM 124

RESULT 100
09G789 PRELIMINARY; PRT; 198 AA.
AC 09G789;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Xylocopa nigrita.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Xylocopa.
OX NCBI_TaxID=135678;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AFR.NIG;
RA Leys R., Cooper S.J.B., Schwarz M.B.;
RT "Molecular phylogeny of the large carpenter bees, genus Xylocopa
(Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BINERALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AY005238; AAC24244.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.
DR PRINTS: PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
FT Respiratory chain; Transmembrane.
FT NON_TER 1
FT 198
SQ SEQUENCE 198 AA; 22966 MW; 67D0AD3C3CD21F032 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;

Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFGLM 11
1111111
DB 117 POHFGLM 124

RESULT 101
09G788 PRELIMINARY; PRT; 198 AA.
AC 09G788;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Xylocopa flavoviridis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Xylocopa.
OX NCBI_TaxID=135679;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MESOTRIAL;
RA Leys R., Cooper S.J.B., Schwarz M.B.;
RT "Molecular phylogeny of the large carpenter bees, genus Xylocopa
(Hymenoptera: Apoidea) based on mitochondrial DNA sequences.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BINERALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AY005239; AAC24245.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.
DR PRINTS: PR01165; CYCOXIDASE1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
FT Respiratory chain; Transmembrane.
FT NON_TER 1
FT 198
SQ SEQUENCE 198 AA; 23006 MW; 2D52B4848E335E50 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFGLM 11
1111111
DB 117 POHFGLM 124

RESULT 102
09G787 PRELIMINARY; PRT; 198 AA.
AC 09G787;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Xylocopa olivieri.

06 Mitochondrion.
 0C Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 0C Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 0C Apoidea; Apidae; Xyllocopa.
 0X NCBI_TaxID=135680;
 0X [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PRO.OLI;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences."
 RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005240: AAG24246.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 RW Respiratory chain; Transmembrane.
 KW NON_TER 1 1
 FT NON_TER 198 198
 SQ SEQUENCE 198 AA; 22906 MW; DC53442DAB0B250E CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
 11 1111
 DB 117 PQOFFGLM 124

RESULT 103
 09G786 PRELIMINARY; PRT; 198 AA.
 ID 09G786;
 AC 09G786;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xyllocopa latipes.
 OG Mitochondrion.
 0C Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 0C Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 0C Apoidea; Apidae; Xyllocopa.
 0X NCBI_TaxID=135681;
 0X [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PLA.B24;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences."
 RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3

CC AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005241: AAG24247.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 RW Respiratory chain; Transmembrane.
 KW NON_TER 1 1
 FT NON_TER 198 198
 SQ SEQUENCE 198 AA; 22917 MW; A36BB24512DDB00 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
 11 1111
 DB 117 PQOFFGLM 124

RESULT 104
 09G785 PRELIMINARY; PRT; 198 AA.
 ID 09G785;
 AC 09G785;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xyllocopa acutipennis.
 OG Mitochondrion.
 0C Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 0C Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 0C Apoidea; Apidae; Xyllocopa.
 0X NCBI_TaxID=135682;
 0X [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HOPL0.T6;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xyllocopa
 (Hymenoptera: Apidae) based on mitochondrial DNA sequences."
 RL Submitted (Jul-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005242: AAG24248.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 RW Respiratory chain; Transmembrane.
 KW NON_TER 1 1
 FT NON_TER 198 198
 SQ SEQUENCE 198 AA; 22896 MW; 219F5F376DCDF4C6 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1 111
 Db 117 PQHFLGLM 124

RESULT 105

096784 PRELIMINARY; PRT; 198 AA.

AC 096784;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xylocopa appendiculata circumvolans.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Xylocopa.
 OX NCBI_Taxid=135722;
 RN [1]
 RC STRAIN=ALLO1;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xylocopa (Hymenoptera: Apidae) based on mitochondrial DNA sequences."; Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4 FERRICYTOCHROME C
 CC -1- COPFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005243; AAC24249.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1.1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane.
 FT NON_TER 1 198
 FT NON_TER 198 198
 SQ SEQUENCE 198 AA; 22931 MW; C4A8B9DE7D3C9E19 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1 111
 Db 117 PQHFLGLM 124

RESULT 106

096783 PRELIMINARY; PRT; 198 AA.

AC 096783;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xylocopa micheneri micheneri.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Xylocopa.
 OX NCBI_Taxid=135684;
 RN [1]
 RC STRAIN=STENO1;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xylocopa (Hymenoptera: Apidae) based on mitochondrial DNA sequences."; Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4 FERRICYTOCHROME C.
 CC -1- COPFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AY005244; AAC24250.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1.1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase; Respiratory chain; Transmembrane.
 FT NON_TER 1 198
 FT NON_TER 198 198
 SQ SEQUENCE 198 AA; 22936 MW; B43C82E6E1731454 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 198;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1 111
 Db 117 PQHFLGLM 124

RESULT 107

096781 PRELIMINARY; PRT; 198 AA.

AC 096781;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Xylocopa gualanensis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Xylocopa.
 OX NCBI_Taxid=135686;
 RN [1]
 RC STRAIN=NEO.NOTO1;
 RA Leys R., Cooper S.J.B., Schwarz M.B.;
 RT "Molecular phylogeny of the large carpenter bees, genus Xylocopa (Hymenoptera: Apidae) based on mitochondrial DNA sequences."; Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2

Query Match 54.1%; Score 33; DB 2; Length 211;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 KPOOFFGLM 11
 11:11111
 Db 16 KPGFFGLM 24

RESULT 111

OY 09RRAS PRELIMINARY; PRT; 234 AA.
 AC 09RRAS;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CONSERVED HYPOTHEICAL PROTEIN.
 GN DR2585.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RI;
 RX MEDLINE=20036896; Pubmed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1.";
 RL Science 286:1571-1577(1999).
 DR EMBL: AF002088; AAF12124.1; -.
 DR HSPB; 026253; 1E2E.
 DR TIGR; DR2585; -.
 DR InterPro; IPR002040; Tachykinin.
 DR PROSITE; PS00267; TACHYKININ; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 234 AA; 25176 MW; 37CEA57E6847F70 CRC64;

Query Match 54.1%; Score 33; DB 2; Length 234;
 Best Local Similarity 75.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PPOFFGLM 11
 1111111
 Db 56 PYSFFGLM 63

RESULT 112

ID 09CR69 PRELIMINARY; PRT; 240 AA.
 AC 09CR69;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE 2300004H16RIK PROTEIN.
 GN 2300004H16RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE=EMBRYO;
 RX MEDLINE=21085660; Pubmed=11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Araiwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuk S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK019970; BAB31941.1; -.
 DR EMBL: AK012917; BAB28548.1; -.
 DR MGI; MGI:1913752; 2300004H16RIK.
 SQ SEQUENCE 240 AA; 28034 MW; 17DCB43406E5A309 CRC64;

Query Match 54.1%; Score 33; DB 11; Length 240;
 Best Local Similarity 75.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOOFF 8
 1111111
 Db 38 RPNPOAF 45

RESULT 113

ID 09TGG7 PRELIMINARY; PRT; 265 AA.
 AC 09TGG7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Halictus farinosus.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoidea; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.
 OX NCBI_TaxID=77575;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N., Mitchell P.L., Packer L.;
 RT "Mitochondrial DNA differentiation between two cryptic Halictus
 RT (Hymenoptera: Halictidae) species.";
 RL Ann. Entomol. Soc. Amer. 91:387-391(1998).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTONS ORIGINATING IN
 CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) - 2 H(2)O + 4
 CC FE(II)CYTOCHROME C.
 CC -1- FACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF045372; AAD47364.1; -.
 DR InterPro; IPR000883; COX1.
 DR Pfam; PF00115; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 265 265

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF045377; AAD47369.1; -.
 DR InterPro: IPR000883; COX1.1.
 DR Pfam: PF00115; COX1.1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT 266 266
 SQ SEQUENCE 266 AA; 30290 MW; A9CF473DA4E74910 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 266;
 Best Local Similarity 75.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQDFGLM 11
 111111
 DB 184 PQHFLGLM 131

RESULT 117
 O9T2M6 PRELIMINARY; PRT; 266 AA.
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Halictus ligatus.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoecrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.
 ON NCBI_TaxID=77576;
 RP SEQUENCE FROM N.A.
 RA Danforth B.N., Mitchell P.L., Packer L.;
 RT "Mitochondrial DNA differentiation between two cryptic Halictus
 RT (Hymenoptera: Halictidae) species.";
 RL Ann. Entomol. Soc. Amer. 91:387-391(1998).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 CC AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF045375; AAD47367.1; -.
 DR EMBL: AF045374; AAD47366.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1.1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT 266 266
 SQ SEQUENCE 266 AA; 30308 MW; 1DCF473DA4E1E57A CRC64;

Query Match 54.1%; Score 33; DB 8; Length 266;
 Best Local Similarity 75.0%; Pred. No. 2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQDFGLM 11
 111111
 DB 184 PQHFLGLM 191

RESULT 118
 O53361 PRELIMINARY; PRT; 299 AA.
 ID O53361
 AC O53361
 DT 01-JUN-1998 (TREMblrel. 06, Created)
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
 DE PUTATIVE ACID PHOSPHATASE.
 GN RV3310 OR MTV016.09.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 ON NCBI_TaxID=1773;
 RP SEQUENCE FROM N.A.
 RA STRAIN-H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogan A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrall B.G.;
 RT Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 DR EMBL: AL021841; CA117082.1; -.
 DR TubercuList; RV3310; -.
 KM Complete proteome.
 SQ SEQUENCE 299 AA; 31807 MW; C5E8C49CF62C8B8F8 CRC64;

Query Match 54.1%; Score 33; DB 2; Length 299;
 Best Local Similarity 66.7%; Pred. No. 2.3e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPQDFGL 10
 111111
 DB 181 PKPNYRGL 189

RESULT 119
 O9NE15 PRELIMINARY; PRT; 299 AA.
 ID O9NE15
 AC O9NE15
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE HYPOTHETICAL 32.7 KDA PROTEIN.
 GN I5808.12.
 OS Leishmania major.
 OC Eukaryota; Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.
 ON NCBI_TaxID=5664;
 RP SEQUENCE FROM N.A.
 RA STRAIN-FRIEDLIN;
 RA Masuy D., Purnelle B., Goffeau A., Ivens A.C., Quail M.,
 RA Rajandream M.A., Barrall B.G.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN-FRIEDLIN;
 RX MEDLINE=9816435; PubMed=9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;

```
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AJ354572; CAB89649.1; -.
KW Hypothetical protein.
SQ SEQUENCE 299 AA; 32690 MW; AE7F37FB37BDADC0 CRC64;

Query Match 54.1%; Score 33; DB 5; Length 299;
Best Local Similarity 55.6%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKPOFFGL 10
   |||:| |
Db 141 PKPEFTGV 149

RESULT 120
086462
ID 086462 PRELIMINARY; PRT; 301 AA.
AC 086462;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FHU.
GN FHU.
OS Rhizobium leguminosarum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_Taxid=384;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8401(PRLJ1);
RA Stevens J.B., Johnston A.W.B.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE OF 9-301 FROM N.A.
RC STRAIN=8401(PRLJ1);
RA MEDLINE=99231845; PubMed=10217493;
RX Stevens J.B., Carter R.A., Hussain H., Carson K.C., Dilworth M.J.,
  Johnston A.W.B.;
RA "The fhu genes of Rhizobium leguminosarum, specifying siderophore
  uptake proteins: fhuD are adjacent to a pseudogene version of
  fhuA.";
RL Microbiology 145:593-601(1999).
DR EMBL; AJ007906; CAA07723.1; -.
DR EMBL; AJ007906; CAA07724.1; -.
DR InterPro; IPR002491; Peripla_BP.
DR Pfam; PF01497; Peripla_BP_2; 1.
SQ SEQUENCE 301 AA; 33073 MW; BB0B3723B6C987EC CRC64;

Query Match 54.1%; Score 33; DB 2; Length 301;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOFFGL 11
   |||:| |
Db 284 PRPMFAGIL 293

RESULT 121
083931
ID 083931 PRELIMINARY; PRT; 320 AA.
AC 083931;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE MEMBRANE FUSION PROTEIN, PUTATIVE.
GN TP0965.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_Taxid=160;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=NITC10LS;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
  Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
  Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
  Khalak H., Richardson P., Howell J.K., Chidambaram M., Uterback T.,
  McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
  Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
  Venter J.C.;
RA "Complete genome sequence of Treponema pallidum, the syphilis
  agent spirochete.";
RL Science 281:375-388(1998).
DR EMBL; AE001264; AAC65920.1; -.
DR TIGR; TP0965; -.
KW Complete proteome.
SQ SEQUENCE 320 AA; 35353 MW; 860841FE865B70BC CRC64;

Query Match 54.1%; Score 33; DB 2; Length 320;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 KPOFFGL 11
   |||:| |
Db 162 KPDIYFCTL 170

RESULT 122
09R2U3
ID 09R2U3 PRELIMINARY; PRT; 327 AA.
AC 09R2U3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TRANSPOSASE, PUTATIVE.
GN DR80020.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_Taxid=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1.
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
  Dodson R.J., Haft D.H., Gwin M.L., Nelson W.C., Richardson D.L.,
  Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
  Vamathevan J.J., Lam P., McDonald L., Uterback T., Zaleski C.,
  Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann K.D.,
  Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
  Fraser C.M.;
RA "Genome sequence of the radioresistant bacterium Deinococcus
  radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL; AE001826; AAF12398.1; -.
DR TIGR; DRB0020; -.
KW Plasmid; Complete proteome.
SQ SEQUENCE 327 AA; 37956 MW; 2FACFA526D0BF569 CRC64;

Query Match 54.1%; Score 33; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOFFGL 11
   |||:| |
Db 297 RPKPOFFAIL 307

RESULT 123
09R2R1
ID 09R2R1 PRELIMINARY; PRT; 327 AA.
```

AC Q9R2R1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSPOSASE, PUTATIVE.
GN DRB0057.
OS Deinococcus radiodurans.
OG Plasmid MPl.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Uterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL: AE001826; AAF12602.1; -;
DR TIGR: DRB0057; -;
KW Plasmid; Complete proteome.
SQ SEQUENCE 327 AA; 38026 MW; 972646ABAFE4DE0 CRC64;

Query Match 54.18; Score 33; DB 2; Length 327;
Best Local Similarity 54.58; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPOFFGLM 11
| | | | | : :
Db 297 RPKPOFFMAIL 307

RESULT 124
Q9R2J3
ID Q9R2J3; PRELIMINARY; PRT; 327 AA.
AC Q9R2J3;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSPOSASE, PUTATIVE.
GN DRB0134.
OS Deinococcus radiodurans.
OG Plasmid MPl.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Uterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL: AE001826; AAF12606.1; -;
DR TIGR: DRB0134; -;
KW Plasmid; Complete proteome.
SQ SEQUENCE 327 AA; 38018 MW; ED4DAD9413470AC CRC64;

Query Match 54.18; Score 33; DB 2; Length 327;

Best Local Similarity 54.58; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPOFFGLM 11
| | | | | : :
Db 297 RPKPOFFMAIL 307

RESULT 125
Q9RY10
ID Q9RY10; PRELIMINARY; PRT; 327 AA.
AC Q9RY10;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSPOSASE, PUTATIVE.
GN DR0144.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Uterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL: AE001876; AAF09729.1; -;
DR TIGR: DR0144; -;
KW Complete proteome.
SQ SEQUENCE 327 AA; 37974 MW; 2B8BF12290FB169 CRC64;

Query Match 54.18; Score 33; DB 2; Length 327;
Best Local Similarity 54.58; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RPKPOFFGLM 11
| | | | | : :
Db 297 RPKPOFFMAIL 307

RESULT 126
Q9R3L4
ID Q9R3L4; PRELIMINARY; PRT; 327 AA.
AC Q9R3L4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSPOSASE, PUTATIVE.
GN DRB0005 OR DRB0102.
OS Deinococcus radiodurans.
OG Plasmid MPl.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Uterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;

RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RI.":
RL Science 286:1571-1577(1999).
DR EMBL; AE001826; AAF12607.1; -.
DR EMBL; AE001826; AAF12603.1; -.
DR TIGR; DRB0005; -.
DR TIGR; DRB0102; -.
KM Plasmid: Complete proteome.
SQ SEQUENCE 327 AA; 37960 MW; 5FRCAD9AC84EB57D CRC64;

Query Match 54.1%; Score 33; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOOFFGLM 11
Db 297 RPKPOOFFMAIL 307

RESULT 127

O9CP29 PRELIMINARY; PRT; 334 AA.
AC O9CP29;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE DPPP.
GN DPPP OR PM0237.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxId=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
CC PROTEIN-DEPENDENT TRANSPORT SYSTEMS.
DR EMBL; AE006058; AAK02321.1; -.
DR InterPro: IPR000515; BPD.transp.
DR Pfam: PF00528; BPD.transp. 1.
DR PROSITE: PS00402; BPD_TRANS_PNN_MEMBR; 1.
KM Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 334 AA; 37057 MW; 7979D793F7C9B1A8 CRC64;

Query Match 54.1%; Score 33; DB 2; Length 334;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOFF 8
Db 60 RPLPEQYF 67

RESULT 128

O9B210 PRELIMINARY; PRT; 390 AA.
AC O9B210;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BA702N8.1 (FYN-RELATED KINASE) (FRAGMENT).
OX FRK.
RN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd C.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL357141; CAC27542.1; -.
KM Kinase.
FT NON_TER
SQ SEQUENCE 390 AA; 44994 MW; F9C5984DEIDCD09 CRC64;

Query Match 54.1%; Score 33; DB 4; Length 390;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
Db 344 POOFFNIM 351

RESULT 129

O95684 PRELIMINARY; PRT; 399 AA.
AC O95684;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE FGFR1 ONCOGENE PARTNER (FOP).
GN FOP.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99135870; PubMed=9949182;
RA Popovici C., Zhang B., Gregoire M.J., Jonveaux P.,
RA Lafage-Pochitaloff M., Birbaud D., Pebusque M.J.;
RT "The t(6;8)(q27;p11) translocation in a stem cell myeloproliferative
RT disorder fuses a novel gene, FOP, to fibroblast growth factor receptor
RT 1".
RL Blood 93:1381-1389(1999).
DR EMBL; Y18046; CAA77020.1; -.
SQ SEQUENCE 399 AA; 43064 MW; 7A4B65F627B9D272 CRC64;

Query Match 54.1%; Score 33; DB 4; Length 399;
Best Local Similarity 55.6%; Pred. No. 3.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKPOOFFGL 10
Db 261 PKPEKTYGL 269

RESULT 130

O9TCF5 PRELIMINARY; PRT; 405 AA.
AC O9TCF5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS LasioGLOSSUM lustrans.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; LasioGLOSSUM.
OX NCBI_TaxId=88524;
RN [1]

RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus *Lasloglossum* (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999)
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER 3 (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICCYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF104643; AAF14158.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1
FT TER 405
SQ SEQUENCE 405 AA; 45511 MW; 7EA7D84C2074C929 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 405;
Best Local Similarity 75.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQOFFGLM 11
Db 324 PQHFLGLM 331

RESULT 131
Q9B4P4 PRELIMINARY; PRT; 407 AA.
AC Q9B4P4;
DT 01-JUN-2001 (TREMBLREL. 17, Created)
DT 01-JUN-2001 (TREMBLREL. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE CYTOCHROME OXIDASE SUBUNIT I (FRAGMENT).
OS Diadasia australis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Diadasiinae.
OX NCBI_TaxID=143975;
RN [1]
RP SEQUENCE FROM N.A.
RA Stiles S.D., Wolf P.G.;
RT "Phylogenetic relationships within Diadasiinae, a group of specialist
bees";
RL Submitted (ANG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF300529; AAK20573.1; -.
KW Mitochondrion.
FT NON_TER 1
FT TER 407
SQ SEQUENCE 407 AA; 46368 MW; 8CEA48F5D9ACD9D4 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 407;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQOFFGLM 11
Db 326 PQHFLGLM 333

RESULT 132
Q9XP15 PRELIMINARY; PRT; 409 AA.
AC Q9XP15;
DT 01-NOV-1999 (TREMBLREL. 12, Created)
DT 01-NOV-1999 (TREMBLREL. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
OS Apanteles canariensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Ichneumonidae; Braconidae; Microgasterinae; Apanteles.
OX NCBI_TaxID=92962;
RN [1]
RP SEQUENCE FROM N.A.
RA Mardulyn P., Whitfield J.B.;
RT "Phylogenetic signal in the COI, 16S, and 28S genes for inferring
relationships among genera of Microgasterinae (Hymenoptera;
Braconidae): evidence of a high diversification rate in this group of
parasitoids";
RL Mol. Phylogenet. Evol. 0:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICCYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF102703; AAD40857.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1
FT TER 409
SQ SEQUENCE 409 AA; 46433 MW; 9FF4509A5DC374FC CRC64;

Query Match 54.1%; Score 33; DB 8; Length 409;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 PQOFFGLM 11
Db 331 PQHFLGLM 338

RESULT 133
Q9B4P2 PRELIMINARY; PRT; 411 AA.
AC Q9B4P2;
DT 01-JUN-2001 (TREMBLREL. 17, Created)
DT 01-JUN-2001 (TREMBLREL. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE CYTOCHROME OXIDASE SUBUNIT I (FRAGMENT).
OS Diadasiinae.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Diadasiinae.
OX NCBI_TaxID=143976;
RN [1]

RP SEQUENCE FROM N.A.
 RA Sipes S.D., Wolf P.G.;
 RT "Phylogenetic relationships within Diadasia, a group of specialist
 bees."
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF300530; AAK20575.1; -
 KW Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 411 411
 SQ SEQUENCE 411 AA; 46637 MW; 3ABDAX7CEB92B6E CRC64;

Query Match 54.1%; Score 33; DB 8; Length 411;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
 |||
 DB 332 POHFLGLM 339

RESULT 134
 O9G464 PRELIMINARY; PRT; 412 AA.
 ID O9G464;
 AC O9G464;
 DT 01-MAR-2001 (TREMBLREL. 16, Created)
 DT 01-MAR-2001 (TREMBLREL. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 OS Diadasia laticauda.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Diadasia.
 OX NCBI_TaxID=143982;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sipes S.D., Wolf P.G.;
 RT "Phylogenetic relationships within Diadasia, a group of specialist
 bees."
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
 FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF300521; AAG45968.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 412 412
 SQ SEQUENCE 412 AA; 47166 MW; 63F6CFE500F74B71 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 412;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
 |||
 DB 331 POHFLGLM 338

RESULT 135
 O9B4M3 PRELIMINARY; PRT; 412 AA.
 ID O9B4M3;
 AC O9B4M3;
 DT 01-JUN-2001 (TREMBLREL. 17, Created)
 DT 01-JUN-2001 (TREMBLREL. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
 DE CYTOCHROME OXIDASE SUBUNIT I (FRAGMENT).
 OS Meliphiopsis sp. BBSL-209588.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Meliphilopsis.
 OX NCBI_TaxID=143966;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sipes S.D., Wolf P.G.;
 RT "Phylogenetic relationships within Diadasia, a group of specialist
 bees."
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF300549; AAK20613.1; -
 KW Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 412 412
 SQ SEQUENCE 412 AA; 46994 MW; 0E6D5420BD58AC97 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 412;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
 |||
 DB 331 POHFLGLM 338

RESULT 136
 O9B4K0 PRELIMINARY; PRT; 412 AA.
 ID O9B4K0;
 AC O9B4K0;
 DT 01-JUN-2001 (TREMBLREL. 17, Created)
 DT 01-JUN-2001 (TREMBLREL. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
 DE CYTOCHROME OXIDASE SUBUNIT I (FRAGMENT).
 OS Diadasia tuberculifrons.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Diadasia.
 OX NCBI_TaxID=143992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sipes S.D., Wolf P.G.;
 RT "Phylogenetic relationships within Diadasia, a group of specialist
 bees."
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF300567; AAK20649.1; -
 KW Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 412 412
 SQ SEQUENCE 412 AA; 46828 MW; 6E781E7F98B2DB38 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 412;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
 |||
 DB 331 POHFLGLM 338

RESULT 137
ID 09TEC4 PRELIMINARY: PRT: 413 AA.
AC 09TEC4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum medipolillum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88484;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF103957; AAF14080.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1.
DR PRINTS; PR01165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1.1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT 413 413
SQ SEQUENCE 413 AA; 46590 MW; 52064ACD9D9D6C85 CRC64;

Query Match 54.18; Score 33; DB 8; Length 413;
Best Local Similarity 75.08; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
|||
Db 332 POHFLGLM 339

RESULT 138
ID 09TCL2 PRELIMINARY: PRT: 413 AA.
AC 09TCL2;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Agapostemon kohliellus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Agapostemon.
OX NCBI_TaxID=88594;
RN [1]
RP SEQUENCE FROM N.A.

RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF102833; AAF04748.1; -.
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1.
DR PRINTS; PR01165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1.1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT 413 413
SQ SEQUENCE 413 AA; 46760 MW; 2784C73AE626101 CRC64;

Query Match 54.18; Score 33; DB 8; Length 413;
Best Local Similarity 75.08; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
|||
Db 332 POHFLGLM 339

RESULT 139
ID 09TCL1 PRELIMINARY: PRT: 413 AA.
AC 09TCL1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Agapostemon sericeus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Agapostemon.
OX NCBI_TaxID=88595;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF102834; AAF04749.1; -.

DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 413
SQ SEQUENCE 413 AA; 46893 MW; F5D3BC2C8A998A75 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
1111111
Db 332 PQHFLGLM 339

RESULT 140
O9TCKL0 PRELIMINARY; PRT; 413 AA.
AC O9TCKL0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Agapostemon tyleri.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Agapostemon.
OX NCBI_TaxID=88596;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF102835; AAF04750.1; -
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 413
SQ SEQUENCE 413 AA; 46813 MW; 2752202431487D91 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 PQOFFGLM 11
1111111
Db 332 PQHFLGLM 339

RESULT 141
O9TCK9 PRELIMINARY; PRT; 413 AA.
AC O9TCK9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Agapostemon viequesensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Agapostemon.
OX NCBI_TaxID=88597;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF102836; AAF04751.1; -
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 413
SQ SEQUENCE 413 AA; 46785 MW; A31278D249EA0992 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 PQOFFGLM 11
1111111
Db 332 PQHFLGLM 339

RESULT 142
O9TCK8 PRELIMINARY; PRT; 413 AA.
AC O9TCK8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Halictus confusus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.
OX NCBI_TaxID=88589;
RN [1]

RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus *LasioGLOSSUM* (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL; AF102837; AAF04752.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46706 MW; 2756DAA10ECC98A4 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1111
 DB 332 PQOFFGLM 339

RESULT 143
 O9TCK7 PRELIMINARY; PRT; 413 AA.
 AC 09TCK7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE 1 (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Halictus farinosus.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.
 OX NCBI_TaxID=77575;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus *LasioGLOSSUM* (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL; AF102837; AAF04754.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46532 MW; E06C6135A9A88719 CRC64;

DR EMBL; AF102838; AAF04753.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46551 MW; 93BC11F7D9B7CAF8 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1111
 DB 332 PQOFFGLM 339

RESULT 144
 O9TCK6 PRELIMINARY; PRT; 413 AA.
 AC 09TCK6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE 1 (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Halictus poeyi.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.
 OX NCBI_TaxID=77577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus *LasioGLOSSUM* (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL; AF102839; AAF04754.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS; PR01165; CYCOXIDASE1.
 DR PROSITE; PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46532 MW; E06C6135A9A88719 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1111

Db 332 PQHFLGLM 339

RESULT 145

09TCK3 PRELIMINARY; PRT; 413 AA.

AC 09TCK5; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

GN COI.

OS Halictus ligatus.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.

OX NCBI_TaxID=77576;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT "Phylogeny of the bee genus Lasiglossus (Hymenoptera: Halictidae) based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

CC -1- FERROCYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

DR EMBL: AF102840; AAF04755.1; -.

DR InterPro: IPR000883; COX1.

DR Pfam: PF00115; COX1.1.

DR PRINTS: PR01165; CYCOXIDASE1.

DR PROSITE: PS00077; COX1.1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.

FT NON_TER 1

FT NON_TER 413

SO SEQUENCE 413 AA; 46573 MW; 588FF805C2D6A667 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;

Best Local Similarity 75.0%; Pred. No. 3.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQHFLGLM 11

Db 332 PQHFLGLM 339

RESULT 146

09TCK4 PRELIMINARY; PRT; 413 AA.

AC 09TCK4; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

GN COI.

OS Halictus poeyi.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.

OX NCBI_TaxID=77577;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT "Phylogeny of the bee genus Lasiglossus (Hymenoptera: Halictidae) based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

CC -1- FERROCYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

DR EMBL: AF102841; AAF04756.1; -.

DR InterPro: IPR000883; COX1.

DR Pfam: PF00115; COX1.1.

DR PRINTS: PR01165; CYCOXIDASE1.

DR PROSITE: PS00077; COX1.1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.

FT NON_TER 1

FT NON_TER 413

SO SEQUENCE 413 AA; 46543 MW; 265AD8259F877825 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;

Best Local Similarity 75.0%; Pred. No. 3.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQHFLGLM 11

Db 332 PQHFLGLM 339

RESULT 147

09TCK3 PRELIMINARY; PRT; 413 AA.

AC 09TCK3; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).

GN COI.

OS Halictus rubicundus.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Halictus.

OX NCBI_TaxID=77578;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;

RT "Phylogeny of the bee genus Lasiglossus (Hymenoptera: Halictidae) based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

CC -1- FERROCYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF102842; AAF04757.1; -
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46748 MW; A11B06DC9A2ADDC CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
DB 332 PQHFLGLM 339

RESULT 148
Q9TCK2 PRELIMINARY; PRT; 413 AA.
AC Q9TCK2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Mexalictus arizonensis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Mexalictus.
OX NCBI_TaxID=85398;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data."
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF102843; AAF04758.1; -
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46775 MW; C5053197B478563 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11

DB 332 PQHFLGLM 339

RESULT 149
Q9TCK1 PRELIMINARY; PRT; 413 AA.
AC Q9TCK1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Sphecodes minor.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Sphecodes.
OX NCBI_TaxID=85399;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data."
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF102844; AAF04759.1; -
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46913 MW; C0AB94DA87069F2 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
DB 332 PQHFLGLM 339

RESULT 150
Q9TCK0 PRELIMINARY; PRT; 413 AA.
AC Q9TCK0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS LasioGLOSSUM convexum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; LasioGLOSSUM.

OX NCBI_TaxID=88480;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus *Lasloglossum* (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 H⁺
 CC -1- FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF103951; AAF14074.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KN Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46624 MW; E4392FMA4930B278 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGLM 11
 |||
 Db 332 PQHFLGLM 339

RESULT 151
 O9TCJ9 PRELIMINARY; PRT: 413 AA.
 AC O9TCJ9; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum conspicuum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoecita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88479;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus *Lasloglossum* (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 H⁺
 CC -1- FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF103952; AAF14075.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KN Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46552 MW; AFBED43EBD1BF88 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGLM 11
 |||
 Db 332 PQHFLGLM 339

RESULT 152
 O9TCJ8 PRELIMINARY; PRT: 413 AA.
 AC O9TCJ8; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum cognatum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoecita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88478;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus *Lasloglossum* (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 H⁺
 CC -1- FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF103953; AAF14076.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KN Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46567 MW; D24FCEE382033F3 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


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CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103956; AAF14079.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 413
SQ SEQUENCE 413 AA; 46594 MW; 904A10DE4121240A CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
DB 332 PQHFLGLM 339

RESULT 156
Q9TJC4 PRELIMINARY; PRT; 413 AA.
AC Q9TJC4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI;
OS Lasloglossum mirandum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88486;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
    based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
    CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
    3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
    CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
    CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
    AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
    AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
    FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103958; AAF14081.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 413
SQ SEQUENCE 413 AA; 46600 MW; 3069F02ED575037D CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 4 PQOFFGLM 11
DB 332 PQHFLGLM 339

RESULT 157
Q9TJC3 PRELIMINARY; PRT; 413 AA.
AC Q9TJC3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI;
OS Lasloglossum parasphecodum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88486;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
    based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
    CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
    3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
    CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
    CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
    AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
    AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
    FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103959; AAF14082.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 413
SQ SEQUENCE 413 AA; 46675 MW; E2840F36A36E9806 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
DB 332 PQHFLGLM 339

RESULT 158
Q9TJC2 PRELIMINARY; PRT; 413 AA.
AC Q9TJC2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI;
OS Lasloglossum cressoni1.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; LasioGLOSSUM.
OX NCBI_TaxID=88489;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103963; AAF14086.1; --
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46572 MW; D71006CA01E29CC2 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
DB 332 POFHFLGLM 339

RESULT 159
O9TCJ1 PRELIMINARY; PRT; 413 AA.
AC O9TCJ1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS LasioGLOSSUM cuprelicolle.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; LasioGLOSSUM.
OX NCBI_TaxID=88450;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
FERRICYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103964; AAF14087.1; --
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46646 MW; 9CFE64F7E68448D6 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
DB 332 POFHFLGLM 339

RESULT 160
O9TCJ0 PRELIMINARY; PRT; 413 AA.
AC O9TCJ0:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS LasioGLOSSUM gundlachii.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; LasioGLOSSUM.
OX NCBI_TaxID=88491;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus LasioGLOSSUM (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103965; AAF14088.1; --
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46797 MW; 8E706566A052E577 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGLM 11
111111
DB 332 PQOFGLM 339

RESULT 161

O9TC19 PRELIMINARY: PRT: 413 AA.
AC O9TC19: 01-MAY-2000 (TREMBLREL. 13, Created)
DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum hyalinum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88492;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF103966; AAF14089.1; -
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT 413 413
SQ SEQUENCE 413 AA; 46616 MW; 80B4F5724DC71914 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGLM 11
111111
DB 332 PQOFGLM 339

RESULT 162
O9TC19 PRELIMINARY: PRT: 413 AA.
AC O9TC19: 01-MAY-2000 (TREMBLREL. 13, Created)
DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum imitatum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88493;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF103967; AAF14090.1; -
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT 413 413
SQ SEQUENCE 413 AA; 46754 MW; 25FF845E518E90B3 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGLM 11
111111
DB 332 PQOFGLM 339

RESULT 163
O9TC19 PRELIMINARY: PRT: 413 AA.
AC O9TC19: 01-MAY-2000 (TREMBLREL. 13, Created)
DT 01-MAY-2000 (TREMBLREL. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLREL. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum parvum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88494;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103968; AAF14091.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PRO1165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46646 MW; 25C3C451CEB8AAEE CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
1111111
Db 332 POHFLGLM 339

RESULT 164
O9TC16 PRELIMINARY; PRT; 413 AA.
AC O9TC16;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum pilosum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88495;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICCYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103969; AAF14092.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PRO1165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46586 MW; 9EB109D1E87B135E CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
1111111
Db 332 POHFLGLM 339

RESULT 165
O9TC15 PRELIMINARY; PRT; 413 AA.
AC O9TC15;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum rohweri.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88496;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICCYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103970; AAF14093.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PRO1165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413 413
SQ SEQUENCE 413 AA; 46646 MW; 542C37934BEDCDP4 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
1111111
Db 332 POHFLGLM 339

RESULT 166
O9TC14 PRELIMINARY; PRT; 413 AA.
AC O9TC14;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum tegulare.
OC Mitochondrion.

CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
CC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88497;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
RT based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HERE A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: AF103971; AAF14094.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46634 MW; 97BED229E977472A CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
|||
Db 332 PQHFLGLM 339

RESULT 167
09TC13 PRELIMINARY; PRT; 413 AA.
AC 09TC13;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum vierecki.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88497;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
RT based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HERE A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4

CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: AF103972; AAF14095.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46533 MW; 804CD6287DFC43F5 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
|||
Db 332 PQHFLGLM 339

RESULT 168
09TC12 PRELIMINARY; PRT; 413 AA.
AC 09TC12;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum umbrilipenne.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88498;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
RT based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HERE A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: AF103975; AAF14098.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 1
FT NON_TER 413 413
SQ SEQUENCE 413 AA; 46611 MW; 797998620C724B9D CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;

Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
11 1 111
Db 332 POHFLGLM 339

RESULT 169

09TC11 PRELIMINARY; PRT; 413 AA.
AC 09TC10; 09TC10; PRELIMINARY; PRT; 413 AA.
DT 01-MAY-2000 (TREMUREL. 13, Created)
DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)
DT 01-JUN-2001 (TREMUREL. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum albidipes.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88501;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data."
RL Syst. Entom. 24:0-(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103976; AAF14099.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 413
FT NON_TER 1 413
SQ SEQUENCE 413 AA; 46780 MW; 0CEAICE291B2BA58 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
11 1 111
Db 332 POHFLGLM 339

RESULT 170

09TC10 PRELIMINARY; PRT; 413 AA.
AC 09TC10; 09TC10; PRELIMINARY; PRT; 413 AA.
DT 01-MAY-2000 (TREMUREL. 13, Created)
DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)
DT 01-JUN-2001 (TREMUREL. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum albidipes.

06 Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88501;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data."
RL Syst. Entom. 24:0-(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103977; AAF14100.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KM Respiratory chain; Transmembrane.
FT NON_TER 1 413
FT NON_TER 1 413
SQ SEQUENCE 413 AA; 46762 MW; 87506DFE6D80B63 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
11 1 111
Db 332 POHFLGLM 339

RESULT 171

09TC9 PRELIMINARY; PRT; 413 AA.
AC 09TC9; 09TC9; PRELIMINARY; PRT; 413 AA.
DT 01-MAY-2000 (TREMUREL. 13, Created)
DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)
DT 01-JUN-2001 (TREMUREL. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum ardistum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88502;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae) based on mitochondrial COI sequence data."
RL Syst. Entom. 24:0-(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF103978; AAF14101.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT 413 413
 SQ SEQUENCE 413 AA; 46692 MW; EDAAD377A243FEE3 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 POOFFGLM 11
 11 1111
 Db 332 PQHFLGLM 339

RESULT 172

09TCH8 PRELIMINARY; PRT; 413 AA.

ID 09TCH8
 AC 09TCH8:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum boreale.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88503;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF103979; AAF14102.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT 413 413
 SQ SEQUENCE 413 AA; 46758 MW; 6006A87084EAC5ED CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 POOFFGLM 11
 11 1111
 Db 332 PQHFLGLM 339

RESULT 173

09TCH7 PRELIMINARY; PRT; 413 AA.

ID 09TCH7
 AC 09TCH7:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum calceatum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88504;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF103980; AAF14103.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT 413 413
 SQ SEQUENCE 413 AA; 46730 MW; 12EC845EB3C62A73 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 POOFFGLM 11
 11 1111
 Db 332 PQHFLGLM 339

RESULT 174

09TCH6 PRELIMINARY; PRT; 413 AA.

ID 09TCH6
 AC 09TCH6:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.

OS Lastloglossum c:clnclipes.
OG Mitochondrion.
OC Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
OC Pterygota: Neoptera: Endopterygota: Hymenoptera: Apocrita: Aculeata:
OC Apoidea: Halictidae: Halictinae: Halictini: Lastloglossum.
OX NCBI_TaxID=88505;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lastloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103981; AAF14104.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 413
SQ SEQUENCE 413 AA; 46549 MW; D338190C949874BE CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
11 1 111
Db 332 PQHFLGLM 339

RESULT 175
Q9TCH5 PRELIMINARY; PRT; 413 AA.
AC Q9TCH5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lastloglossum commagense.
OG Mitochondrion.
OC Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
OC Pterygota: Neoptera: Endopterygota: Hymenoptera: Apocrita: Aculeata;
OC Apoidea: Halictidae: Halictinae: Halictini: Lastloglossum.
OX NCBI_TaxID=88505;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lastloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3

CC -1- AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103982; AAF14105.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 413
SQ SEQUENCE 413 AA; 46786 MW; F26D5CD2286DC68 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
11 1 111
Db 332 PQHFLGLM 339

RESULT 176
Q9TCH4 PRELIMINARY; PRT; 413 AA.
AC Q9TCH4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lastloglossum duplex.
OG Mitochondrion.
OC Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
OC Pterygota: Neoptera: Endopterygota: Hymenoptera: Apocrita: Aculeata;
OC Apoidea: Halictidae: Halictinae: Halictini: Lastloglossum.
OX NCBI_TaxID=88507;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lastloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103983; AAF14106.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 413
SQ SEQUENCE 413 AA; 46710 MW; EF400F726EB13989 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFGLM 11
|||
DB 332 POHFLGLM 339

RESULT 177
O9TCH3 PRELIMINARY; PRT; 413 AA.

AC 09TCH3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum fulvicorne.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88508;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRITYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF103984; AAF14107.1; -
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413
SQ SEQUENCE 413 AA; 46820 MW; D239B6B0B760199B CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFGLM 11
|||
DB 332 POHFLGLM 339

RESULT 178
O9TCH2 PRELIMINARY; PRT; 413 AA.

AC 09TCH2:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum lineare.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88511;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2

GN COI.
OS Lasloglossum laticeps.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88510;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRITYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL; AF103985; AAF14108.1; -
DR InterPro; IPR000883; COX1.
DR Pfam; PF00115; COX1; 1.
DR PRINTS; PR01165; CYCOXIDASE1.
DR PROSITE; PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT 413
SQ SEQUENCE 413 AA; 46644 MW; 64E59D92A8C48D69 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFGLM 11
|||
DB 332 POHFLGLM 339

RESULT 179
O9TCH1 PRELIMINARY; PRT; 413 AA.

AC 09TCH1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum lineare.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88511;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2

CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY) .
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
CC FERROCYTOCHROME C .
CC -1- CORACOIN: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY) .
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN .
CC -1- SUBCELLULAR LOCATION: INTERMEMBRANE PROTEIN (BY SIMILARITY) .
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY .
DR EMBL: AF103986; AAF14109.1; - .
DR InterPro: IPR000883; COX1 .
DR Pfam: PFC0115; COX1, 1 .
DR PRINTS: PR01165; CYCOKIDASE1 .
DR PROSITE: PS00077; COX1, 1 .
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane .
FT NON_TER 1 1
FT TER 413 413
SQ SEQUENCE 413 AA; 46614 MW; E1A54281BDC78C62 CRC64;

Query Match	54.18;	Score 33;	DB 8;	Length 413;
Best Local Similarity	75.08;	Pred. NO. 3.2e+02;		
Matches	6;	Conservative	0;	Mismatches 2;
			Indels	0;
			Gaps	0;

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OY      4 PQQFFGLM 11
         11 1 111
Db      332 PQHFLGLM 339

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Db 332 PQHFLGLM 339

RESULT	180
09TCH0	
ID	09TCH0
AC	PRELIMINARY;
DT	09TCH0;
DT	01-MAY-2000 (TEMBLrel. 13, Created)
DT	01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT	01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN	COI.
OS	Lasloglossum marginatum.
OC	Mitochondrion.
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC	Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC	Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX	NCBI_TaxID=88513;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Danforth B.N.;
RT	"phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
RL	based on mitochondrial COI sequence data.";
Syst. Entom.	24:0-0(1999).
-1-	FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1	
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE	
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN	
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2	
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A	
AND COPPER B (BY SIMILARITY).	
-1-	CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
CC	FERROCYTOCHROME C.
-1-	COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC	-1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY
EMBL:	AF103987; AAF14110.1; -.
InterPro:	IPR000883; COX1.
DR	Pfam: PF00115; COX1; 1.
DR	PRINTS: PR01165; CYCOXIDASE1.
DR	PROSITE: PS00677; COX1; 1.
KM	Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
Respiratory chain; Transmembrane.	
FT	NON_TER 1 1
FT	NON_TER 1 1
SEQUENCE	413 AA; 46477 MW; 3236CDD0FC6782BC CRC64;

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Query Match      54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      4 PQQFFGLM 11
        11 1 1 1 1
Db      332 PQQFFGLM 339

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QY	4	PQEFFGLM	11
		111111	
Db	332	PQHFLGLM	339

Db 332 PÖHFLGLM 339

RESULT	181
Q9TCG9	
ID	Q9TCG9 PRELIMINARY; PRT; 413 AA.
AC	Q9TCG9;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN	COI.
OS	Lasioglossum malachurum.
OG	Mitochondrion.
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC	Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
CC	Apoidea; Halictidae; Halictinae; Halictini; Lasioglossum.
CC	NCB1_Taxid=68512.
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Danforth B.N.;
RT	"Phylogeny of the bee genus Lasioglossum (Hymenoptera: Halictidae)
RL	based on mitochondrial COI sequence data.";
SQ	Syst. Entom. 24:0-0(1999).
CC	-1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE CATALYTIC SUBUNIT OF THE ENZYME. ELECTRON S ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3 AND COPPER B (BY SIMILARITY).
CC	-1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4 FERRICYTOCHROME C.
CC	-1- COPACTORY: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC	-1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR	EMBL; AF103988; AAP411.1; .
DR	InterPro; IPR000883; COX1.
DR	Pfam; PF00115; COX1; 1.
DR	PRINTS; PR01165; CYCOXIDASE1.
DR	PROSITE; PS00077; COX1; 1.
KW	Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW	Respiratory chain; Transmembrane.
FT	NON_TER 1
FT	NON_TER 413
SQ	SEQUENCE 413 AA; 46425 MW; 55326AAE95988C5C CRC64;
Query Match	54.1%; Score 33; DB 8; Length 413;
Best Local Similarity	75.0%; Pred. NO. 3.2e+02;
Matches	6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	4 PQDFGLM 11
Db	332 PQDFGLM 339
RESULT	182
Q9TCG8	
ID	Q9TCG8 PRELIMINARY; PRT; 413 AA.
AC	Q9TCG8;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)

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Query Match          54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      4 POFFGLM 11
        ||| |||
Db       332 POFFGLM 339

RESULT 182
Q9TGC8      ID      PRELIMINARY;      PRT;      413 AA.
Q9TGC8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

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Qy	4	POQFFGLM	11
		111111	
Db	332	POHFLGLM	339
RESULT	182		
ID	09TCG8		PRELL
AC	09TCG8		
DT	01-MAY-2000	(TIME	
DT	01-MAY-2000	(TIME	
DT	01-JUN-2001	(TIME	

DB	332	POHFLGLM	339
RESULT	182		
Q9TCG8			
ID	Q9TCG8	PRELL	
AC	Q9TCG8;		
DT	01-MAY-2000	(ITEM	
DT	01-MAY-2000	(ITEM	
DT	01-JUN-2001	(ITEM	

RESULT	182	
09TCG8	ID	09TCG8
09TCG8	PRELIMINARY;	PRT: 413 AA.
AC	09TCG8;	
DT	01-MAY-2000	(TREMBLrel. 13, Created)
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum morio.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88514;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103989; AAF14113.1; -.
DR InterPro: IPR008883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 413
SQ SEQUENCE 413 AA; 46651 MW; EB0E1376047B2E9C CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGSLM 11
Db 332 PQHFLGLM 339

RESULT 183
O9TGC7 PRELIMINARY; PRT; 413 AA.
AC O9TGC7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum nigripes.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88515;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN

CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF103990; AAF14113.1; -.
DR InterPro: IPR008883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 413
SQ SEQUENCE 413 AA; 46726 MW; 082E1BE63D8B2472 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFGSLM 11
Db 332 PQHFLGLM 339

RESULT 184
O9TGC4 PRELIMINARY; PRT; 413 AA.
AC O9TGC4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum pauxillum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_TaxID=88516;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
FERRICYTOCHROME C.
CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
DR EMBL: AF104634; AAF14149.1; -.
DR InterPro: IPR008883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 413
SQ SEQUENCE 413 AA; 46726 MW; 082E1BE63D8B2472 CRC64;

SO SEQUENCE 413 AA; 46537 MW; F9A83E9A392PC1B4 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;

Best Local Similarity 75.0%; Pred. No. 3.2e+02; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
|||
Db 332 PQHFLGLM 339

RESULT 185

09TCG3 PRELIMINARY; PRT; 413 AA.

AC 09TCG3;
DT 01-MAY-2000 (TRIMBLREL. 13, Created)
DT 01-MAY-2000 (TRIMBLREL. 13, Last sequence update)
DT 01-JUN-2001 (TRIMBLREL. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.

OS Lasloglossum pectorale.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Eukaryota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.

OX NCBI_TaxID=88517;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

-1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN

CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2

CC AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4

CC FERROCYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

DR EMBL: AF104635; AAF1450.1; -

DR InterPro: IPR000883; COX1.

DR Pfam: PF00115; COX1.1.

DR PRINTS: PRO1165; CYCOXIDASE1.

DR PROSITE: PS00077; COX1.1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.

FT NON_TER 1 1

FT 413 413

SO SEQUENCE 413 AA; 46505 MW; B1CADF1B8BC0A59E CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;

Best Local Similarity 75.0%; Pred. No. 3.2e+02; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
|||
Db 332 PQHFLGLM 339

RESULT 186

09TCG3 PRELIMINARY; PRT; 413 AA.

AC 09TCG3;
DT 01-MAY-2000 (TRIMBLREL. 13, Created)
DT 01-MAY-2000 (TRIMBLREL. 13, Last sequence update)

DT 01-JUN-2001 (TRIMBLREL. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.

OS Lasloglossum pollium.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Eukaryota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.

OX NCBI_TaxID=88518;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

-1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN

CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2

CC AND COPPER B (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4

CC FERROCYTOCHROME C.

CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).

CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.

DR EMBL: AF104636; AAF1451.1; -

DR InterPro: IPR000883; COX1.

DR Pfam: PF00115; COX1.1.

DR PRINTS: PRO1165; CYCOXIDASE1.

DR PROSITE: PS00077; COX1.1.

KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.

FT NON_TER 1 1

FT 413 413

SO SEQUENCE 413 AA; 46641 MW; D5674CD65A42648F CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;

Best Local Similarity 75.0%; Pred. No. 3.2e+02; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
|||
Db 332 PQHFLGLM 339

RESULT 187

09TCG1 PRELIMINARY; PRT; 413 AA.

DT 01-MAY-2000 (TRIMBLREL. 13, Created)

DT 01-MAY-2000 (TRIMBLREL. 13, Last sequence update)

DT 01-JUN-2001 (TRIMBLREL. 17, Last annotation update)

DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.

OS Lasloglossum puncticolle.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Eukaryota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;

OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.

OX NCBI_TaxID=88519;

RN [1]

RP SEQUENCE FROM N.A.

RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
based on mitochondrial COI sequence data.";

RL Syst. Entom. 24:0-0(1999).

-1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE

CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- CORAFCTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
CC EMBL: AF104637; AAF14152.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 413 AA: 46562 MW: 01E87C05419878E4 CRC64:

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
1111111
Db 332 POFFGLM 339

RESULT 188

AC 09TCG0 PRELIMINARY; PRT; 413 AA.
ID 09TCG0:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lastloglossum quebecense.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lastloglossum.
OX NCBI_TaxID=88520;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lastloglossum (Hymenoptera: Halictidae)
RT based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- CORAFCTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
CC EMBL: AF104638; AAF14153.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1

FT NON_TER 413 413
SQ SEQUENCE 413 AA: 46804 MW: F26C0D973D6DC6C8 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
1111111
Db 332 POFFGLM 339

RESULT 189

AC 09TCF9 PRELIMINARY; PRT; 413 AA.
ID 09TCF9:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lastloglossum gattaca.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lastloglossum.
OX NCBI_TaxID=88509;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lastloglossum (Hymenoptera: Halictidae)
RT based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERRICYTOCHROME C.
CC -1- CORAFCTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
CC EMBL: AF104639; AAF14154.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1.1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1.1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 413 AA: 46676 MW: D957CF136ECF98E8 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
1111111
Db 332 POFFGLM 339

RESULT 190

AC 09TCF8 PRELIMINARY; PRT; 413 AA.
ID 09TCF8:
DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum subtronicum.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104640; AAF14155.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1.1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1.1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT 413 413
 SQ SEQUENCE 413 AA; 46747 MW; 8C54AB0B0A4128F CRC64;
 Query Match 54.18; Score 33; DB 8; Length 413;
 Best Local Similarity 75.08; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 PQOFFGLM 11
 111111
 Db 332 PQHFLGLM 339
 RESULT 191
 09TCE7 PRELIMINARY; PRT; 413 AA.
 AC 09TCE7;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum truncatum.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88522;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-

CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104641; AAF14156.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1.1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1.1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT 413 413
 SQ SEQUENCE 413 AA; 46665 MW; 7BC4C502C65DF1C3 CRC64;
 Query Match 54.18; Score 33; DB 8; Length 413;
 Best Local Similarity 75.08; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 PQOFFGLM 11
 111111
 Db 332 PQHFLGLM 339
 RESULT 192
 09TCE6 PRELIMINARY; PRT; 413 AA.
 AC 09TCE6;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum villosulum.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88523;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) -> 2 H(2)O + 4
 FERRICYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104642; AAF14157.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1.1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1.1.
 KM Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.

FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46624 MW; D4DC061F0229DC4 CRC64;

Query Match
 Best Local Similarity 54.1%; Score 33; DB 8; Length 413;
 Matches 6; Conservativity 75.0%; Pred. No. 3.2e+02;
 Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
 || || || ||
 Db 332 POHFLGLM 339

RESULT 193
 O9TCF4 PRELIMINARY; PRT; 413 AA.

ID O9TCF4;
 AC O9TCF4;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum callizonium.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88525;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104644; AAF14159.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46516 MW; 65F0037DB563C2AA CRC64;

Query Match
 Best Local Similarity 54.1%; Score 33; DB 8; Length 413;
 Matches 6; Conservativity 75.0%; Pred. No. 3.2e+02;
 Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
 || || || ||
 Db 332 POHFLGLM 339

RESULT 194
 O9TCF3 PRELIMINARY; PRT; 413 AA.
 AC O9TCF3;
 AC O9TCF3;

DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum corticeum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88526;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
 CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 FERROCYTOCHROME C.
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104645; AAF14160.1; -
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KM Respiratory chain; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA; 46652 MW; C112DA8C1C043D38 CRC64;

Query Match
 Best Local Similarity 54.1%; Score 33; DB 8; Length 413;
 Matches 6; Conservativity 75.0%; Pred. No. 3.2e+02;
 Mismatches 2; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
 || || || ||
 Db 332 POHFLGLM 339

RESULT 195
 O9TCF2 PRELIMINARY; PRT; 413 AA.
 ID O9TCF2;
 AC O9TCF2;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum desertum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88527;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY

CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERROCYTOCHROME C.
CC -1- COPACITOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: AF104646; AAF14161.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KM Copper: Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 413
SQ SEQUENCE 413 AA; 46596 MW; AE84F89B5170695D CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQDFGLM 11
11 1 111
DB 332 PQDFGLM 339

RESULT 196
O9TCE1 PRELIMINARY; PRT: 413 AA.
AC O9TCE1;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (PC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum discum.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_Taxid=88528;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
RT based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERROCYTOCHROME C.
CC -1- COPACITOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: AF104647; AAF14162.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;

KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 413
SQ SEQUENCE 413 AA; 46538 MW; FBF3614973886F93 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQDFGLM 11
11 1 111
DB 332 PQDFGLM 339

RESULT 197
O9TCE0 PRELIMINARY; PRT: 413 AA.
AC O9TCE0;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE I (PC 1.9.3.1) (FRAGMENT).
GN COI.
OS Lasloglossum fuscipenne.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
OX NCBI_Taxid=88529;
RN [1]
RP SEQUENCE FROM N.A.
RA Danforth B.N.;
RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
RT based on mitochondrial COI sequence data.";
RL Syst. Entom. 24:0-0(1999).
CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. COI IS THE
CC CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
CC CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
CC AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
CC AND COPPER B (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
CC FERROCYTOCHROME C.
CC -1- COPACITOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL: AF104648; AAF14163.1; -.
DR InterPro: IPR000883; COX1.
DR Pfam: PF00115; COX1; 1.
DR PRINTS: PR01165; CYCOXIDASE1.
DR PROSITE: PS00077; COX1; 1.
KW Copper; Heme; Inner membrane; Mitochondrion; Oxidoreductase;
KW Respiratory chain; Transmembrane.
FT NON_TER 1
FT NON_TER 413
SQ SEQUENCE 413 AA; 46668 MW; 87B42FB5498C1E81 CRC64;

Query Match 54.1%; Score 33; DB 8; Length 413;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQDFGLM 11
11 1 111
DB 332 PQDFGLM 339

RESULT 198
O9TCE9 PRELIMINARY; PRT: 413 AA.
ID O9TCE9

AC 09TCE9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (FRAGMENT).
 GN COI.
 OS Lasloglossum laevigatum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Halictidae; Halictinae; Halictini; Lasloglossum.
 OX NCBI_TaxID=88530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danforth B.N.;
 RT "Phylogeny of the bee genus Lasloglossum (Hymenoptera: Halictidae)
 based on mitochondrial COI sequence data.";
 RL Syst. Entom. 24:0-0(1999).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
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 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104649; AAF1464.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 DR Copper: Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 KM NON_TER 1
 FT NON_TER 1
 FT 413
 SQ SEQUENCE 413 AA; 46529 MW; 561747FD6BA4F59A CRC64;
 OY 4 POOFFGLM 11
 DB 332 POHFLGLM 339
 Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 3 FORM THE FUNCTIONAL CORE OF THE ENZYME. ELECTRONS ORIGINATING IN
 CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBUNIT 2
 AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED BY HEME A3
 AND COPPER B (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
 CC -1- COFACTOR: TWO HEME (A AND A3) GROUPS AND COPPER B (BY SIMILARITY).
 CC -1- PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
 DR EMBL: AF104650; AAF1465.1; -.
 DR InterPro: IPR000883; COX1.
 DR Pfam: PF00115; COX1; 1.
 DR PRINTS: PR01165; CYCOXIDASE1.
 DR PROSITE: PS00077; COX1; 1.
 DR Copper: Heme; Inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 KM NON_TER 1
 FT NON_TER 1
 FT 413
 SQ SEQUENCE 413 AA; 46334 MW; 0FA4851A84ECAD0E CRC64;
 OY 4 POOFFGLM 11
 DB 332 POHFLGLM 339
 Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

KW Copper; Heme; inner membrane; Mitochondrion; Oxidoreductase;
 KW Respiratory chain; Transmembrane.
 FT NON_TER 1
 FT NON_TER 413 413
 SQ SEQUENCE 413 AA: 46508 MW: E352300D9EFA2E6 CRC64:

Query Match 54.1%; Score 33; DB 8; Length 413;
 Best Local Similarity 75.0%; Pred. NO. 3.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
 11 1 11
 Db 332 PQHFLGLM 339

Search completed: April 1, 2002, 16:20:04
 Job time: 150 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 1, 2002, 16:17:29 ; Search time 23.26 Seconds
(without alignments)
36.024 Million cell updates/sec

Title: US-09-988-792-1
Perfect score: 61
Sequence: 1 RPKQQQFFGLM 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	11	1	SPHO
2	61	100.0	11	1	substance P - hors
3	61	100.0	63	2	substance P - guin
4	61	100.0	72	2	tachykinin gamma c
5	61	100.0	72	2	tachykinin A gamma
6	61	100.0	97	2	preprotachykinin-A
7	61	100.0	112	2	tachykinin delta p
8	61	100.0	115	1	substance P alpha
9	61	100.0	115	1	substance P gamma
10	61	100.0	129	1	tachykinin 1 precu
11	61	100.0	130	1	neurokinin 1 precu
12	61	100.0	130	1	substance P beta p
13	61	100.0	130	2	neurokinin 1 precu
14	61	100.0	130	2	tachykinin 1 precu
15	58	95.1	11	2	substance P - chic
16	50	82.0	11	2	substance P - rain
17	49	80.3	11	2	substance P - Atla
18	48	78.7	11	2	probable substance
19	44	72.1	11	2	substance P-like p
20	44	72.1	11	2	substance P-like p
21	44	72.1	12	2	tachykinin - Afric
22	41	67.2	11	2	ranatachykinin A -
23	41	67.2	3828	2	trithorax protein
24	38	62.3	205	2	hypothetical prote
25	38	62.3	257	2	small nuclear ribo
26	38	62.3	293	2	hypothetical prote
27	37	60.7	11	2	kassinin-like pept
28	37	60.7	11	2	upreolisin - frog
29	37	60.7	249	2	hypothetical prote

30	36	59.0	11	2	D60409
31	36	59.0	11	2	B60409
32	36	59.0	12	2	S07436
33	36	59.0	12	2	S07206
34	36	59.0	321	2	A64173
35	36	59.0	373	2	T02976
36	36	59.0	629	2	T19563
37	36	59.0	728	2	E69486
38	35	57.4	133	2	A25777
39	35	57.4	206	2	T33064
40	35	57.4	297	2	A83049
41	35	57.4	347	2	T05737
42	35	57.4	474	2	T15511
43	35	57.4	494	2	E86671
44	35	57.4	512	2	A82296
45	35	57.4	832	2	S76815
46	35	57.4	1043	2	T23875
47	35	57.4	1092	2	H69071
48	35	57.4	1611	2	A84743
49	35	57.4	1736	2	F86178
50	34.5	56.6	216	2	F96657
51	34	55.7	167	2	T36290
52	34	55.7	306	2	H81036
53	34	55.7	316	2	T13601
54	34	55.7	318	2	A81982
55	34	55.7	359	2	T52337
56	34	55.7	493	2	S73890
57	34	55.7	498	1	S48058
58	34	55.7	502	2	JX0334
59	34	55.7	503	2	A40843
60	34	55.7	504	2	A22631
61	34	55.7	583	2	S30930
62	34	55.7	583	2	S34785
63	34	55.7	585	1	S33544
64	34	55.7	587	1	S33543
65	34	55.7	588	2	S30929
66	34	55.7	588	2	S34786
67	34	55.7	628	2	D86466
68	34	55.7	666	2	S56781
69	34	55.7	1799	1	S44920
70	33	54.1	71	2	G81889
71	33	54.1	101	2	G71054
72	33	54.1	234	2	F75254
73	33	54.1	282	2	T15304
74	33	54.1	299	2	E70842
75	33	54.1	320	2	H71259
76	33	54.1	327	2	A75633
77	33	54.1	327	2	C75624
78	33	54.1	327	2	E75618
79	33	54.1	327	2	C75556
80	33	54.1	327	2	B73620
81	33	54.1	404	2	A54871
82	33	54.1	416	2	F75434
83	33	54.1	454	2	T37933
84	33	54.1	502	1	D64110
85	33	54.1	505	1	SYECKT
86	33	54.1	505	1	SYECKU
87	33	54.1	505	2	I38396
88	33	54.1	505	2	E86108
89	33	54.1	505	2	F85944
90	33	54.1	512	2	I49552
91	33	54.1	521	2	A32431
92	33	54.1	546	2	F84647
93	33	54.1	712	2	T02552
94	33	54.1	755	2	T47731
95	33	54.1	1057	1	A39288
96	33	54.1	1741	2	T13610
97	32.5	53.3	325	2	S14230
98	32	52.3	11	2	S07201
99	32	52.5	180	2	S77046
100	32	52.5	210	2	A69898
101	32	52.5	225	2	G75448
102	32	52.5	263	1	S23009

kassinin-like pept
kassinin-like pept
tachykinin - Afric
kassinin - Senegal
conserved hypotnet
probable DNA bindi
hypothetical prote
translacion elonga
T-cell receptor be
hypothetical prote
hypothetical prote
probable hordenin C
hypothetical prote
lysine--trna ligas
lysyl--trna synthet
hypothetical prote
hypothetical prote
DNA-directed DNA p
probable myosin he
hypothetical prote
hypothetical prote
probable integral
riboflavin kinase/
hypothetical prote
FAD synthase NMA06
phosphoprotein pho
hypothetical prote
cytochrome P450 Cy
cytochrome P450 3A
cytochrome P450 3
cytochrome P450 3A
cytochrome P450 3A
catechol oxidase (
catechol oxidase (
catechol oxidase (
catechol oxidase (
catechol oxidase (
hypothetical prote
hypothetical prote
ZK688_5 protein -
hypothetical prote
hypothetical prote
conserved hypotnet
hypothetical prote
probable acid phos
probable membrane
probable transposa
probable transposa
probable transposa
probable transposa
probable transposa
Gal beta-1, 3galNA
hypothetical prote
transcription acti
lysine--trna ligas
lysine--trna ligas
lysine--trna ligas
protein-tyrosine k
hypothetical prote
hypothetical prote
protein-tyrosine k
cytochrome-c oxida
hypothetical prote
cellulose synthase
hypothetical prote
dorsal-ventral pat
parallel sister ch
pyruvate dehydroge
phylalaemin - frog
hypothetical prote
conserved hypotnet
conserved hypotnet
insulin-like growt

103	32	52.5	271	2	B35407	tryptophan synthas
104	32	52.5	288	2	C75426	probable transposa
105	32	52.5	288	2	A75638	probable transposa
106	32	52.5	299	2	E69288	ISA0963-2 transpos
107	32	52.5	299	2	H69462	ISA0963-6 transpos
108	32	52.5	299	2	E69413	ISA0963-3 transpos
109	32	52.5	299	2	F69422	ISA0963-4 transpos
110	32	52.5	305	2	D96769	hypothetical prote
111	32	52.5	313	2	G86336	hypothetical prote
112	32	52.5	327	2	A75631	probable transposa
113	32	52.5	345	2	B83371	conserved hypotet
114	32	52.5	357	2	A69426	ISA0963-5 transpos
115	32	52.5	361	2	C71242	hypothetical prote
116	32	52.5	368	2	T15492	hypothetical prote
117	32	52.5	370	2	T05598	hypothetical prote
118	32	52.5	382	1	B64158	hypothetical prote
119	32	52.5	418	2	H72026	3,4-dihydroxy-2-bu
120	32	52.5	418	2	F86599	GTP cyclohydrolase
121	32	52.5	419	2	F82991	transcription term
122	32	52.5	419	2	H81667	transcription term
123	32	52.5	426	2	E83172	transcription term
124	32	52.5	427	2	G72246	transcription term
125	32	52.5	432	2	F81320	transcription term
126	32	52.5	445	2	S73859	hypothetical prote
127	32	52.5	462	2	A42401	macrophage elastas
128	32	52.5	464	2	A71509	probable transcrip
129	32	52.5	464	2	D72058	transcription term
130	32	52.5	464	2	G86566	transcription term
131	32	52.5	469	1	KCPG1	interstitial colla
132	32	52.5	478	2	F82175	conserved hypotet
133	32	52.5	484	2	T16695	hypothetical prote
134	32	52.5	493	2	JC7205	lysine--cRNA ligas
135	32	52.5	508	2	JC6200	cholesterol monoox
136	32	52.5	513	2	T35456	hypothetical prote
137	32	52.5	515	2	F70128	transcription term
138	32	52.5	518	2	T19562	hypothetical prote
139	32	52.5	519	2	C71346	probable transcrip
140	32	52.5	532	2	T49467	related to COP1-in
141	32	52.5	567	2	T08405	hypothetical prote
142	32	52.5	612	2	T35430	probable long-chain
143	32	52.5	614	2	T25208	hypothetical prote
144	32	52.5	617	2	A81095	excinuclease ABC c
145	32	52.5	628	2	G81845	alpha-amylase ABC s
146	32	52.5	632	2	J50631	hypothetical prote
147	32	52.5	637	2	T00548	p6 protein - mous
148	32	52.5	837	2	A57542	desmocollin - bovi
149	32	52.5	896	2	T45858	hypothetical prote
150	32	52.5	1039	2	T22982	DNA-directed RNA p
151	32	52.5	1116	2	S41915	type I restriction
152	32	52.5	1163	2	D64315	formin isoform IV
153	32	52.5	1206	2	S24407	limb deformity (ld
154	32	52.5	1213	2	A41724	conserved hypotet
155	32	52.5	1415	2	C83070	formin - mouse
156	32	52.5	1468	2	S11515	vitellogenin vit-6
157	32	52.5	1651	2	B43081	hypothetical prote
158	32	52.5	1718	2	T14603	hypothetical prote
159	32	52.5	1817	2	T34249	SEC16 protein - ye
160	32	52.5	2195	2	S61103	glialdin omega-5 -
161	31	50.8	32	2	A59156	hypothetical prote
162	31	50.8	79	2	D69969	terteodoxin--thiore
163	31	50.8	97	2	JT0703	nuclear receptor p
164	31	50.8	113	2	S43435	hypothetical prote
165	31	50.8	126	2	S72785	conserved hypotet
166	31	50.8	126	2	D69293	hypothetical HIF-f
167	31	50.8	133	2	T40979	hypothetical prote
168	31	50.8	136	2	T45725	hypothetical prote
169	31	50.8	138	2	T14185	chitinase (EC 3.2.
170	31	50.8	143	2	S67619	ribosomal protein
171	31	50.8	159	2	E81982	probable phosphata
172	31	50.8	172	2	S68232	antimicrobial prote
173	31	50.8	176	2	A75624	hypothetical prote
174	31	50.8	183	2	E69286	transcription init
175	31	50.8	193	2	E96766	hypothetical prote
176	31	50.8	206	2	F71012	hypothetical prote
177	31	50.8	216	2	T22453	hypothetical prote
178	31	50.8	219	2	C81038	phosphoglycolate p
179	31	50.8	226	2	T24530	hypothetical prote
180	31	50.8	226	2	S40944	hypothetical prote
181	31	50.8	254	1	WMBVT3	30K protein - toma
182	31	50.8	264	1	WMBVL2	30K protein - toma
183	31	50.8	266	2	E71612	ribosomal protein
184	31	50.8	269	2	A26162	holocytochrome-c s
185	31	50.8	271	2	D55552	conserved hypotet
186	31	50.8	278	2	S48776	hypothetical prote
187	31	50.8	283	2	A35935	NADH dehydrogenase
188	31	50.8	304	2	G64175	hypothetical prote
189	31	50.8	320	2	D96750	unknown protein F2
190	31	50.8	323	1	PRLJHD	proteinase (EC 3.4
191	31	50.8	337	2	T19592	hypothetical prote
192	31	50.8	338	2	G69027	phosphoribosylform
193	31	50.8	338	2	S75196	hypothetical prote
194	31	50.8	355	2	T24822	hypothetical prote
195	31	50.8	371	2	C72077	conserved hypotet
196	31	50.8	371	2	F86546	hypothetical prote
197	31	50.8	377	2	T40024	probable cytochrom
198	31	50.8	379	2	D83803	tRNA-guanine trans
199	31	50.8	385	2	G72569	hypothetical prote
200	31	50.8	391	2	F82369	conserved hypotet
201	31	50.8	398	2	T46312	hypothetical prote
202	31	50.8	406	2	A35401	cytochrome P450 10
203	31	50.8	455	2	E96737	probable DEAD/DEAH
204	31	50.8	455	2	D86166	protein F21B7.12 (
205	31	50.8	466	2	E70865	trigger factor tlg
206	31	50.8	469	2	C86170	hypothetical prote
207	31	50.8	476	2	G81091	glu-cRNA(Gln) amid
208	31	50.8	479	2	T15427	hypothetical prote
209	31	50.8	485	2	S75655	anthranilate synth
210	31	50.8	488	1	QOBEHS	alkaline exonuclea
211	31	50.8	488	2	T44030	alkaline exonuclea
212	31	50.8	488	2	T44215	lysine--tRNA ligas
213	31	50.8	488	2	S69892	cytochrome-c oxida
214	31	50.8	496	2	T11376	hypothetical prote
215	31	50.8	529	1	S76167	hypothetical prote
216	31	50.8	532	2	T27549	hypothetical prote
217	31	50.8	546	2	T19139	hypothetical prote
218	31	50.8	558	2	T56545	glycpan precursor
219	31	50.8	566	2	T49988	hypothetical prote
220	31	50.8	583	2	S65227	probable ribonucle
221	31	50.8	596	2	T30498	gelatinase A (EC 3
222	31	50.8	660	1	A28153	gelatinase A (EC 3
223	31	50.8	662	2	A42496	gelatinase A (EC 3
224	31	50.8	662	2	S34780	gelatinase A (EC 3
225	31	50.8	662	2	S70365	gelatinase A (EC 3
226	31	50.8	663	1	S46492	gelatinase A (EC 3
227	31	50.8	667	2	T01999	hypothetical prote
228	31	50.8	678	2	S77215	hypothetical prote
229	31	50.8	692	2	T13161	A-kinase anchor pr
230	31	50.8	705	2	S70691	polyribonucleotide
231	31	50.8	735	2	T49622	hypothetical prote
232	31	50.8	757	1	LIRRH	hormone-sensitiv
233	31	50.8	761	2	A53414	A-kinase anchor pr
234	31	50.8	775	2	B72074	hypothetical prote
235	31	50.8	775	2	C81594	hypothetical prote
236	31	50.8	775	2	D86549	hypothetical prote
237	31	50.8	797	2	T27518	hypothetical prote
238	31	50.8	864	2	A49070	hypothetical prote
239	31	50.8	922	2	T40372	ecdysone-inducible
240	31	50.8	948	2	T26417	trp asp repeat pro
241	31	50.8	997	2	T15243	hypothetical prote
242	31	50.8	1019	2	T50251	hypothetical prote
243	31	50.8	1139	2	T33368	hypothetical coile
244	31	50.8	1222	2	T14805	hypothetical prote
245	31	50.8	1323	2	H85202	hypothetical prote
246	31	50.8	1765	2	T42388	sodium channel alp
247	31	50.8	1840	2	T30250	GTL protein - mous
248	31	50.8	2517	2	S58380	probable RNA-direc

249	31	50.8	3712	1	YCCEVC	alpha-aminoadipyl-
250	30.5	50.0	445	2	EB2075	hypothetical prote
251	30.5	50.0	574	2	FB3991	hypothetical prote
252	30.5	50.0	2201	2	AS4774	ATP binding casset

ALIGNMENTS

RESULT 1
SPHO

Substance P - horse
C:Species: Equus caballus (domestic horse)
C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996
C:Accession: A01558
R:Studer, R.O.; Trzeciak, A.; Lergler, W.
Helv. Chim. Acta 56, 860-866, 1973
A:Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.
A:Reference number: A01558
A:Accession: A01558
A:Molecule type: protein
A:Residues: 1-11 <STU>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; hormone
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match
Best Local Similarity 100.0%; Score 61; DB 1; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOQFFGLM 11
|||||
DB 1 RRPQOQFFGLM 11

RESULT 2

A60654

Substance P - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995
C:Accession: A60654
R:Murphy, R.
Neuropeptides 14, 105-110, 1989
A:Title: Primary amino acid sequence of guinea-pig substance P.
A:Reference number: A60654; MUID:90044685
A:Accession: A60654
A:Molecule type: protein
A:Residues: 1-11 <MUR>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match
Best Local Similarity 100.0%; Score 61; DB 1; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOQFFGLM 11
|||||
DB 1 RRPQOQFFGLM 11

RESULT 3

JC2412

tachykinin gamma chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1995 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: JC2412
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in th
A:Reference number: JC2411; MUID:94324969

A:Accession: JC2412
A:Molecule type: mRNA
A:Residues: 1-63 <KHA>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:12-21/Product: substance P #status predicted <SUP>
F:21/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match
Best Local Similarity 100.0%; Score 61; DB 2; Length 63;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOQFFGLM 11
|||||
DB 11 RRPQOQFFGLM 21

RESULT 4

I62742

tachykinin A gamma chain precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: I62742; JC5453
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mo
A:Reference number: JC5450; MUID:91209287
A:Accession: I62742
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-72 <RES>
A:Cross-references: GB:M68909; NID:9200469; PIDN:AAA39970.1; PID:9554261
C:Comment: This protein contains two tachykinin peptide hormone substance-P which is
C:Genetics:
A:Gene: gamma-PPT-A
C:Superfamily: substance P precursor
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-33/Product: substance-P #status predicted <STP>
F:48-57/Product: neurokinin-A #status predicted <NKA>

Query Match
Best Local Similarity 100.0%; Score 61; DB 2; Length 72;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOQFFGLM 11
|||||
DB 23 RRPQOQFFGLM 33

RESULT 5

JC5455

preprotachykinin-A gamma precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 16-Jul-1999
C:Accession: JC5455; I45967
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mo
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5455
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-72 <CHI>
A:Cross-references: GB:M68912; NID:9163593; PIDN:AAA30725.1; PID:9552336
C:Comment: This protein contains two tachykinin peptide hormone substance-P which is
C:Genetics:
A:Gene: PPT-A
C:Superfamily: substance P precursor
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-33/Product: substance-P #status predicted <STP>
F:48-57/Product: neurokinin-A #status predicted <NKA>

Query Match 100.0%; Score 61; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 23 RPKPOQFFGLM 33

RESULT 6
S12958
tachykinin delta precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S12958; J02413
R:Harmer, A.J.; Hyde, V.; Chapman, K.
FEBS Lett. 275, 22-24, 1990
A:Title: Identification and cDNA sequence of delta-preprotachykinin, a fourth splicing
A:Reference number: S12958; MUID:91085565
A:Accession: S12958
A:Molecule type: mRNA
A:Residues: 1-97 <HAK>
A:Cross-references: GB:X56306; NID:956067; PIDN:CAA39752.1; PID:956068
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in th
A:Reference number: J02411; MUID:94324969
A:Accession: J02413
A:Molecule type: mRNA
A:Residues: 48-92 <KHA>
A:Cross-references: GB:S72369; NID:9632805; PIDN:AAB31499.1; PID:9632806
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:58-68/Product: substance P #status predicted <SUP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 100.0%; Score 61; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 58 RPKPOQFFGLM 68

RESULT 7
SPRTA
substance P alpha precursor - rat
N:Alternate names: preprotachykinin alpha
N:Contains: substance P
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1988 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: B26590
R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Hershey, A.D.
Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987
A:Title: Three rat preprotachykinin mRNAs encode the neuropeptides substance P and neuro
A:Reference number: A94187; MUID:87118268
A:Accession: B26590
A:Molecule type: mRNA
A:Residues: 1-112 <KRA>
A:Cross-references: GB:M4184; NID:9206329; PIDN:AAA1925.1; PID:9206330
C:Comment: Alternative splicing of the mRNA for substance P precursor yields the alpha f
C:Comment: The alpha form is processed to yield substance P.
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykin
F:1-112/Product: substance P alpha precursor #status predicted <PREA>
F:1-15/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: substance P #status predicted <SBP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gly

Query Match 100.0%; Score 61; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 58 RPKPOQFFGLM 68

RESULT 8
SPRG
substance P gamma precursor - rabbit
N:Alternate names: gamma-neuropeptide K; gamma-preprotachykinin I precursor; tachykin
N:Contains: neurokinin A; neuropeptide K; substance P
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 10-Nov-1992 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: JN0709; A60302; A60200; S18922
R:Maegert, H.J.; Heililand, A.; Rose, M.; Forssmann, W.G.
Biochem. Biophys. Res. Commun. 195, 128-131, 1993
A:Title: Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.
A:Reference number: JN0709; MUID:93371392
A:Accession: JN0709
A:Molecule type: mRNA
A:Residues: 1-115 <MA2>
A:Cross-references: EMBL:X62994; NID:91565; PIDN:CAA44728.1; PID:91566
R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
Regul. Pept. 18, 346, 1987
A:Title: gamma-Neuropeptide K: a peptide isolated from rabbit gut that is derived fro
A:Reference number: A60302
A:Accession: A60302
A:Molecule type: protein
A:Residues: 72-92 <KAG>
R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.
J. Neurochem. 50, 1412-1417, 1988
A:Title: Neuropeptide-gamma: a peptide isolated from rabbit intestine that is derived
A:Reference number: A60200; MUID:86199570
A:Accession: A60200
A:Molecule type: protein
A:Residues: 72-92 <KA2>
C:Comment: The gamma alternatively spliced form is processed to yield substance P and
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachy
F:1-15/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: substance P #status predicted <SBP>
F:72-92/Product: gamma-neuropeptide K #status experimental <NPK>
F:83-92/Product: neurokinin A #status predicted <NKA>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following
F:92/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 100.0%; Score 61; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 58 RPKPOQFFGLM 68

RESULT 9
S47039
tachykinin 1 precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S47039
R:Heililand, A.; Kruloffier, M.; Uergeren Maegert, H.J.; Forssmann, W.G.
submitted to the EMBL Data Library, July 1994
A:Reference number: S47038
A:Accession: S47039
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-115 <HEI>

A:Cross-references: EMBL:X80663; NID:g520938; PIDN:CAA56692.1; PID:g550939
C:Superfamily: substance P precursor

Query Match 100.0%; Score 61; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRPQOFGGLM 11
|||||
Db 58 RRPQOFGGLM 68

RESULT 10

SPRUB
neurokinin 1 precursor, beta splice form [validated] - human
M:Alternate names: neurokinin A; neurokinin alpha; neuromedin L; neuropeptide K; preprotachykinin 1; neurokinin 1 precursor, alpha splice form; neurokinin 1 precursor; Homo sapiens (man)
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1988 #sequence_revision 26-May-1995 #text_change 19-May-2000
C:Accession: A24805; A60425; S00069; S03033; JC5451; JC5450; A59269; A59270; B59270; 162
R:Harman, A.J.; Armstrong, A.; Pascall, J.C.; Chapman, K.; Koste, R.; Curtis, A.; Goling, P.B.S. Lett. 208, 67-72, 1986
A:Title: cDNA sequence of human beta-preprotachykinin, the common precursor to substance P and neurokinin B
A:Reference number: A24805; MUID:87030957
A:Accession: A24805
A:Molecule type: mRNA
A:Residues: 1-129 <HAR>
A:Cross-references: GB:M28109; EMBL:X54469; NID:g29482; PIDN:CAA38351.1; PID:g29483
R:McGregor, G.P.; Conlon, J.M.
Peptides 11, 907-910, 1990
A:Title: Characterization of the C-terminal flanking peptide of human beta-preprotachykinin
A:Reference number: A60425; MUID:91133934
A:Accession: A60425
A:Molecule type: Protein
A:Residues: 111-126 <MCG>
A:Experimental source: neuroendocrine tumor of adrenal medulla
R:Theodorsson-Norheim, E.; Joernvall, H.; Andersson, M.; Norheim, I.; Oberg, K.; Jacobsen, J. Biochem. 166, 693-697, 1987
A:Title: Isolation and characterization of neurokinin A, neurokinin A(3-10) and neurokinin B
A:Reference number: S00069; MUID:87275962
A:Accession: S00069
A:Molecule type: protein
A:Residues: 98-107 <THE>
R:Kage, R.; Thim, L.; Creutzfeldt, W.; Conlon, J.M.
Biochem. J. 253, 203-207, 1988
A:Title: Post-translational processing of preprotachykinins. Isolation of protachykinin-A
A:Reference number: S03033; MUID:88339887
A:Accession: S03033
A:Molecule type: protein
A:Residues: 20-30 <KAG>
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Iwell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5451
A>Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 36-73,89-122 <CH11>
A:Cross-references: GB:M68907; NID:g190292; PIDN:AAA60160.1; PID:g553619
A:Accession: JC5450
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 36-86, 'P', 88-122 <CH12>
A:Cross-references: GB:M68906; NID:g190290; PIDN:AAA60159.1; PID:g553618
R:Tan, A.; Teo, H.P.
submitted to GenBank, October 1995
A:Reference number: A59269
A:Accession: A59269
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-129 <TAN>
A:Cross-references: GB:U37529; NID:g1017792; PIDN:AAA79195.1; PID:g1017793

A:Experimental source: tissue brain cortex
R:rai, J.P.; Douglas, S.D.; Rappaport, E.; Wu, J.M.; Ho, W.Z.

submitted to GenBank, February 1998
A:Description: Identification of a delta isoform of preprotachykinin mRNA in human mo
A:Reference number: A59270
A:Accession: A59270

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 36-96, 'W', 116-118 <LA11>

A:Cross-references: GB:AF050656; NID:g3098594; PIDN:AAC15702.1; PID:g3098595

A:Experimental source: alpha splice form; tissue blood; tissue brain; cell type monoc

A:Accession: B59270

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 36-73,89-96, 'W', 116-122 <LA12>

A:Cross-references: GB:AF050658; NID:g3098598; PIDN:AAC15704.1; PID:g3098599

A:Experimental source: delta splice form; tissue blood; tissue brain; cell type monoc

C:Comment: This protein is processed to produce the tachykinin peptide hormones neuro

kin X).

C:Genetics:

A:Gene: GDB:TAC1; TAC2; NKNA, PPT-A

A:Cross-references: GDB:119452; OMIM:162320

A:Map position: 7q21-q22

C:Superfamily: substance P precursor

C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachy

F:1-129/Product: neurokinin 1 precursor, beta splice form #status predicted <SP>

F:1-96, 'W', 116-118/Product: neurokinin 1 precursor, alpha splice form #status predict

F:1-73,89-129/Product: neurokinin 1 precursor, gamma splice form #status predicted <S

F:1-73,89-96, 'W', 116-122/Product: neurokinin 1 precursor, alpha splice form #status p

F:1-19/Domains: signal sequence #status predicted <SIG>

F:20-57/Domains: amino-terminal propeptide #status predicted <PRO>

F:58-68/Product: neurokinin 1 #status experimental <NK1>

F:72-107/Product: neuropeptide K #status predicted <NK>

F:98-107/Product: neurokinin 2 #status experimental <NK2>

F:100-107/Product: neurokinin 2(3-10) #status experimental <NK23>

F:101-107/Product: neurokinin 2(4-10) #status experimental <NK24>

F:111-126/Domains: carboxyl-terminal propeptide #status experimental <CTP>

F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following

F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following

OY 1 RRPQOFGGLM 11
|||||
Db 58 RRPQOFGGLM 68

RESULT 11

SPRUB
substance P beta precursor - rat
M:Alternate names: preprotachykinin beta; preprotachykinin gamma; substance K
N:Contains: neurokinin A; substance P; substance P gamma precursor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1988 #sequence_revision 26-May-1995 #text_change 18-Jun-1999
C:Accession: A37163; A26590; C26590; A25067; JC2411
R:Carter, M.S.; Krause, J.E.
J. Neurosci. 10, 2203-2214, 1990
A:Title: Structure, expression, and some regulatory mechanisms of the rat preprotachy

A:Cross-references: GB:M15191; NID:g206341; PIDN:AAAA1928.1; PID:g206342; GB:M35277
A:Accession: C26590
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KR2>
A:Cross-references: GB:M34183; NID:g206343; PIDN:AAAA1929.1; PID:g206344
R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
A:Title: Sequence analysis of cloned cDNA for rat substance P precursor: existence of a
A:Reference number: A25067; MUID:87025808
A:Accession: A25067
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KAW>
A:Cross-references: GB:M14312; NID:g206339; PIDN:AAA41927.1; PID:g206340
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for substance P in th
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2411
A:Molecule type: mRNA
A:Residues: 48-110 <KHA>
A:Experimental source: Intestine
C:Comment: Alternative splicing of the mRNA for substance P precursor yields the beta an
C:Comment: The beta and gamma forms are processed to yield substance P and neurokinin A
C:Genetics:
A:Introns: 41/3; 74/1; 89/1; 97/1; 115/1
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykin
F:1-130/Product: substance P beta precursor #status predicted <PREB>
F:1-73, 89-130/Product: substance P gamma precursor #status predicted <REG>
F:1-15/Domain: signal sequence #status predicted <SIG>
F:58-68/Product: substance P #status predicted <SBP>
F:96-107/Product: neurokinin A #status predicted <NKA>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following g
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following g

Query Match 100.0%; Score 61; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
Db 58 RPKPOQFFGLM 68

RESULT 12
SPBOB
neurokinin 1 precursor, beta splice form [validated] - bovine
N:Alternate names: neurokinin A; preprotachykinin; substance K; substance P
N:Contains: neurokinin 1; neurokinin 1 precursor, alpha splice form; neurokinin 1 precu
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Feb-1984 #sequence, revision 19-Feb-1984 #text, change 16-Jun-2000
C:Accession: A05093; A01557; B25067; A61460; JC5454; I45966
R:Nawa, H.; Kotani, H.; Nakanishi, S.
Nature 312, 729-734, 1984
A:Title: Tissue-specific generation of two preprotachykinin mRNAs from one gene by alter
A:Reference number: A05093; MUID:85086245
A:Accession: A05093
A:Molecule type: DNA
A:Residues: 1-130 <NMI>
A:Cross-references: GB:X02351; GB:M14786; NID:g655; PIDN:CAA26206.1; PID:g1197197
R:Nawa, H.; Hirose, T.; Takashima, H.; Inayama, S.; Nakanishi, S.
Nature 306, 32-36, 1983
A:Title: Nucleotide sequences of cloned cDNAs for two types of bovine brain substance P
A:Reference number: A93318; MUID:84039802
A:Accession: A01559
A:Molecule type: mRNA
A:Residues: 1-130 <NMI>
A:Cross-references: GB:X00075; NID:g758; PIDN:CAA24939.1; PID:g759
A:Accession: A01557
A:Molecule type: mRNA
A:Residues: 1-96, 'M', 116-130 <NMI>
A:Cross-references: GB:X00076; NID:g762; PIDN:CAA24942.1; PID:g763

R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
A:Title: Sequence analysis of cloned cDNA for rat substance P precursor: existence of
A:Reference number: A25067; MUID:87025808
A:Accession: B25067
A:Molecule type: mRNA
A:Residues: 1-73, 89-130 <KAW>
R:McGregor, G.P.; Kage, R.; Thim, L.; Conlon, J.M.
J. Neurochem. 53, 1871-1877, 1989
A:Title: Quantitation and characterization of peptides from the C-terminal flanking r
A:Reference number: A61460; MUID:90039314
A:Accession: A61460
A:Molecule type: Protein
A:Residues: 111-126 <MCG>
A:Experimental source: corpus striatum
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schultze, W.; Iyell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mo
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5454
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 36-120, 'A', 122 <CHT>
A:Cross-references: GB:M68911; NID:g163591; PIDN:AAA30724.1; PID:g552335
C:Comment: The protein is processed to produce neurokinin 1 (substance P) and neuroki
C:Genetics:
A:Gene: PPT-A
A:Introns: 41/3; 74/1; 89/1; 97/1; 115/1
C:Superfamily: substance P precursor
C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachy
F:1-130/Product: neurokinin 1 precursor, beta splice form #status predicted <SBP>
F:1-96, 'M', 116-130/Product: neurokinin 1 precursor, alpha splice form #status predict
F:1-73, 89-130/Product: neurokinin 1 precursor, gamma splice form #status predicted <S
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F:58-68/Product: neurokinin 1 #status experimental <SBP>
F:96-107/Product: neurokinin 2 #status predicted <NKA>
F:111-126/Domain: carboxyl-terminal propeptide #status experimental <CNP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following

Query Match 100.0%; Score 61; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
Db 58 RPKPOQFFGLM 68

RESULT 13
S47038
tachykinin 1 precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 13-Jan-1995 #sequence, revision 13-Jan-1995 #text, change 16-Jul-1999
C:Accession: S47038
R:Heiland, A.; Krueffer, M.; Juergen Maegerl, H.J.; Forssmann, W.G.
submitted to the EMBL Data Library, July 1994
A:Reference number: S47038
A:Accession: S47038
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <HEI>
A:Cross-references: EMBL:X80662; NID:g520917; PIDN:CAA56691.1; PID:g520918
C:Superfamily: substance P precursor

Query Match 100.0%; Score 61; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11

DB 58 RPKPOQFFGLM 68
|||||
RESULT 14
152526
neurokinin 1 precursor - mouse
N:Alternate names: neurokinin A; preprotachykinin; substance K; substance P
N:Contains: neurokinin 1; neurokinin 2
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-2000
C:Accession: J52526; J5452; I62741
R:Kako, K.; Muneoka, E.; Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 14, 253-259, 1993
A>Title: Cloning and sequence analysis of mouse cDNAs encoding preprotachykinin A and B.
A:Reference number: J52526
A:Accession: J52526
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-130 <KAK>
A:Cross-references: GB:DJ7584; MID:9407345; PIDN:BA04508.1; PID:9435121
R:Chikata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A>Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse
A:Reference number: J5450; MID:91209287
A:Accession: J5450
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 36-122 <CHT>
A:Cross-references: GB:M68908; MID:9200467; PIDN:AAA39969.1; PID:9554260
C:Genetics:
A:Gene: PPT-A
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F:58-68/Product: neurokinin 1 #status predicted <NK1>
F:98-107/Product: neurokinin 2 #status predicted <NK2>
F:111-126/Domain: carboxy-terminal propeptide #status predicted <CTP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following gl
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following gl

Query Match 100.0%; Score 61; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
DB 58 RPKPOQFFGLM 68

RESULT 15
JN0023
substance P - chicken
C:Species: Gallus gallus (chicken)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997
C:Accession: JN0023
R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A>Title: [Arg3]substance P and neurokinin A from chicken small intestine.
A:Reference number: JN0023; MID:88204263
A:Accession: JN0023
A:Molecule type: protein
A:Residues: 1-11 <CON>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; tachykinin
F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 95.1%; Score 58; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00015;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
DB 1 RPKPOQFFGLM 11

RESULT 16
S23308
substance P - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S23308
R:Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A>Title: Substance-P-related and neurokinin-A-related peptides from the brain of the
A:Reference number: S23186; MID:92298992
A:Accession: S23308
A:Molecule type: protein
A:Residues: 1-11 <JEN>
A:Experimental source: brain
C:Function:
A:Description: may play a physiological role in the regulation of cardiovascular and
A:Note: substance P is derived by post-translational processing of preprotachykinin A
C:Superfamily: unassigned animal peptides
C:Keywords: neuropeptide; amidated carboxyl end; tachykinin
F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 82.0%; Score 50; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.0042;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
DB 1 RPKPOQFFGLM 11

RESULT 17
S23306
substance P - Atlantic cod
C:Species: Gadus morhua (Atlantic cod)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C:Accession: S23306
R:Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A>Title: Substance-P-related and neurokinin-A-related peptides from the brain of the
A:Reference number: S23186; MID:92298992
A:Accession: S23306
A:Molecule type: protein
A:Residues: 1-11 <JEN>
A:Experimental source: brain
C:Function:
A:Description: may play a physiological role in the regulation of cardiovascular and
A:Note: substance P is derived by post-translational processing of preprotachykinin A
C:Superfamily: unassigned animal peptides
C:Keywords: neuropeptide; amidated carboxyl end; tachykinin
F:11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 80.3%; Score 49; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.0064;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
DB 1 RPKPOQFFGLM 11

RESULT 18
S33300
probable substance P - smaller spotted catshark
C:Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999

C:Accession: S33300
R:Maugh, D.; Wang, Y.; Hazen, N.; Balmert, R.J.; Conlon, J.M.
Eur. J. Biochem. 214, 469-474, 1993
A:Title: Primary structures and biological activities of substance-P-related peptides from
A:Reference number: S33300; MUID:93292508
A:Accession: S33300
A:Molecule type: protein
A:Residues: 1-11 <MAU>
A:Experimental source: brain
C:Function:
A:Description: may play a physiological role in the regulation of cardiovascular and gas
A:Note: substance P is derived by post-translational processing of preprotachykinin A
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 78.7%; Score 48; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.0098;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
: | : | | | | |
Db 1 KPRGQFFGLM 11

RESULT 19
F60409
Substance P-like peptide II - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C:Accession: F60409
R:Stimaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro
A:Reference number: A60409; MUID:90287814
A:Accession: F60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 72.1%; Score 44; DB 2; Length 11;
Best Local Similarity 63.6%; Pred. No. 0.052;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
: | : | | | | |
Db 1 QPNPEFFGLM 11

RESULT 20
E60409
Substance P-like peptide I - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C:Accession: E60409
R:Stimaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro
A:Reference number: A60409; MUID:90287814
A:Accession: E60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 72.1%; Score 44; DB 2; Length 11;

Best Local Similarity 63.6%; Pred. No. 0.052;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
: | : | | | | |
Db 1 QPNPEFFGLM 11

RESULT 21
S10059
tachykinin - African tree frog (Kassina maculata)
N:Alternate names: hylambates-kassinin
C:Species: Kassina maculata
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Sep-2000
C:Accession: S10059
R:Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.
Biomed. Res. 2, 613-617, 1981
A:Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, 1
A:Reference number: S07436
A:Accession: S10059
A:Molecule type: protein
A:Residues: 1-12 <YAS>
A:Experimental source: skin
A:Note: the source is designated as Hylambates maculatus
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 72.1%; Score 44; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 0.057;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOFFGLM 11
| | | | | | |
Db 3 KPDQFVGLM 12

RESULT 22
A61033
raatachykinin A - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C:Accession: A61033; JE0426
R:Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.
Regul. Pept. 42(Suppl.1), S12, 1992
A:Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and 1
A:Reference number: A61033
A:Accession: A61033
A:Molecule type: protein
A:Residues: 1-11 <KAN>
R:Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 177, 588-595, 1991
A:Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and 1
A:Reference number: JE0426; MUID:91254337
A:Accession: JE0426
A:Molecule type: protein
A:Residues: 1-11 <KO2>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; neuropeptide
F:1/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 67.2%; Score 41; DB 2; Length 11;
Best Local Similarity 54.5%; Pred. No. 0.19;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
: | : | | | | |
Db 1 KPSDRFVGLM 11

RESULT 23

T13857
trithorax protein - fruit fly (Drosophila virilis)
C:Species: Drosophila virilis
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13857
R:Mazo, A.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z17801
A:Accession: T13857
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3828 <MAZ>
A:Cross-references: EMBL:Z50038; NID:g899253; PID:g899254; PIDN:CAA90349.1
C:Genetics:
A:Cross-references: FlyBase:FBgn0014844
A:Introns: 337/3; 529/1; 721/1; 791/1; 3668/2; 3713/1; 3771/3
C:Superfamily: Drosophila trithorax protein
C:Keywords: DNA binding; transcription regulation; zinc finger

Query Match 67.2%; Score 41; DB 2; Length 3828;
Best Local Similarity 60.0%; Pred. No. 66;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFGL 10
|||: |||
DB 618 RPKPKNYFGL 627

RESULT 24
T30016
hypothetical protein F38E9.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T30016
R:Wu, X.; Gattung, S.
submitted to the EMBL Data Library, January 1996
A:Description: The sequence of C. elegans cosmid F38E9.
A:Reference number: Z20722
A:Accession: T30016
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-205 <WUX>
A:Cross-references: EMBL:U46668; PIDN:AAA93346.1; CESP:F38E9.4
C:Genetics:
A:Gene: CESP:F38E9.4

Query Match 62.3%; Score 38; DB 2; Length 205;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 RPKPOQF 8
|||: |||
DB 151 RPKPOQF 157

RESULT 25
T10586
small nuclear ribonucleoprotein-associated protein homolog F9F13.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 19-May-2000
C:Accession: T10586
R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z16991
A:Accession: T10586
A:Molecule type: DNA
A:Residues: 1-257 <BEV>
A:Cross-references: EMBL:AL080253; GSPDB:GN00062; ATSP:F9F13.90
A:Experimental source: cultivar Columbia; BAC clone F9F13
C:Genetics:
A:Gene: ATSP:F9F13.90

A:Map position: 4
C:Superfamily: proline-rich protein

Query Match 62.3%; Score 38; DB 2; Length 257;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFPG 9
|||: |||
DB 189 RPKPOQFPG 197

RESULT 26
T04951
hypothetical protein F7J7.140 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-Aug-1999
C:Accession: T04951
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.
submitted to the Protein Sequence Database, July 1998
A:Reference number: Z15391
A:Accession: T04951
A:Molecule type: DNA
A:Residues: 1-293 <BEV>
A:Cross-references: EMBL:AL021960
A:Experimental source: cultivar Columbia; BAC clone F7J7
C:Genetics:
A:Map position: 4
A:Introns: 107/2; 214/3
A:Note: F7J7.140
C:Superfamily: L-aminocyclopropane-1-carboxylate oxidase

Query Match 62.3%; Score 38; DB 2; Length 293;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 RPKPOFFGLM 11
|||: |||
DB 159 RPKPEVYGLM 168

RESULT 27
C60409
kassinin-like peptide K-II - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C:Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000
C:Accession: C60409
R:Stimaco, M.; Severini, C.; De Biae, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melch
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Aus
A:Reference number: A60409; MUID:90287814
A:Accession: C60409
A:Molecule type: protein
A:Residues: 1-11 <STM>
A:Note: this peptide was also found in a deamidated form
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 60.7%; Score 37; DB 2; Length 11;
Best Local Similarity 54.5%; Pred. No. 0.99;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
|||: |||
DB 1 QPNPDERVGLM 11

RESULT 28

S07203
uperolein - frog (Uperoleia marmorata)
C:Species: Uperoleia marmorata
C>Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C:Accession: S07203
R:Anastasi, A.; Erspamer, V.; Eudean, R.
A:Title: Structure of uperolein, a physalaemin-like endecapeptide occurring in the skin
A:Reference number: S07203; MUID:75131227
A:Accession: S07203
A:Molecule type: protein
A:Residues: 1-11 <ANA>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 60.7%; Score 37; DB 2; Length 11;
Best Local Similarity 54.5%; Pred. No. 0.99;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
: 1 1 1 1 1 1 1 1 1 1 1 1
Db 1 QPDPNPFVGLM 11

RESULT 29
G75189
hypothetical protein PAB2321 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: G75189
R:Anonymous; Genoscope
Submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: G75189
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <KAM>
A:CROSS-references: GB:A7248283; GB:AL096836; NID:95457433; PIDN:CAB48966.1; PID:9545747
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2321

Query Match 60.7%; Score 37; DB 2; Length 249;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGL 10
: 1 1 1 1 1 1 1 1 1 1 1 1
Db 124 RIKPEKFFGI 133

RESULT 30
D60409
kassinin-like peptide K-III - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
C:Accession: D60409
R:Stimaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro
A:Reference number: A60409; MUID:90287814
A:Accession: D60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 59.0%; Score 36; DB 2; Length 11;
Best Local Similarity 54.5%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
: 1 1 1 1 1 1 1 1 1 1 1 1
Db 1 QPDPNPFVGLM 11

RESULT 31
B60409
kassinin-like peptide K-I - frog (Pseudophryne guentheri)
C:Species: Pseudophryne guentheri
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000
C:Accession: B60409
R:Stimaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melch
Peptides 11, 299-304, 1990
A:Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Aus
A:Reference number: A60409; MUID:90287814
A:Accession: B60409
A:Molecule type: protein
A:Residues: 1-11 <SIM>
A:Note: this peptide was also found in a deamidated form
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 59.0%; Score 36; DB 2; Length 11;
Best Local Similarity 54.5%; Pred. No. 1.5;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
: 1 1 1 1 1 1 1 1 1 1 1 1
Db 1 QPDPNPFVGLM 11

RESULT 32
S07436
tachykinin - African tree frog (Kassina maculata)
N:Alternate names: hylambatin
C:Species: Kassina maculata
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Sep-2000
C:Accession: S07436
R:Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.
Biomol. Res. 2, 613-617, 1981
A:Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, 1
A:Reference number: S07436
A:Accession: S07436
A:Molecule type: protein
A:Residues: 1-12 <YAS>
A:Experimental source: skin
A:Note: the source is designated as Hylambates maculatus
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
F:12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 59.0%; Score 36; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.6;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 RPKPOQFFGLM 11
: 1 1 1 1 1 1 1 1 1 1 1 1
Db 3 PDPDRFVGLM 12

RESULT 33
S07206
kassinin - Senegal running frog

C:Species: *Kassina senegalensis* (Senegal running frog)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 02-Sep-2000
C:Accession: S07206
R:Anastasi, A.; Montecucchi, P.; Erspamer, V.; Visser, J.
E:Experientia 33, 857-858, 1977
A:Title: Amino acid composition and sequence of kassinin, a tachykinin dodecapeptide from
A:Reference number: S07206; MUID:77246385
A:Accession: S07206
A:Molecule type: protein
A:Residues: 1-12 <ANK>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end
F:12/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 59.0%; Score 36; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 2 PKPOQFGLM 11
3 PKSDQFVGLM 12

RESULT 34
A64173
conserved hypothetical protein H11608 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 19-May-2000
C:Accession: A64173
R:Feischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Shirley, R.; Liu, L.I.; Glodex, A.; Kelley, J.M.; Weidman, J.
Science 269, 496-512, 1995
A:Authors: Guehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: A64173
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-321 <TRIGR>
A:Cross-references: GB:L42023; NID:g1574444; PIDN:AAC23252.1; PID:g1574450; TIGR:H11608
C:Genetics:
A:Start codon: GTG
C:Superfamily: conserved hypothetical protein HPI443

Query Match 59.0%; Score 36; DB 2; Length 321;
Best Local Similarity 54.5%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 1 RPKPOQFFGLM 11
281 RQKPEAFEGFV 291

RESULT 35
T02976
probable DNA binding protein PCF2 - rice
C:Species: *Oryza sativa* (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T02976
R:Kosugi, S.; Ohashi, Y.
Plant Cell 9, 1607-1619, 1997
A:Title: PCF1 and PCF2 specifically bind to cis elements in the rice proliferating cell
A:Reference number: Z14803; MUID:97480096
A:Accession: T02976
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: mRNA
A:Residues: 1-373 <KOS>
A:Cross-references: EMBL:D87261; NID:g2580439; PIDN:BA23143.1; PID:g2580440
A:Experimental source: cultivar Nipponbare

Query Match 59.0%; Score 36; DB 2; Length 373;
Best Local Similarity 54.5%; Pred. No. 52;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 1 RPKPOQFFGLM 11
55 KPEPVEFGCM 65

RESULT 36
T19563
hypothetical protein C29F3.2 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T19563; T23034
R:Matthews, L.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19142
A:Accession: T19563
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: DNA
A:Residues: 1-629 <WID>
A:Cross-references: EMBL:Z81043; PIDN:CAB02804.1; GSPDB:GN00023; CESP:C29F3.2
A:Experimental source: clone C29F3
R:White, S.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z19657
A:Accession: T23034
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: DNA
A:Residues: 1-629 <WID>
A:Cross-references: EMBL:AL023813; PIDN:CA19424.1; GSPDB:GN00023; CESP:C29F3.2
A:Experimental source: clone H02K04
C:Genetics:
A:Gene: CESP:C29F3.2
A:Map position: 5
A:introns: 23/1; 111/3; 177/3; 207/2; 287/1; 381/3; 399/3; 417/1; 476/2; 528/3; 537/2

Query Match 59.0%; Score 36; DB 2; Length 629;
Best Local Similarity 75.0%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 RPKPOQFF 8
380 QPPPOQFF 387

RESULT 37
E69486
translation elongation factor EF-2 (fus) homolog - *Archaeoglobus fulgidus*
C:Species: *Archaeoglobus fulgidus*
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C:Accession: E69486
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodex, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utlacker, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woesle, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: E69486
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-728 <KLE>
A:Cross-references: GB:AF000972; GB:AF000782; NID:g2689295; PIDN:AA89360.1; PID:g264
C:Superfamily: translation elongation factor 2; translation elongation factor Tu homo
C:Keywords: GTP binding; nucleotide binding; P-loop
F:21-150/Domain: translation elongation factor Tu homology <ETU>
F:27-34/Region: nucleotide-binding motif A (P-loop)
F:147-150/Region: GTP-binding NKXD motif

F:202-204/Region: GTP-binding SAK/L motif
F:33,34,70,147,148,150,202/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta

Query Match 59.0%; Score 36; DB 2; Length 728;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPQOFFGL 1.0
|||: |||
Db 720 PKPEDFVGL 728

RESULT 38

A25777 T-cell receptor beta-2 chain precursor V region (MOLT-4) - human

C:Species: Homo sapiens (man)

C>Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 29-Aug-1997

C:Accession: A25777

R:Turnaciliffe, A.; Kafford, R.; Milstein, C.; Forster, A.; Rabbitts, T.H.

Proc. Natl. Acad. Sci. U.S.A. 82, 5068-5072, 1985

A:Title: Sequence and evolution of the human T-cell antigen receptor beta chain genes.

A:Reference number: A94053; MUID:85270467

A:Accession: A25777

A:Molecule type: mRNA

A:Residues: 1-133 <TUN>

A:Cross-references: GB:M12886

C:Genetics:

A:Gene: GDB:TCRB

A:Cross-references: SDB:120405; OMIM:186930

A:Map position: 7q35-7q35

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

Query Match 57.4%; Score 35; DB 2; Length 133;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKPQOFFG 9
||: |||
Db 118 PKNEOFFG 125

RESULT 39

T33064 hypothetical protein F56C3.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000

C:Accession: T33064

R:Stonking, T.

submitted to the EMBL Data Library, May 1998

A:Description: The sequence of C. elegans cosmid F56C3.

A:Reference number: Z21276

A:Accession: T33064

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-206 <STO>

A:Cross-references: EMBL:AF067214; PIDN:AACT1009.1; GSPDB:GN00028; CESP:F56C3.9

A:Experimental source: strain Bristol N2; clone F56C3

C:Genetics:

A:Gene: CESP:F56C3.9

A:Map position: X

A:Introns: 43/2; 87/1; 116/1; 141/2; 184/3

Query Match 57.4%; Score 35; DB 2; Length 206;
Best Local Similarity 62.5%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOFF 8
||: |||
Db 188 KRPPOOFF 195

RESULT 40

A83049 hypothetical protein PA4779 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: A83049

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

oy, S.; Olson, M.V

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337

A:Accession: A83049

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-297 <STO>

A:Cross-references: GB:AE004891; GB:AE004091; NID:99951037; PIDN:AA08165.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA4779

Query Match 57.4%; Score 35; DB 2; Length 297;
Best Local Similarity 54.5%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOOFFGLM 11
||: |||
Db 111 RPRPGLFGL 121

RESULT 41

T05737

probable hordein C - barley

C:Species: Hordeum vulgare (barley)

C>Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 20-Aug-1999

C:Accession: T05737

R:Entwistle, J.

Carlsberg Res. Commun. 53, 247-258, 1988

A:Title: Primary structure of a C-hordein gene from barley.

A:Reference number: Z15444; MUID:89351278

A:Accession: T05737

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-347 <ENT>

A:Cross-references: EMBL:M36941; NID:q167062; PIDN:AAA92333.1; PID:q893242

A:Experimental source: cv. Boml, immature endosperm

C:Superfamily: gliadin

Query Match 57.4%; Score 35; DB 2; Length 347;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKPQOFF 8
||: |||
Db 60 PTPQOFF 66

RESULT 42

T15511 hypothetical protein C15C7.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15511

R:Leimbach, D.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid C15C7.

A:Reference number: Z18363

A:Accession: T15511

A:Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: DNA
A: Residues: 1-474 <LEI>
A: Cross-references: EMBL:U41528; NID: g1109795; PID: g1109800; PIDN: AAA83156.1; CESP: C15C7
C: Genetics:
A: Gene: CESP: C15C7.1
A: Introns: 31/3; 67/2; 106/1; 202/3; 235/3; 364/3; 410/3

Query Match 57.4%; Score 35; DB 2; Length 474;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQFGL 10
DB 457 PRPSAFGL 465

RESULT 43
E86671
lysine--tRNA ligase (EC 6.1.1.6) [imported] - Lactococcus lactis subsp. lactis (strain I
N: Alternate names: lysyl-tRNA synthetase
C: Species: Lactococcus lactis subsp. lactis
C: Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 31-Mar-2001
C: Accession: E86671
R: Bolotin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarne, K.; Weissbach, J.; Ehrlich
Genome Res. In press, 2001
A: Title: The complete genome sequence of the lactic acid bacterium.
A: Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
A: Reference number: A86625
A: Accession: E86671
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-494 <STO>
A: Cross-references: GB: A8005176; NID: g12723244; PIDN: AAK04471.1; GSPDB: GN00146
A: Experimental source: strain H1403
C: Genetics:
A: Gene: lysS
C: Superfamily: lysine--tRNA ligase
C: Keywords: ligase

Query Match 57.4%; Score 35; DB 2; Length 494;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFGL 10
DB 143 RPLPEKFGHL 152

RESULT 44
A82296
lysyl-tRNA synthetase, heat inducible VC0664 [imported] - Vibrio cholerae (strain N16961
C: Species: Vibrio cholerae
C: Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C: Accession: A82296
R: Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
charlson, D.; Emolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
Nature 406, 477-483, 2000
A: Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A: Reference number: A82035; MUID: 20406833
A: Accession: A82296
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-512 <HEI>
A: Cross-references: GB: AE004152; GB: AE003852; NID: g9655096; PIDN: AAF93829.1; GSPDB: GN001
A: Experimental source: serogroup O1, strain N16961; biotype El Tor
C: Genetics:
A: Gene: VC0664
A: Map position: 1
C: Superfamily: lysine--tRNA ligase

Query Match 57.4%; Score 35; DB 2; Length 512;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFGL 10
DB 152 RPLPEKFGHL 161

RESULT 45
S76815
hypothetical protein sl11477 - Synechocystis sp. (strain PCC 6803)
C: Species: Synechocystis sp.
A: Variety: PCC 6803
C: Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C: Accession: S76815
R: Kaneo, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,
O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A: Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
s.
A: Reference number: S74322; MUID: 97061201
A: Accession: S76815
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-832 <KAN>
A: Cross-references: EMBL: D90916; GB: AB001339; NID: g1653715; PIDN: BAA18727.1; PID: g165
A: Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C: Superfamily: Synechocystis hypothetical protein sl11477

Query Match 57.4%; Score 35; DB 2; Length 832;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFGL 10
DB 669 RPKQMFGL 678

RESULT 46
T23875
hypothetical protein R03E1.1 - Caenorhabditis elegans
C: Species: Caenorhabditis elegans
C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Feb-2000
C: Accession: T23875
R: McMurray, A.
submitted to the EMBL Data Library, March 1997
A: Reference number: Z19812
A: Accession: T23875
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-1043 <WIL>
A: Cross-references: EMBL: Z92837; PIDN: CAB07400.1; GSPDB: GN00028; CESP: R03E1.1
A: Experimental source: clone R03E1
C: Genetics:
A: Gene: CESP: R03E1.1
A: Map position: X
A: Introns: 34/3; 92/3; 164/3; 344/3; 512/2; 558/2; 830/3; 864/3; 1003/3

Query Match 57.4%; Score 35; DB 2; Length 1043;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQFGL 11
DB 955 PRQVFFNML 964

RESULT 47
H69071
DNA-directed DNA polymerase (EC 2.7.7.7) chain 2 MTH1536 [similarity] - Methanobacter

C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Mar-2001
C:Accession: H69071
R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
Otu, D.; Spadefora, R.; Vicaire, R.; Wang, Y.; Mierzbowski, J.; Gibson, R.; Jiwani, N.
K.I.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funcn
A:Reference number: A69000; MUID:98037514
A:Accession: H69071
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1092 <MTX>
A:Cross-references: GB:AE000913; GB:AE000666; NID:g2622646; PIDN:AAB86010.1; PID:g262265
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1536
C:Superfamily: Pyrococcus furiosus DNA-directed DNA polymerase chain 2
C:Keywords: nucleotidyltransferase

Query Match 57.4%; Score 35; DB 2; Length 1092;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PKPOFFGLM 11
|||: |||
Db 932 KPEQYTGIM 940

RESULT 48
A84743
Probable myosin heavy chain [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: A84743
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
Euse, D.; Niemann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: A84743
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1611 <STO>
A:Cross-references: GB:AE002093; NID:g6598338; PIDN:AAF18589.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g33240
A:Map position: 2
C:Superfamily: myosin MYO2; myosin motor domain homology

Query Match 57.4%; Score 35; DB 2; Length 1611;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOFFGLM 11
|||: |||
Db 1338 PQPSTFGRM 1347

RESULT 49
F86178
Hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F86178
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huiztar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F86178
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1736 <STO>
A:Cross-references: GB:AE005172; NID:g2494118; PIDN:AAB80627.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Superfamily: myosin MYO2; myosin motor domain homology

Query Match 57.4%; Score 35; DB 2; Length 1736;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOFFGLM 11
|||: |||
Db 1402 PQPSTFGRM 1411

RESULT 50
F96657
Hypothetical protein F16M19.10 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: F96657
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
Chin, C.W.; Hughes, B.; Huiztar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F96657
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-216 <STO>
A:Cross-references: GB:AE005173; NID:g10092246; PIDN:AAG12661.1; GSPDB:GN00141
C:Genetics:
A:Gene: F16M19.10
A:Map position: 1

Query Match 56.6%; Score 34.5; DB 2; Length 216;
Best Local Similarity 53.8%; Pred. No. 56;
Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 1 RPKPOQ--FGL 10
|||||: |||
Db 168 RPKPOQVYKFGI 180

RESULT 51
T36290
Probable integral membrane protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T36290
R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M
submitted to the EMBL Data Library, May 1998
A:Reference number: Z21603
A:Accession: T36290
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-167 <SEB>
A:Cross-references: EMBL:AL049819; PIDN:CAB42667.1; GSPDB:GN00070; SCOEDB:SCE7.08C
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCE7.08C

Query Match 55.7%; Score 34; DB 2; Length 167;
Best Local Similarity 55.6%; Pred. No. 54;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOFFG 9
||| :|||
Db 18 REPPLRFYC 26

RESULT 52
H81036
riboflavin kinase/FMN adenylyltransferase NMB1834 [Imported] - Neisseria meningitidis (S

C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: H81036

R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
rt, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755

A:Accession: H81036

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-306 <TEB>

A:Cross-references: GB:AE002534; GB:AE002098; NID:g7227095; PIDN:AAF2169.1; PID:g722708

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB1834

C:Superfamily: conserved hypothetical protein H10963

Query Match 55.7%; Score 34; DB 2; Length 306;
Best Local Similarity 55.6%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 RPKPOFFGL 10
|:|:| :|||
Db 56 PPKKEFFAL 64

RESULT 53
T13601
hypothetical protein 80H7.5 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000

C:Accession: T13601

R:Benos, P.
submitted to the EMBL Data Library, April 1999

A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A:Reference number: Z17667

A:Accession: T13601

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-316 <BEN>

A:Cross-references: EMBL:AL031027; NID:el313443; PID:el310143; PIDN:CAA19842.1

C:Genetics:

A:Cross-references: FlyBase:FBgn0000481

Query Match 55.7%; Score 34; DB 2; Length 316;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOFF 8
||| :|||
Db 49 RPKSROFF 56

RESULT 54

A81982

PAD synthase NMA0621 [similarity] - Neisseria meningitidis (strain Z2491 serogroup A)

N:contains: FMN adenylyltransferase (EC 2.7.7.2); riboflavin kinase (EC 2.7.1.26)

C:Species: Neisseria meningitidis

C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

C:Accession: A81982

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo

; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491

A:Reference number: A81775; MUID:20222556

A:Accession: A81982

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-318 <PAR>

A:Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83911.1; PID:g737

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: rbf; NMA0621

C:Superfamily: conserved hypothetical protein H10963

C:Keywords: nucleotidyltransferase; phosphotransferase

Query Match 55.7%; Score 34; DB 2; Length 318;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 RPKPOFFGL 10
|:|:| :|||
Db 68 PPKKEFFAL 76

RESULT 55
T52337
phosphoprotein phosphatase (EC 3.1.3.16) 2C [Imported] - common ice plant

C:Species: Mesembryanthemum crystallinum (common ice plant)

C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000

C:Accession: T52337

R:Miyaizaki, S.; Koga, R.; Bohner, H.J.; Fukuhara, T.
Mol. Gen. Genet. 261, 307-316, 1999

A:Title: Tissue- and environmental response-specific expression of 10 PP2C transcrip

A:Reference number: Z26045; MUID:99200489

A:Accession: T52337

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-359 <MIY>

A:Cross-references: EMBL:AF075580; PIDN:AC36698.1

C:Genetics:

A:Gene: PP2C

C:Keywords: phosphoric monoester hydrolase

Query Match 55.7%; Score 34; DB 2; Length 359;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 RPKPOFFGL 10
||| :|||
Db 84 PKPSAFYGV 92

RESULT 56
S73890
hypothetical protein yarl homolog A65_orf493 - Mycoplasma pneumoniae (strain ATCC 293
N:Alternate names: hypothetical protein A65_orf493
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342

C>Date: 27-Feb-1997 #sequence,revision 25-Apr-1997 #text_change 17-Mar-2000
C:Accession: S73890
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Hermann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumoniae*
A:Reference number: S73327; MUID:97105885
A:Accession: S73890
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-493 <HIM>
A:Cross-references: EMBL:AE000056; GB:U00089; NID:91674263; PIDN:AA96212.1; PID:9167426
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Gene: ysr1
A:Genetic code: SGC3
C:Superfamily: hypothetical protein ymda

Query Match 55.7%; Score 34; DB 2; Length 493;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PKPOFFEG 11
|||
Db 281 PKLHFFEL 290

RESULT 57
S48058
cytochrome P450 CYP5B1 - black swallowtail
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Papilio polyxenes (black swallowtail)
C>Date: 10-Sep-1999 #sequence,revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: S48058
R:Prapalpong, H.; Barenbaum, M.R.; Schuler, M.A.
Nucleic Acids Res. 22, 3210-3217, 1994
A:Title: Transcriptional regulation of the Papilio polyxenes CYP6B1 gene.
A:Reference number: S48058; MUID:94344788
A:Accession: S48058
A:Molecule type: DNA
A>Status: preliminary
A:Residues: 1-498 <2RA>
A:Cross-references: EMBL:Z29624; NID:9520879; PIDN:CA82732.1; PID:9520880
R:Chen, M.B.; Schuler, M.A.; Barenbaum, M.R.
Proc. Natl. Acad. Sci. U.S.A. 89, 10920-10924, 1992
A:Title: A host-inducible cytochrome P-450 from a host-specific caterpillar: molecular
A:Reference number: A46367; MUID:9306355
A:Accession: A46367
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-23, 'N', 25-154, 'NS', 157-498 <COH>
A:Cross-references: GB:M80828; NID:9160763; PIDN:AAA29789.1; PID:9160764
A>Note: sequence extracted from NCBI backbone (NCBIN:118719, NCBI:P:118720)
C:Genetics:
A:Introns: 445/1
C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F:300-465/Domain: cytochrome P450 homology <P45>
F:443/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 55.7%; Score 34; DB 1; Length 498;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PKPOFFEG 9
|||
Db 34 PKVPFFEG 41

RESULT 58
JX0334
cytochrome P450 3A R1J3 - rat

N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Mar-1994 #sequence,revision 28-Oct-1994 #text_change 28-Jul-2000
C:Accession: JX0334; S39797
R:Komori, M.; Oda, Y.
J. Biochem. 116, 114-120, 1994
A:Title: A major glucocorticoid-inducible P450 in rat liver is not P450 3A1.
A:Reference number: JX0334; MUID:95096005
A:Accession: JX0334
A:Molecule type: mRNA
A:Residues: 1-502 <KOM>
A:Cross-references: GB:D29967; NID:9479038; PIDN:BA06233.1; PID:9479039

A:Experimental source: Liver
R:Kirita, S.; Matsubara, T.
Arch. Biochem. Biophys. 307, 253-258, 1993
A:Title: cDNA cloning and characterization of a novel member of steroid-induced cytochrome P450
A:Reference number: S39797; MUID:94099605
A:Accession: S39797
A:Molecule type: mRNA
A:Residues: 1-106, 'D', 108-502 <KIR>
A:Cross-references: EMBL:D13912; NID:9220835; PIDN:BA03008.1; PID:9220836; GB:X96721
C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C:Keywords: chromoprotein; heme; iron; metalloprotein; monooxygenase; oxidoreductase;
F:301-463/Domain: cytochrome P450 homology <P45>
F:441/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 55.7%; Score 34; DB 2; Length 502;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PKPOFFEG 9
|||
Db 41 PKPLPFFEG 48

RESULT 59
A40843
cytochrome P450 3 - golden hamster
N:Contains: oxidoreductase (EC 1.-.-.-)
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 27-Mar-1992 #sequence,revision 27-Mar-1992 #text_change 28-Jul-2000
C:Accession: A40843
R:Teitel, J.; Gil, G.
J. Biol. Chem. 266, 21030-21036, 1991
A:Title: Cloning, expression, and regulation of lithocholic acid 6beta-hydroxylase.
A:Reference number: A40843; MUID:92041973
A:Accession: A40843
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-503 <TEI>
A:Cross-references: GB:M73992
C:Genetics:
A:Gene: CYP3A10
C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase
F:302-464/Domain: cytochrome P450 homology <P45>
F:442/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 55.7%; Score 34; DB 2; Length 503;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PKPOFFEG 9
|||
Db 41 PKPLPFFEG 48

RESULT 60
A22631
cytochrome P450 3A1, pregnenolone 16-alpha-carbonitrile-inducible - rat
N:Alternate names: testosterone 6beta-hydroxylase

N:Contains: unspecific monooxygenase (EC 1.14.14.1) cytochrome P450 PCN1
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 28-Jul-2000
C:Accession: A22631; PX0035; S21697; S36137; S27107; S30378; I59218
R:Gonzalez, F.J.; Nebert, D.W.; Hardwick, J.P.; Kasper, C.B.
J. Biol. Chem. 260, 7435-7441, 1985
A:Title: Complete cDNA and protein sequence of a pregnenolone 16-alpha-carbonitrile-indu
A:Reference number: A22631; MUID:85207783
A:Accession: A22631
A:Molecule type: mRNA
A:Residues: 1-504 <GON>
A:Cross-references: GB:M10161; NID:9203777; PIDN:AAA41035.1; PID:9203778
R:Natata, K.; Gonzalez, F.J.; Yamazoe, Y.; Kato, R.
J. Biochem. 107, 718-725, 1990
A:Title: Purification and characterization of four catalytically active testosterone 6be
nally related forms.
A:Reference number: PX0032; MUID:90375438
A:Accession: PX0035
A:Molecule type: protein
A:Residues: 1-26 <NAG>
A:Experimental source: liver, Sprague-Dawley male rat
R:Lechner, M.C.
submitted to the EMBL Data Library, December 1991
A:Reference number: S21697
A:Accession: S21697
A:Molecule type: mRNA
A:Residues: 1-206, 'A', 208-212, 'T', 214-231, 'V', 233-504 <LEC>
A:Cross-references: EMBL:X64401; NID:956038; PIDN:CAA45743.1; PID:956039
R:Albeiro, V.; Lechner, M.C.
Arch. Biochem. Biophys. 293, 147-152, 1992
A:Title: Cloning and characterization of a novel CYP3A1 allelic variant: Analysis of CYP
A:Reference number: S36137; MUID:92117688
A:Accession: S36137
A:Molecule type: mRNA
A:Residues: 205-206, 'A', 208-212, 'T', 214-231, 'V', 233-234 <RTB>
A:Cross-references: EMBL:X64401
R:Teilhada, M.B.; Pereira, T.M.; Lechner, M.C.
Arch. Biochem. Biophys. 298, 715-725, 1992
A:Title: Effect of dexamethasone and phenobarbital on run-on transcription rate and CYP3
A:Reference number: S27107; MUID:93037516
A:Accession: S27107
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-24 <TEL>
A:Cross-references: EMBL:X62086
R:Cooper, K.O.; Reik, L.M.; Jayyosi, Z.; Bandiera, S.; Kelley, M.; Ryan, D.E.; Daniel, H
Arch. Biochem. Biophys. 301, 345-354, 1993
A:Title: Regulation of two members of the steroid-inducible cytochrome P450 subfamily (3
A:Reference number: S30378; MUID:93213168
A:Accession: S30378
A:Molecule type: protein
A:Residues: 1-25 <COO>
R:Burger, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 2145-2149, 1992
A:Title: Paradoxical transcriptional activation of rat liver cytochrome P-450 3A1 by dex
to primary monolayer cultures of adult rat hepatocytes.
A:Reference number: I59218; MUID:92196074
A:Accession: I59218
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-24 <BUR>
A:Cross-references: GB:M66850; NID:9205919; PIDN:AAA41780.1; PID:9205920
C:Genetics: CYP3A1; P450P
C:Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F:303-465/Domain: cytochrome P450 homology <P45>
F:443/Binding site: heme iron (Cys) (axial ligand) #status predicted

Qy 2 PKPQDFG 9 55.7%; Score 34; DB 2; Length 583;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 41 PKPLPFG 48
RESULT 61
catechol oxidase (EC 1.10.3.1) p2 precursor - potato (fragment)
S30930
N:Alternate names: polyphenol oxidase
C:Species: Solanum tuberosum (potato)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Feb-2000
A:Accession: S30930
R:Hunt, M.D.; Eannetta, N.T.; Yu, H.; Newman, S.M.; Steffens, J.C.
Plant Mol. Biol. 21, 59-68, 1993
A:Title: cDNA cloning and expression of potato polyphenol oxidase.
A:Reference number: S30929; MUID:93144692
A:Accession: S30930
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-583 <HUN>
C:Superfamily: catechol oxidase
C:Keywords: chloroplast; copper; oxidoreductase
F:1-84/Domain: transit peptide (chloroplast) (fragment) #status predicted <TNP>
F:85-583/Product: catechol oxidase #status predicted <MAT>
F:193-202/Binding site: copper (His) #status predicted
F:324-328, 359/Binding site: copper (His) #status predicted

Qy 2 PKPQDFG 9 55.7%; Score 34; DB 2; Length 583;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 296 PCPSQFFG 303
RESULT 62
catechol oxidase (EC 1.10.3.1) precursor - potato (fragment)
S34785
N:Alternate names: polyphenol oxidase
C:Species: Solanum tuberosum (potato)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Feb-2000
A:Accession: S34785
R:Hunt, M.D.; Eannetta, N.T.; Yu, H.; Newman, S.M.; Steffens, J.C.
submitted to the EMBL Data Library, June 1992
A:Reference number: S34785
A:Accession: S34785
A:Molecule type: mRNA
A:Residues: 1-583 <HUN>
A:Cross-references: EMBL:M95196
R:Hunt, M.D.; Eannetta, N.T.; Yu, H.; Newman, S.M.; Steffens, J.C.
Plant Mol. Biol. 21, 59-68, 1993
A:Title: cDNA cloning and expression of potato polyphenol oxidase.
A:Reference number: S30929; MUID:93144692
A:Contents: annotation
C:Superfamily: catechol oxidase
C:Keywords: chloroplast; copper; oxidoreductase
F:1-83/Domain: transit peptide (chloroplast) (fragment) #status predicted <MAT>
F:84-583/Product: catechol oxidase #status predicted
F:193-202/Binding site: copper (His) #status predicted

Qy 2 PKPQDFG 9 55.7%; Score 34; DB 2; Length 583;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 296 PCPSQFFG 303

RESULT 63
S33544
catechol oxidase (EC 1.10.3.1) precursor [similarity] - tomato
N:Alternate names: polyphenol oxidase precursor
C:Species: Lycopersicon esculentum (tomato)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
R:Newman, S.M.; Eannetta, N.T.; Yu, H.; Prince, J.P.; de Vicente, C.; Tanksley, S.D.; St
Plant Mol. Biol. 21, 1035-1051, 1993
A:Title: Organisation of the tomato polyphenol oxidase gene family.
A:Reference number: S33539; MUID:93257620
A:Accession: S33544
A:Molecule type: DNA
A:Residues: 1-585 <NEW>
A:Cross-references: EMBL:Z12838; NID:91403355; PIDN:CAA78300.1; PID:922735
R:Newman, S.M.; Eannetta, N.T.; Yu, H.; Prince, J.P.; de Vicente, C.; Tanksley, S.D.; St
submitted to the EMBL Data Library, June 1992
A:Description: Organization of the tomato polyphenol oxidase gene family.
A:Reference number: S22965
A:Accession: S22970
A:Molecule type: DNA
A:Residues: 1-582; 'ELKGIYLDLDYLDKLDNFILMLITLITSS' <NE2>
A:Cross-references: EMBL:Z12838
C:Superfamily: catechol oxidase
C:Keywords: oxidoreductase
F:197,206/Binding site: copper (His) #status predicted
F:326,330,361/Binding site: copper (His) #status predicted

Query Match 55.7%; Score 34; DB 1; Length 585;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PKPOOFFG 9
1 1 1111
Db 300 PCPSQFFG 307

RESULT 64
S33543
catechol oxidase (EC 1.10.3.1) E, precursor [similarity] - tomato
N:Alternate names: polyphenol oxidase
C:Species: Lycopersicon esculentum (tomato)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
A:Accession: S33543; JQ1672; S22969
R:Newman, S.M.; Eannetta, N.T.; Yu, H.; Prince, J.P.; de Vicente, C.; Tanksley, S.D.; St
Plant Mol. Biol. 21, 1035-1051, 1993
A:Title: Organisation of the tomato polyphenol oxidase gene family.
A:Reference number: S33539; MUID:93257620
A:Accession: S33543
A:Molecule type: DNA
A:Residues: 1-587 <NEW>
A:Cross-references: EMBL:Z12837; NID:91403354; PIDN:CAA78299.1; PID:922733
R:Shahar, T.; Hentley, N.; Gutfinger, T.; Hareven, D.; Lifschitz, E.
Plant Cell 4, 135-147, 1992
A:Title: The tomato 66.3-kD polyphenol oxidase gene: molecular identification and develop
A:Reference number: JQ1672; MUID:92338844
A:Accession: JQ1672
A:Molecule type: DNA
A:Residues: 1-310; 'UWVUNV', 316-409, 'V', 411-540, 'V', 542-566, 'I', 568-573, 'G', 575-587 <SHA>
A:Cross-references: GB:S40548; NID:9251894; PIDN:AMB22610.1; PID:9251895
A:Experimental source: tomato flowers cv Tiny Tim LA154
C:Genetics:
A:Gene: P2
C:Superfamily: catechol oxidase
C:Keywords: copper; oxidoreductase
F:197,206/Binding site: copper (His) #status predicted
F:328,332,363/Binding site: copper (His) #status predicted

QY 2 PKPOOFFG 9
1 1 1111
Db 300 PCPSQFFG 307

RESULT 65
S30929
catechol oxidase (EC 1.10.3.1) P1 precursor - potato (fragment)
N:Alternate names: polyphenol oxidase
C:Species: Solanum tuberosum (potato)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Feb-2000
C:Accession: S30929
R:Hunt, M.D.; Eannetta, N.T.; Yu, H.; Newman, S.M.; Steffens, J.C.
Plant Mol. Biol. 21, 59-68, 1993
A:Title: cDNA cloning and expression of potato polyphenol oxidase.
A:Reference number: S30929; MUID:93144692
A:Accession: S30929
A:Molecule type: mRNA
A:Residues: 1-588 <HUN>
A:Cross-references: EMBL:S54002
C:Superfamily: catechol oxidase
C:Keywords: chloroplast; copper; oxidoreductase
F:1-88/Domain: transit peptide (chloroplast) (fragment) #status predicted <MAP>
F:89-588/Product: catechol oxidase #status predicted
F:198,207/Binding site: copper (His) #status predicted
F:329,333,364/Binding site: copper (His) #status predicted

Query Match 55.7%; Score 34; DB 2; Length 588;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PKPOOFFG 9
1 1 1111
Db 301 PCPSQFFG 308

RESULT 66
S34786
catechol oxidase (EC 1.10.3.1) precursor - potato (fragment)
N:Alternate names: polyphenol oxidase
C:Species: Solanum tuberosum (potato)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Feb-2000
A:Accession: S34786
R:Hunt, M.D.; Eannetta, N.T.; Yu, H.; Newman, S.M.; Steffens, J.C.
submitted to the EMBL Data Library, June 1992
A:Reference number: S34785
A:Accession: S34786
A:Molecule type: mRNA
A:Residues: 1-588 <HUN>
A:Cross-references: EMBL:M95197
R:Hunt, M.D.; Eannetta, N.T.; Yu, H.; Newman, S.M.; Steffens, J.C.
Plant Mol. Biol. 21, 59-68, 1993
A:Title: cDNA cloning and expression of potato polyphenol oxidase.
A:Reference number: S30929; MUID:93144692
A:Contents: annotation
C:Superfamily: catechol oxidase
C:Keywords: chloroplast; copper; oxidoreductase
F:1-88/Domain: transit peptide (chloroplast) (fragment) #status predicted <MAP>
F:89-588/Product: catechol oxidase #status predicted
F:198,207/Binding site: copper (His) #status predicted

Query Match 55.7%; Score 34; DB 1; Length 587;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

RESULT 67
D86466
hypothetical protein AAD39611.1 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D86466
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizart, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marzalli,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: D86466
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-628 <STO>
C:Cross-references: GB:AE05172; NID:g5091623; PIDN:AA039611.1; GSPDB:GN0141
C:Genetics:
A:Map position: 1

Query Match
Best Local Similarity 55.7%; Score 34; DB 2; Length 628;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFF 8
1 111111
DB 267 RRPQEFF 274

RESULT 68
S56781
hypothetical protein YJ1010C - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein J1357
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 05-Nov-1999
C:Accession: S56781
R:To Van, D.; Pereira, J.; Jacq, C.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S56776
A:Accession: S56781
A:Molecule type: DNA
A:Residues: 1-666 <DEH>
A:Cross-references: EMBL:Z49285; NID:g1006722; PIDN:CAA89301.1; PID:g1006723; GSPDB:GN00
C:Genetics:
A:Gene: MIPS:YJ1010C
A:Map position: 10L

Query Match
Best Local Similarity 55.7%; Score 34; DB 2; Length 666;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOQFFGLM 11
1 111111
DB 48 QPQMFGLV 56

RESULT 69
S44920
ZK688.5 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S44920
R:Wilson, R.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid ZK688.
A:Reference number: S44913

A:Accession: S44920
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1799 <WIL>
A:Cross-references: EMBL:L16621; NID:g289775; PID:g289783
C:Genetics:
A:Insertions: 40/3; 96/2; 269/2; 357/1; 486/3; 1129/3; 1194/1; 1425/1; 1503/1; 15
C:Superfamily: Caenorhabditis elegans ZK688.5 protein; ubiquitin homology
F:21-96/Domain: ubiquitin homology <UBH>

Query Match
Best Local Similarity 85.7%; Score 34; DB 1; Length 1799;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQF 7
1 111111
DB 552 RPTPOQF 558

RESULT 70
G81889
hypothetical protein NMA1216 [imported] - Neisseria meningitidis (strain Z2491 serogr
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: G81889
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: A81775; MUID:20222556
A:Accession: G81889
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84476.1; PID:g737
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1216

Query Match
Best Local Similarity 54.1%; Score 33; DB 2; Length 71;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOQFFG 9
1 111111
DB 40 KPERFFG 46

RESULT 71
G71054
hypothetical protein PH1133 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C:Accession: G71054
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137
A:Accession: G71054
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-101 <KAW>
A:Cross-references: GB:AP000005; NID:g3236137; PIDN:BAA30233.1; PID:g3257550
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBa
C:Genetics:
A:Gene: PH1133
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1133

```

Query Match 54.1%; Score 33; DB 2; Length 101;
 Best Local Similarity 75.0%; Pred. No. 49;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 PPOFFGLM 11
 |||||
 DB 18 PPOFFGLM 25

RESULT 72

F75254
 conserved hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: F75254
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Yamathayan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Mc
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 S:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896
 A:Accession: F75254
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-234 <WHIT>
 A:Cross-references: GB:AE002089; GB:AE000513; NID:96460427; PIDN:AAF12124.1; PID:9646041
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2585
 A:Map position: 1

Query Match 54.1%; Score 33; DB 2; Length 234;
 Best Local Similarity 75.0%; Pred. No. 1,1e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PPOFFGLM 11
 |||||
 DB 56 PPOFFGLM 63

RESULT 73

T15304
 hypothetical protein B0280.10 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
 C:Accession: T15304
 R:Puliton, L.
 S:Submitted to the EMBL Data Library, June 1994
 A:Description: The sequence of C. elegans cosmid B0280.
 A:Reference number: S48966
 A:Accession: T15304
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-282 <FUL>
 A:Cross-references: EMBL:U10439; NID:9500762; PID:9500771; PIDN:AAAI9088.1; CESP:B0280.1
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:B0280.10
 A:Introns: 39/3; 89/1; 119/1; 133/2; 183/1; 212/3; 243/3
 C:Superfamily: Caenorhabditis elegans hypothetical protein B0280.10

Query Match 54.1%; Score 33; DB 2; Length 282;
 Best Local Similarity 62.5%; Pred. No. 1,4e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOOFFG 9
 |||||
 DB 15 PKPOOFFG 22

RESULT 74

E70842
 probable acid phosphatase - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C:Accession: E70842

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garrier, T.; Churcher, C.; Harris, D.; Gordon
 ; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, S.; Skelton, S.; Squares, S.
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
 A:Reference number: A70500; MUID:98295987
 A:Accession: E70842
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-299 <COL>
 A:Cross-references: GB:AL021841; GB:AL123456; NID:93261517; PIDN:CAAI7082.1; PID:e125
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV3310

Query Match 54.1%; Score 33; DB 2; Length 299;
 Best Local Similarity 66.7%; Pred. No. 1,5e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOOFFGL 10
 |||||
 DB 181 PKPOOFFGL 189

RESULT 75

H71259
 probable membrane fusion protein - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
 C:Accession: H71259
 R:Fraser, C.M.; Norris, S.J.; Welstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Childsbaram, M.; Uterback, T.; M
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 S:Science 281, 375-388, 1998
 A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A:Reference number: A71250; MUID:98332770
 A:Accession: H71259
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-320 <COL>
 A:Cross-references: GB:AE001264; GB:AE000520; NID:93323278; PIDN:MAC65920.1; PID:9332
 A:Experimental source: strain Nichols
 C:Genetics:
 A:Gene: TP0965

Query Match 54.1%; Score 33; DB 2; Length 320;
 Best Local Similarity 55.6%; Pred. No. 1,6e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 KPOOFFGLM 11
 |||||
 DB 162 KPOOFFGLM 170

RESULT 76

A75633
 Probable transposase - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: A75633
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
 ; M.; Shen, M.; Yamathayan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.;
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 S:Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896
A:Accession: A75633
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <WHI>
A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12606.1; PID:g6460902; TIGR:DRB01
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRB0134
A:Map position: megaplasmid
A:Genome: plasmid
A:Note: plasmid MP1

Query Match 54.1%; Score 33; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
| | | | | : :
Db 297 RMRPOQFFMAIL 307

RESULT 77
C75624
probable transposase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: C75624
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: C75624
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <WHI>
A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12602.1; PID:g6460898; TIGR:DRB00
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRB0057
A:Map position: megaplasmid
A:Genome: plasmid
A:Note: plasmid MP1

Query Match 54.1%; Score 33; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
| | | | | : :
Db 297 RMRPOQFFMAIL 307

RESULT 78
E75618
probable transposase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: E75618; C75629
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: E75618
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <WHI>

A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12607.1; PID:g6460903; TIGR:DR
A:Experimental source: strain R1
A:Accession: C75629
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <WHI>
A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12607.1; PID:g6460903; TIGR:DR
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRB0005; DRB0102
A:Map position: megaplasmid
A:Genome: plasmid
A:Note: plasmid MP1

Query Match 54.1%; Score 33; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
| | | | | : :
Db 297 RMRPOQFFMAIL 307

RESULT 79
C75556
probable transposase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: C75556
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: C75556
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <WHI>
A:Cross-references: GB:AE001876; GB:AE000513; NID:g6457800; PIDN:AAF09729.1; PID:g645
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0144
A:Map position: 1

Query Match 54.1%; Score 33; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
| | | | | : :
Db 297 RMRPOQFFMAIL 307

RESULT 80
B75620
probable transposase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: B75620
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: B75620
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <WHI>
A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12598.1; PID:g6460894; TIGR:DR

```
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRB0020
A:Map position: megaplasmid
A:Genome: plasmid
A:Note: plasmid MP1
```

Very Match	54.1%;	Score 33;	DB 2;	Length 327;
1st Local Similarity	54.5%;	Pred. No. 1.6e+02;		
Matches	6;	Conservative	2;	Mismatches 3;
				Indels 0;
				Gaps 0;

```

OY      1 RPKPQQEFGIM 11
          | | | | |
Db      297 RWKPPQFMAIL 307

```

RESULT 81
A:54871
Gal beta-1, 3GalNAc-specific GalNAc alpha2, 6-sialyl]transferase - chicken
C:Species: Gallus gallus (chicken)
C:Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 24-Sep-1999
C:Accession: A54871
R:Kurosawa, N.; Kojima, N.; Inoue, M.; Hamamoto, T.; Tsuji, S.
J. Biol. Chem. 269, 19048-19053, 1994
A:Title: Cloning and expression of Galbeta1,3GalNAc-specific GalNAc alpha2,6-sialyl]trans
A:Reference number: A54871; MUID:94308168
A:Accession: A54871
A:Status: Preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-404 <KUS>
A:Cross-references: GB:J7775; NID:G550104; PIDN:CAA54813.1; PID:G550105
C:Superfamily: galactosyl-1,3-N-acetyl]galactosaminyl-specific alpha-2,6-sialyl]transferase

Query Match	54.1%	Score 33;	DB 2;	Length 404;
Best Local Similarity	62.5%;	Pred. NO. 2e+02;		
Matches	5;	Conservative	3;	Mismatches
			0;	Indels
			0;	Gaps
			0;	

QY	3	KPQQFFGL	10
		:11::111	
Db	288	EPQKXFGL	295

```

RESULT      82
F75434
hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: F75434
R:White, O.; Eelsen, J.A.; Heldelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: F75434
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-416 <WHI>
A:Cross-references: GB:AE001962; GB:AE000513; NID:g6458855; PIDN:AAF10703.1; PID:g6458860
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1127
A:Map position: 1

```

```

Query Match      54.1%; Score 33; DB 2; length 416;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0.
OY      2 PKPQQPFGLM 11
      1 1111111111

```

QY 2 PKPQQFFGLM 11
 | |:: |||:

Db 1.39 PTPRRLFGLL 148

RESULT 83
T37933
Transcription activator GCN5 homolog - fission yeast (*Schizosaccharomyces pombe*)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000
C:Accession: T37933
R:McDougal, R.C., Rajandream, M.A., Barrell, B.G., Bothe, G., Pohl, T.
submitted to the EMBL data library, August 1999
.:Reference number: Z21755

Query Match	54.18;	Score 33;	DB 2;	Length 454;
Best Local Similarity	36.48;	Pred. NO. 2.2e+02;		
Matches	4;	Conservative	5;	Mismatches 2;
				Indels 0;
				Gaps 0.

```
QY      1 RPKPQQFFGLM 11
          :|:|:|:|:|:
Db     342 KPRPKPFFAVL 352
```

RESULT 84
D64110
Lysine--tRNA ligase (EC 6.1.1.6) - Haemophilus influenzae (strain Rd KW20)
N/Alternate names: Lysyl-tRNA synthetase
C/Species: Haemophilus influenzae
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: D64110
R:/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
/Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodet, A.; Kelley, J.M.; Medman
/D.M.; Brindon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.;
Science 269, 496-512, 1995
A:/Authors: Gnehm, C.T., McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter
A:/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:/Reference number: A64000; MUID:95350630
A:/Accession: D64110
A:/Status: nucleic acid sequence not shown; translation not shown
A:/Molecule type: DNA
A:/Residues: 1-502 <TIGR>
A:/Cross-references: GB:U32800; GB:IL42023; NID:g15741133; PIDN:AC22865.1; PID:g1574141
C:/Superfamily: Lysine-tRNA ligase
/Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis

Query Match	54.1%;	Score 33;	DB 1;	Length 502;
Best Local Similarity	60.0%;	Pred. No. 2.5e+02;		
Matches	6;	Conservative	1;	Mismatches 3;
			Indels	0;
			Gaps	0;

```

QY      1 RPKPQQFFGL 10
          |||: ||
Db     147 RPLPKFHL 156

```

```

RESULT      85
SYEEXT
lysine--tRNA ligase (EC 6.1.1.6) - Escherichia coli
N:Alternate names: lysyl-tRNA synthetase I
C:Species: Escherichia coli
C:Date: 30-Jun-1991 #sequence_revstion 21-Nov-1997 #text_change 18-Jun-1999
:Accession: B65073; J50401; A38066; B31325

```

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: B65073
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-505 <BLAT>
A:Cross-references: GB:AE000372; GB:U00096; NID:92367171; PIDN:AACT5928.1; PID:91789256;
A:Experimental source: strain K-12, substrain MG1655
R:Leveque, F.; Plateau, P.; Dessen, P.; Blanquet, S.
Nucleic Acids Res. 18, 305-312, 1990
A:Title: Homology of *lys*S and *lys*U, the two *Escherichia coli* genes encoding distinct *lys*
A:Reference number: J50401; MUID:90221811
A:Accession: J50401
A:Molecule type: DNA
A:Residues: 1-396, 398-444, 'V', 445-505 <LE1>
A:Cross-references: GB:X16542
A:Experimental source: strain EM20031
A:Accession: A38066
A:Molecule type: protein
A:Residues: 1-28 <LE2>
R:Kawakami, K.; Joensson, Y.H.; Bjoerk, G.R.; Ikeda, H.; Nakamura, Y.
Proc. Natl. Acad. Sci. U.S.A. 85, 5620-5624, 1988
A:Title: Chromosomal location and structure of the operon encoding peptide-chain-release
A:Reference number: A32651; MUID:88289768
A:Accession: B31325
A:Molecule type: DNA
A:Residues: 1-505 <KAN>
A:Cross-references: GB:J03795; NID:9146339; PIDN:AAA23959.1; PID:9146341
C:Comment: In *E. coli*, *lys*S is activated and transferred to tRNA by two distinct forms
coded by the *lys*U gene.
C:Genetics:
A:Gene: *lys*S; *herc*
A:Map position: 62 min
C:Superfamily: *lys*Sine-tRNA ligase
C:Keywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase; protein biosynthesis
F:2-505/Product: *lys*Sine-tRNA ligase #status predicted <MAT>

Query Match 54.1%; Score 33; DB 1; Length 505;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKQOQFGL 10
|||:|:|
DB 151 RPLPDKFHGL 160

RESULT 86
STECKU
lysine-tRNA ligase (EC 6.1.1.6), thermoinducible - *Escherichia coli*
N:Alternate names: *lys*Y1-tRNA synthetase II; *lys*Y1-tRNA synthetase, thermoinducible
C:Species: *Escherichia coli*
C>Date: 30-Jun-1991 #sequence_revision 31-Oct-1997 #text_change 18-Jun-1999
C:Accession: S56356; H65222; J50400; JY0093
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A:Title: Analysis of the *Escherichia coli* genome VI: DNA sequence of the region from 92.
A:Reference number: S56314; MUID:95334362
A:Accession: S56356
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-505 <BUR>
A:Cross-references: EMBL:U14003; NID:91263172; PIDN:AA97029.1; PID:9536974
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: H65222

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-505 <BLAT>
A:Cross-references: GB:AE000485; GB:U00096; NID:91790563; PIDN:AACT7090.1; PID:917905
A:Experimental source: strain K-12, substrain MG1655
R:Leveque, F.; Plateau, P.; Dessen, P.; Blanquet, S.
Nucleic Acids Res. 18, 305-312, 1990
A:Title: Homology of *lys*S and *lys*U, the two *Escherichia coli* genes encoding distinct
A:Reference number: J50401; MUID:90221811
A:Accession: J50400
A:Molecule type: DNA
A:Residues: 1-445, 'R', 447-505 <LEV>
A:Cross-references: GB:X16542
R:Clark, R.L.; Neidhardt, F.C.
J. Bacteriol. 172, 3237-3243, 1990
A:Title: Roles of the two *lys*Y1-tRNA synthetases of *Escherichia coli*: analysis of nuc
A:Reference number: JY0093; MUID:90264318
A:Accession: JY0093
A:Molecule type: DNA
A:Residues: 1-124, 126-235, 'A', 237-257, 'HVT', 263-267, 'R', 270-350, 'R', 352-370, 'S', 372-3
A:Cross-references: GB:M30630; NID:9146688; PIDN:AAA24096.1; PID:9146689
C:Comment: In *E. coli*, *lys*S is activated and transferred to tRNA by two distinct fo
coded by the *lys*U gene.
C:Genetics:
A:Gene: *lys*U
A:Map position: 94 min
C:Superfamily: *lys*Sine-tRNA ligase
C:Keywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase; protein biosynthesis
F:2-505/Product: *lys*Sine-tRNA ligase #status predicted <MAT>

Query Match 54.1%; Score 33; DB 1; Length 505;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKQOQFGL 10
|||:|:|
DB 151 RPLPDKFHGL 160

RESULT 87
I38396
protein-tyrosine kinase (EC 2.7.1.112) FRK - human
N:Alternate names: FYN-related kinase (FRK)
C:Species: *Homo sapiens* (man)
C>Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 04-Feb-2000
C:Accession: I38396
R:Lee, J.; Wang, Z.; Luoh, S.M.; Wood, W.I.; Scadden, D.T.
Gene 138, 247-251, 1994
A:Title: Cloning of FRK, a novel intracellular SRC-like tyrosine kinase-encoding gene
A:Reference number: I38396; MUID:94171047
A:Accession: I38396
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-505 <RES>
A:Cross-references: EMBL:U00803; NID:9392887; PIDN:AAA18284.1; PID:9392888
C:Genetics:
A:Gene: GDB:FRK
A:Cross-references: GDB:355675
A:Map position: 4q35-4q35
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH
F:49-105/Domain: SH3 homology <SH3>
F:116-208/Domain: SH2 homology <SH2>
F:332-494/Domain: protein kinase homology <KIN>
F:240-248/Region: protein kinase ATP-binding motif
F:262/Active site: *lys* #status predicted

Query Match 54.1%; Score 33; DB 2; Length 505;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
||||: :|
Db 459 PQOFFYIM 466

RESULT 88
E86108
hypothetical protein lysu [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: E86108
R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouzis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E86108
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-505 <STO>
A:Cross-references: GB:AE005174; NID:912519106; PIDN:AAG59329.1; GSPDB:GN00145; UMGP:257
C:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: lysu
C:Superfamily: lysine--tRNA ligase

Query Match 54.1%; Score 33; DB 2; Length 505;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOFFGL 10
|||:| :|
Db 151 RPLDPKPHGL 160

RESULT 89
F85944
hypothetical protein lysu [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: F85944
R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouzis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: F85944
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-505 <STO>
A:Cross-references: GB:AE005174; NID:912517416; PIDN:AAG58018.1; GSPDB:GN00145; UMGP:242
C:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: lysu
C:Superfamily: lysine--tRNA ligase

Query Match 54.1%; Score 33; DB 2; Length 505;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOFFGL 10
|||:| :|
Db 151 RPLDPKPHGL 160

RESULT 90
I49552
protein-tyrosine kinase (EC 2.7.1.112) bak/lyk - mouse
N:Alternate names: intestinal tyrosine kinase
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 04-Mar-2000

C:Accession: I49552; I48608
R:Oberg-Welsh, C.; Welsh, M.
Gene 152, 239-242, 1995
A:Title: Cloning of BSK, a murine FRK homologue with a specific pattern of tissue dis
A:Reference number: I49552; MUID:95137395
A:Accession: I49552
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-512 <RES>
A:Cross-references: GB:U36132; NID:9556287; PIDN:AA65197.1; PID:9777773
R:Thuvesson, M.; Albrecht, D.; Zurcher, G.; Andres, A.C.; Ziemlecki, A.
Biochem. Biophys. Res. Commun. 209, 582-589, 1995
A:Title: lyk, a novel intracellular protein tyrosine kinase differentially expressed
A:Reference number: I48608; MUID:95251656
A:Accession: I48608
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-153, 'T', 155-236, 'H', 238-512 <RE2>
A:Cross-references: EMBL:Z48757; NID:9736263; PIDN:CAA88658.1; PID:9736264
C:Genetics:
A:Gene: BSK
C:Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH
C:Keywords: Arp; blocked amino end; intestine; lipoprotein; myristylation; phosphotra
F:56-112/Domain: SH3 homology <SH3>
F:123-215/Domain: SH2 homology <SH2>
F:239-501/Domain: protein kinase homology <KIN>
F:247-255/Region: protein kinase Arp-binding motif
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:5/Binding site: palmitate (Cys) (covalent) #status predicted
F:269/Active site: lys #status predicted

Query Match 54.1%; Score 33; DB 2; Length 512;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQOFFYIM 11
||||: :|
Db 466 PQOFFYIM 473

RESULT 91
A32431
cytochrome-c oxidase (EC 1.9.3.1) chain I - honeybee mitochondrion
C:Species: mitochondrion Apis mellifera (honeybee)
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 07-Dec-1999
C:Accession: A32431; A61223; S52961
R:Crozier, R.H.; Crozier, Y.C.; Mackinlay, A.G.
Mol. Biol. Evol. 6, 399-411, 1989
A:Title: The CO-I and CO-II region of honeybee mitochondrial DNA: evidence for variat
A:Reference number: A32431; MUID:90136028
A:Accession: A32431
A:Molecule type: DNA
A:Residues: 1-521 <CRO>
A:Cross-references: GB:M23409; NID:9493737; PIDN:AAA18476.1; PID:9493738
A:Note: this variant of the mitochondrial genome has a small distance between the COI
R:Corruet, J.M.; Garnery, L.; Solignac, M.
Genetics 128, 393-403, 1991
A:Title: Putative origin and function of the intergenic region between COI and COII o
A:Reference number: A61223; MUID:91301463
A:Accession: A61223
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 338-521 <COR>
A:Note: this variant of the mitochondrial genome has a large distance between the COI
R:Crozier, R.H.; Crozier, Y.C.
Genetics 133, 97-117, 1993
A:Title: The mitochondrial genome of the honeybee Apis mellifera: complete sequence a
A:Accession: S52961
A:Molecule type: DNA
A:Residues: 1-521 <CR2>
A:Cross-references: EMBL:L06178; NID:9336279; PIDN:AAB96799.1; PID:9552440

A:Experimental source: Apis mellifera ligustica
A:Note: the authors did not translate the codon for residue 521
C:Genetics:
A:Gene: COI
A:Genome: mitochondrion
A:Genetic code: SGCA
C:Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C:Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane-as
transmembrane protein
F:9-455/Domain: cytochrome-c oxidase chain I homology <COI>
F:53,376/Binding site: heme a iron (His) (axial ligands) #status predicted
F:238,288,289/Binding site: copper (His) #status predicted
F:238-242/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted
F:242/Binding site: oxygen (Tyr) #status predicted
F:366/Binding site: magnesium (His) (shared with chain II) #status predicted
F:374/Binding site: heme a3 iron (His) (axial ligand) #status predicted

Query Match 54.1%; Score 33; DB 2; Length 521;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQQFFGLM 11
||| |||
Db 425 PQQFFGLM 432

RESULT 92
F84647
hypothetical protein At2g25370 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: F84647
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: F84647
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-546 <STO>
A:Cross-references: GB:AE002093; NID:g4432850; PIDN:AAD20698.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g25370
A:Map position: 2

Query Match 54.1%; Score 33; DB 2; Length 546;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKPOOFF 8
||| |||
Db 500 PKPOOFF 506

RESULT 93
T02552
cellulose synthase homolog T26B15.9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C:Accession: T02552; C84734
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, July 1998
A:Description: Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence.
A:Reference number: 214678
A:Accession: T02552
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-712 <ROU>
A:Cross-references: EMBL:AC004681; NID:g3298532; PID:g3298541

A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: C84734
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-712 <STO>
A:Cross-references: GB:AE002093; NID:g3298541; PIDN:AAC25935.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g32530; T26B15.9
A:Map position: 2
A:Introns: 45/2; 151/3; 193/3; 234/3; 301/3; 347/1; 407/3; 524/3

Query Match 54.1%; Score 33; DB 2; Length 712;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 PKPQFFGLM 11
||| |||
Db 437 PKPQFFGLM 446

RESULT 94
T47731
hypothetical protein F18021.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-May-2000
C:Accession: T47731
R:Benes, V.; Wurmbach, E.; Drzonek, H.; Ansoorge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24474
A:Accession: T47731
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-755 <BEN>
A:Cross-references: EMBL:ATP18021
A:Experimental source: cultivar Columbia; BAC clone F18021
C:Genetics:
A:Map position: 3
A:Introns: 219/2; 262/3; 439/3; 485/3; 668/3; 706/3
A:Note: F18021.100
C:Superfamily: Arabidopsis thaliana hypothetical protein F18021.100

Query Match 54.1%; Score 33; DB 2; Length 755;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOFFGL 10
||| |||
Db 24 RPKPOFFGL 33

RESULT 95
A39288
dorsal-ventral patterning protein tollold (EC 3.4.24.-) - fruit fly (Drosophila melan
C:Species: Drosophila melanogaster
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A39288
R:Shmell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
Cell 67, 469-481, 1991
A:Title: The Drosophila dorsal-ventral patterning gene tollold is related to human bo
A:Reference number: A39288; MUID:92034970
A:Accession: A39288
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1057 <SHI>
A:Cross-references: GB:M76976; NID:g157305; PIDN:AAA28491.1; PID:g157306

C:Superfamily: synecocystis hypothetical protein sl10676

Query Match 52.5%; Score 32; DB 2; Length 180;
Best Local Similarity 54.5%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFGLM 11
| : | | | | | :
DB 165 KRPQPFEL 175

RESULT 100

A69898 conserved hypothetical protein yoa2 - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999

C:Accession: A69898

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteaux, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choc A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaute, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinis, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Roche, B.; Roche, M.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot kenchil, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Togonni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipet, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yate, K.; Yoshida, K

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69880; MUID:98044033

A:Accession: A69898

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-210 <KUN>

A:Cross-references: GB:299114; GB:AL009126; NID:q2634230; PIDN:CAB13771.1; PID:el185351;

A:Experimental source: strain 168

C:Genetics:

A:Gene: yoa2

Query Match 52.5%; Score 32; DB 2; Length 210;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPKQFGLM 11
| : | | | | | :
DB 197 KRPYFELM 205

RESULT 101

G75448 conserved hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000

C:Accession: G75448

R:White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896

A:Accession: G75448

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-225 <WHT>

A:Cross-references: GB:AE001952; GB:AE000513; NID:q6458725; PIDN:AAI0575.1; PID:q645872

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR0999

A:Map position: 1

Query Match 52.5%; Score 32; DB 2; Length 225;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKQPFGL 10
| : | | | | | :
DB 78 RRPQPFGL 87

RESULT 102

S23009 insulin-like growth factor-binding protein 1 precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S23009

R:Sneyers, M.; Kettmann, R.; Massart, S.; Renaville, R.; Burny, A.; Portetelle, D. DNA Seq. 1, 407-408, 1991

A:Title: Cloning and characterization of a cDNA encoding the bovine insulin-like grow

A:Reference number: S23009; MUID:92119331

A:Accession: S23009

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-263 <SNE>

A:Cross-references: EMBL:X54979; NID:q435; PIDN:CA38723.1; PID:q436

A:Note: the authors translated the codon TGG for residue 30 as Cys

C:Superfamily: insulin-like growth factor binding protein 1; thyroglobulin type I rep

F:180-255/Domain: thyroglobulin type I repeat homology <THR1>

Query Match 52.5%; Score 32; DB 1; Length 263;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPKQPFGL 10
| : | | | | | :
DB 253 PKQPFGL 261

RESULT 103

B35407 tryptophan synthase (EC 4.2.1.20) alpha chain - Thermus aquaticus

C:Species: Thermus aquaticus

C:Date: 14-Sep-1990 #sequence_revision 14-Sep-1990 #text_change 21-Aug-1998

C:Accession: B35407

R:Koyama, Y.; Furukawa, K. J. Bacteriol. 172, 3490-3495, 1990

A:Title: Cloning and sequence analysis of tryptophan synthetase genes of an extreme t

to competent T. thermophilus cells.

A:Reference number: A35407; MUID:90264352

A:Accession: B35407

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-271 <KOY>

A:Cross-references: GB:M32108

C:Superfamily: tryptophan synthase alpha chain; tryptophan synthase alpha chain homol

C:Keywords: carbon-oxygen lyase; hydro-lyase

F:17-241/Domain: tryptophan synthase alpha chain homology <TRPA>

F:47/Active site: Glu #status predicted

Query Match 52.5%; Score 32; DB 2; Length 271;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 RPKQFGL 10
| : | | | | | :
DB 108 RRPQFGL 114

RESULT 104

C75426
Probable transposase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: C75426
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: C75425
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-288 <WHI>
A:Cross-references: GB:AE001968; GB:AE000513; NID:g6458930; PIDN:AAF10765.1; PID:g645893
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1196
A:Map position: 1

Query Match 52.5%; Score 32; DB 2; Length 288;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RPKQPFGLM 11
|:::|||||
Db 258 RMKQPFMAVL 268

RESULT 105
A75638
Probable transposase - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: A75638
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: A75636
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-288 <WHI>
A:Cross-references: GB:AE001827; NID:g6460959; PIDN:AAF12670.1; PID:g6460967; TIGR:DR00
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0029
A:Map position: Plasmid
A:Genome: Plasmid
A:Note: Plasmid CPl

Query Match 52.5%; Score 32; DB 2; Length 288;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RPKQPFGLM 11
|:::|||||
Db 258 RMKQPFMAVL 268

RESULT 106
E69288
ISA0963-2 transposase homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: E69288
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Moese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: E69288
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-299 <KLE>
A:Cross-references: GB:AE001083; GB:AE000782; NID:g2689406; PIDN:AAB90922.1; PID:g265

Query Match 52.5%; Score 32; DB 2; Length 299;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 KPOQPFGLM 11
|:::|||||
Db 234 KIERFFGLM 242

RESULT 107
H69462
ISA0963-6 transposase homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: H69462
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Moese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: H69462
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-299 <KLE>
A:Cross-references: GB:AE000966; GB:AE000782; NID:g2689309; PIDN:AAB89545.1; PID:g264

Query Match 52.5%; Score 32; DB 2; Length 299;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 KPOQPFGLM 11
|:::|||||
Db 234 KIERFFGLM 242

RESULT 108
E69413
ISA0963-3 transposase homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: E69413
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Moese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: E69413
A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-299 <KLE>
A:Cross-references: GB:AE001013; GB:AE000782; NID:g2689336; PIDN:AAB89935.1; PID:g264

Query Match 52.5%; Score 32; DB 2; Length 299;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQFFGLM 11
| : : | | | | |
Db 234 KIRFFGLM 242

RESULT 109
F69422
ISA0963-4 transposase homolog - *Archaeoglobus fulgidus*
C:Species: *Archaeoglobus fulgidus*
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: F69422
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
R: Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
G: Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Overbeek, R.; Cotton, M.D.; Spriggs, T.; Arltach, P.; Kaane, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343
A:Accession: F69422
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-299 <RLE>
A:Cross-references: GB:AE001009; GB:AE000782; NID:g2689332; PIDN:AA89862.1; PID:g264919

Query Match 52.5%; Score 32; DB 2; Length 299;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOQFFGLM 11
| : : | | | | |
Db 234 KIRFFGLM 242

RESULT 110
D96769
hypothetical protein F9E11.2 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96769
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719
A:Accession: D96769
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-305 <STO>
A:Cross-references: GB:AE005173; NID:g10092421; PIDN:AA612826.1; GSPDB:GN00141
C:Genetics:
A:Gene: F9E11.2
A:Map position: 1

Query Match 52.5%; Score 32; DB 2; Length 305;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPOQFFGLM 11
| : : | | | | |
Db 242 KRYTTRFGLM 251

RESULT 111
G86336
hypothetical protein AAF88158.1 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G86336
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719
A:Accession: G86336
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-313 <STO>
A:Cross-references: GB:AE005172; NID:g9558595; PIDN:AAF88158.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 52.5%; Score 32; DB 2; Length 313;
Best Local Similarity 75.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKQFF 8
| | | | |
Db 232 RPKLQHF 239

RESULT 112
A75631
probable transposase - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: A75631
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Overbeek, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896
A:Accession: A75631
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <WHI>
A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12605.1; PID:g6460901; TIGR:DR
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRB0117
A:Map position: megaplasmid
A:Genome: plasmid
A:Note: plasmid MPI

Query Match 52.5%; Score 32; DB 2; Length 327;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKQFFGLM 11
| | | | |
Db 297 RPKQFFMAVL 307

RESULT 113
B83371

conserved hypothetical protein PA2197 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83371
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardi, K.; Lim,
.; Lory, S.; Olson, M.V.
Mature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337
A:Accession: B83371
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-345 <STO>
A:Cross-references: GB:AE004646; GB:AE004091; NID:g9948213; PIDN:AAG05585.1; GSPDB:GN001
C:Genetics:
A:Gene: PA2197

Query Match 52.5%; Score 32; DB 2; Length 345;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
I:|||||
DB 322 PEAFFGL 329

RESULT 114
A:Accession: A69426
A:Title: 5 transposase homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: A69426
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uetleback, T.; Cocton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Moose, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343
A:Accession: A69426
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-357 <KLE>
A:Cross-references: GB:AE001007; GB:AE000782; NID:g2689330; PIDN:AAB89838.1; PID:g264916

Query Match 52.5%; Score 32; DB 2; Length 357;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPQOFFGLM 11
I:|||||
DB 292 KIERFFGLM 300

RESULT 115
C:Title: 115
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C:Accession: C71242
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137
A:Accession: C71242
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-361 <KAW>
A:Cross-references: GB:AP000001; NID:g3236128; PIDN:BAA29266.1; PID:g3256583
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenB
A:Genetics:
A:Gene: PH0197

Query Match 52.5%; Score 32; DB 2; Length 361;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 PQOFFGLM 11
I:|||||
DB 113 PQOFFGLM 120

RESULT 116
C:Title: 116
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15492
R:Wu, X.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid C14F11.
A:Reference number: Z18360
A:Accession: T15492
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-368 <WUX>
A:Cross-references: EMBL:U39645; NID:g1049344; PID:g1049350; PIDN:AAA80366.1; CESP:C1
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:C14F11.5
A:introns: 42/3; 67/3; 263/2; 299/1; 329/1

Query Match 52.5%; Score 32; DB 2; Length 368;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKPQPF 8
I:|||||
DB 34 PKPQPF 40

RESULT 117
C:Title: 117
C:Species: Arabidopsis thaliana
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C:Accession: T05598
R:Beran, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hobeisel, J.; Mewes, H.W.; Mayer, K
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15419
A:Accession: T05598
A:Molecule type: DNA
A:Residues: 1-370 <BEV>
A:Cross-references: EMBL:AL035394
A:Experimental source: cultivar Columbia; BAC clone F9D16
C:Genetics:
A:Map position: 4
A:introns: 148/2; 193/3; 234/2; 272/3; 322/3
A:Note: F9D16.130

Query Match 52.5%; Score 32; DB 2; Length 370;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 KPQOFFGL 10
I:|||||

DB 272 KPQAFGL 279

RESULT 118

B64158

C:Species: Haemophilus influenzae (strain Rd KW20)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000

C:Accession: B64158

R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.

R:Goayne, J.D.; Scott, J.; Shirley, R.; Liu, L.T.; Glodok, A.; Kelley, J.M.; Weidman, J.

R:D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Georgiagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630

A:Accession: B64158

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-382 <TIGR>

A:Cross-references: GB:U32759; GB:I42023; NID:g1573756; PIDN:AA022412.1; PID:g1573761; T

C:Superfamily: hypothetical protein from Yersinia enterocolitica

Query Match

52.5%; Score 32; DB 1; Length 382;

Best Local Similarity 55.6%; Pred. No. 2.9e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 KPQFFGLM 11

DB 5 KPQYIGMM 13

RESULT 119

H72026

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000

C:Accession: H72026; G81514

R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.

Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

A:Reference number: A72000; MUID:99206606

A:Accession: H72026

A:Molecule type: DNA

A:Residues: 1-418 <ARN>

A:Cross-references: GB:AE001667; GB:AE001363; NID:g4377171; PIDN:AA019010.1; PID:g437718

A:Experimental source: strain CM1029

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

C:; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MOpn and Chlamydia pneumoniae AR39.

A:Reference number: A81500; MUID:20150255

A:Accession: G81514

A:Molecule type: DNA

A:Residues: 1-418 <REA>

A:Cross-references: GB:AE002257; GB:AE002161; NID:g7189902; PIDN:AAF38775.1; PID:g718991

A:Experimental source: strain AR39, HL cells

C:Genetics:

A:Gene: rfbA/rfbB; CP0997

C:Superfamily: rfbA bifunctional protein; 3,4-dihydroxy-2-butanone 4-phosphate synthase

F:19-209/Domain: 3,4-dihydroxy-2-butanone 4-phosphate synthase homology <HBPS>

Query Match

52.5%; Score 32; DB 2; Length 418;

Best Local Similarity 71.4%; Pred. No. 3.1e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 PQQFFGL 10

DB 366 PKRYFGL 372

RESULT 120

F86599

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae (strain J138)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: F86599

R:Shital, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.

A:Reference number: A86491; MUID:20330349

A:Accession: F86599

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-418 <STO>

A:Cross-references: GB:BA000008; NID:g8979246; PIDN:BA099080.1; GSPDB:GN00142

A:Experimental source: strain J138

C:Genetics:

A:Gene: rfbA/rfbB

C:Superfamily: rfbA bifunctional protein; 3,4-dihydroxy-2-butanone 4-phosphate synth

Query Match

52.5%; Score 32; DB 2; Length 418;

Best Local Similarity 71.4%; Pred. No. 3.1e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 PQQFFGL 10

DB 366 PKRYFGL 372

RESULT 121

F82991

C:Species: Pseudomonas aeruginosa

C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: F82991

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;

Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L

; Ivey, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337

A:Accession: F82991

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-419 <STO>

A:Cross-references: GB:AE004936; GB:AE004091; NID:g9951541; PIDN:AMG08624.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: rho; PA5239

C:Superfamily: transcription termination factor rho

C:Keywords: transcription termination

Query Match

52.5%; Score 32; DB 2; Length 419;

Best Local Similarity 71.4%; Pred. No. 3.1e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPQFFGL 9

DB 296 KPRKFFG 302

RESULT 122

H81667

C:Species: Chlamydia muridarum, Chlamydia trachomatis MOpn

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000

C:Accession: H81667

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

C:; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39.
A:Reference number: AB1500; MUID:20150255
A:Accession: H81667
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-419 <JET>
A:Cross-references: GB:AE002345; GB:AE002160; NID:g7190791; PIDN:AMF39581.1; PID:g719080
A:Experimental source: strain N19g (MoPn)
C:Genetics:
A:Gene: TC0778
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 52.5%; Score 32; DB 2; Length 419;
Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOOFFG 9
||:||||
Db 297 KPKRFFG 303

RESULT 123
E83172
Probable transporter PA3781 [Imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: E83172
R:Stover, C.K.; Pham, X.O.; Errin, A.L.; Miroguchi, S.D.; Warriner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A:Reference number: AB2950; MUID:20437337
A:Accession: E83172
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <STO>
A:Cross-references: GB:AE004797; GB:AE004091; NID:g9949950; PIDN:AMG07168.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA3781
C:Superfamily: conserved hypothetical protein H11029

Query Match 52.5%; Score 32; DB 2; Length 426;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 PPOFFGLM 11
||:||||
Db 45 PQRFFGM 52

RESULT 124
G72246
Transcription termination factor Rho - *Thermotoga maritima* (strain MSB8)
C:Species: *Thermotoga maritima*
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: G72246
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing
A:Reference number: A72200; MUID:99287316
A:Accession: G72246
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-427 <ARN>
A:Cross-references: GB:AE001799; GB:AE000512; NID:g4982033; PIDN:AD36538.1; PID:g498203
A:Experimental source: strain MSB8

C:Genetics:
A:Gene: TMI470
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 52.5%; Score 32; DB 2; Length 427;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOOFFG 9
||:||||
Db 300 KPKRFFG 306

RESULT 125
F81320
Transcription termination factor Cj1156 [Imported] - *Campylobacter jejuni* (strain NCTC 8239)
C:Species: *Campylobacter jejuni*
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
C:Accession: F81320
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chli C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Vanyilet, A.; Whitehead, S.; Ba Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals
A:Reference number: AB1250; MUID:20150912
A:Accession: F81320
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-432 <PAR>
A:Cross-references: GB:AL139077; GB:AL11168; NID:g6968444; PIDN:CA873410.1; PID:g696
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: rho; Cj1156
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 52.5%; Score 32; DB 2; Length 432;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOOFFG 9
||:||||
Db 310 KPKRFFG 316

RESULT 126
S75859
Hypothetical protein gl11103 - *Synechocystis* sp. (strain PCC 6803)
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S75859
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
A:Reference number: S74322; MUID:97061201
A:Accession: S75859
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-445 <KAN>
A:Cross-references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BAA18318.1; PID:g165
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: conserved hypothetical protein H11029

Query Match 52.5%; Score 32; DB 2; Length 445;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQOQFGLM 11
||:||||
DB 55 PQRFICIM 62

RESULT 127

macrophage elastase (EC 3.4.24.-) precursor - mouse
M:Alternate names: matrix metalloproteinase 12 (MMP12)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C:Accession: A42401
R:Shapiro, S.D.; Gillfin, G.L.; Gilbert, D.J.; Jenkins, N.A.; Copeland, N.G.; Welgus, H.
J. Biol. Chem. 267, 4664-4671, 1992
A:Title: Molecular cloning, chromosomal localization, and bacterial expression of a murine
A:Reference number: A42401; MUID:92165826
A:Accession: A42401
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-462 <SHA>
A:Cross-references: GB:M82831; NID:g199127; PIDN:AAA9526.1; PID:g199128
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:53-256/Domain: matrix metalloproteinase homology <MMP>
F:269-462/Domain: hemopexin repeat homology <PXN>
F:85,211,215,221/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:211,215,221/Binding site: zinc, catalytic (His) (active) #status predicted
F:212/Active site: Glu #status predicted

Query Match 52.5%; Score 32; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 QOQFGL 10
|||||
DB 61 QOQFGL 66

RESULT 128

probable transcription termination factor - Chlamydia trachomatis (serotype D, strain UW
A1509
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 15-Oct-1999
C:Accession: A71509
R:Stephens, R.S.; Kalman, S.; Jammel, C.J.; Pan, J.; Marathe, R.; Arevint, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A:Reference number: A71570; MUID:99000809
A:Accession: A71509
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <ARN>
A:Cross-references: GB:AE001322; GB:AE001273; NID:g3328916; PIDN:AAC68091.1; PID:g332892
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: rho
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 52.5%; Score 32; DB 2; Length 464;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOQFPG 9
||:||||
DB 342 KPKRFG 348

RESULT 129

D72058
transcription termination factor Rho CP0137 [imported] - Chlamydia pneumoniae (strain

C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: D72058; H81608
R:Kalman, S.; Mitchell, W.; Marathe, R.; Jammel, C.; Fan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606
A:Accession: D72058
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <ARN>

A:Cross-references: GB:AE001645; GB:AE001363; NID:g4376896; PIDN:AAD18749.1; PID:g437
A:Experimental source: strain CWT029
R:Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MOpn and Chlamydia pneumoniae AR39
A:Reference number: A81500; MUID:20150255
A:Accession: H81608
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <REA>
A:Cross-references: GB:AE002175; GB:AE002161; NID:g7189069; PIDN:AAF38020.1; PID:g718
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: rho; CP0137
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 52.5%; Score 32; DB 2; Length 464;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOQFPG 9
||:||||
DB 342 KPKRFG 348

RESULT 130

transcription termination factor [imported] - Chlamydia pneumoniae (strain J138)
G8566
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: G8566
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349
A:Accession: G8566
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <STO>
A:Cross-references: GB:BA000008; NID:g8978982; PIDN:BA98817.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: rho
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 52.5%; Score 32; DB 2; Length 464;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOQFPG 9
||:||||
DB 342 KPKRFG 348

RESULT 131

KCPGI
interstitial collagenase (EC 3.4.24.7) precursor [validated] - pig

N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 15-Sep-2000
C:Accession: S15985; S13597
R:Richards, C.D.; Kafterly, J.A.; Reynolds, J.J.; Saklatvala, J.
Matrix 11, 161-167, 1991
A:Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of
A:Reference number: S15986; MUID:91333421
A:Accession: S15985
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-469 <RIC>
A:Note: part of the sequence, including the amino end of the proenzyme, was confirmed by
R:Clarke, N.J.; O'Hare, M.C.; Cavatton, T.E.; Harper, G.P.
Nucleic Acids Res. 18, 6703, 1990
A:Title: Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR.
A:Reference number: S13597; MUID:91067477
A:Accession: S13597
A:Molecule type: mRNA
A:Residues: 25-469 <CIA>
A:Cross-references: EMBL:X54724; NID:92016; PIDN:CAA38526.1; PID:9930269
R:Li, J.; Brick, P.; Blow, D.M.
submitted to the Brookhaven Protein Data Bank, April 1995
A:Reference number: A65568; PDB:1FBL
A:Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 100-466
C:Comment: Procollagenase can be activated without removal of the activation peptide. St
tion peptide by other proteinases.
C:Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
C:Function:
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
A:Note: also hydro-lyses type X collagen, serpins, and alpha-macroglobulins
C:Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloprote
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-469/Product: procollagenase #status predicted <PRO>
F:20-99/Domain: activation peptide #status experimental <ACT>
F:60-261/Domain: matrix metalloproteinase homology <MMP>
F:100-469/Product: interstitial collagenase #status predicted <MAT>
F:272-466/Domain: hemopexin repeat homology <PNX>
F:92-218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:120,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental
F:219/Active site: Glu #status predicted
F:278-466/Disulfide bonds: #status experimental

Query Match 52.5% Score 32; DB 1; Length 469;
Best Local Similarly 100.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 QQPFGL 10
| | | | |
Db 68 QQPFGL 73

RESULT 132
F82175
conserved hypothetical protein VCI632 [Imported] - Vibrio cholerae (strain N16961 serogr
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: F82175
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Charadson, D.; Ermolaeva, M.D.; Yamatevna, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R.
Nature 406, 477-483, 2000
A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406833
A:Accession: F82175
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-478 <HEI>
A:Cross-references: GB:AE004241; GB:AE003852; NID:99656142; PIDN:AAF94783.1; GSPDB:GN001
A:Experimental source: serogroup O1, strain N16961, biotype El Tor

C:Genetics:
A:Gene: VC1632
A:Map position: 1

Query Match 52.5% Score 32; DB 2; Length 478;
Best Local Similarly 54.5%; Pred. No. 3.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKQPFGL 11
| | | | |
Db 402 RQPFGL 412

RESULT 133
T16695
hypothetical protein R05H11.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16695
R:Pauley, A.
submitted to the EMBL Data Library, May 1994
A:Description: The sequence of C. elegans cosmid R05H11.
A:Reference number: Z18560
A:Accession: T16695
A:Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: DNA
A:Residues: 1-484 <PAU>
A:Cross-references: EMBL:U00056; NID:9485152; PID:9485153; PIDN:AAA50725.1; CESP:R05H
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:R05H11.1
A:Introns: 40/2; 122/2; 167/3; 264/2; 346/3; 380/2; 411/3; 453/3

Query Match 52.5% Score 32; DB 2; Length 484;
Best Local Similarly 55.6%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKQPFGL 10
| | | | |
Db 384 PPKPFGL 392

RESULT 134
JC7205
Lysine--tRNA ligase (EC 6.1.1.6) - Bacillus stearothermophilus
C:Species: Bacillus stearothermophilus
C:Date: 03-Nov-2000 #sequence_revision 03-Nov-2000 #text_change 17-Nov-2000
C:Accession: JC7205
R:Takita, T.; Shimizu, N.; Sukata, T.; Hashimoto, S.; Akita, E.; Yokota, T.; Esaki, N
Biosci. Biotechnol. Biochem. 64, 432-437, 2000
A:Title: Lysyl-tRNA synthetase of Bacillus stearothermophilus molecular cloning and e
A:Reference number: JC7205; MUID:20199468
A:Accession: JC7205
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-493 <TAK>
A:Cross-references: DDBJ:AB012100
C:Superfamily: Lysine--tRNA ligase
C:Keywords: ligase

Query Match 52.5% Score 32; DB 2; Length 493;
Best Local Similarly 50.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKQPFGL 10
| | | | |
Db 141 RPKPFGL 150

RESULT 135

JC6200
cholesterol monooxygenase (side-chain-cleaving) (EC 1.14.15.6) cytochrome P450 [similar]
N:Alternate names: cytochrome P450sc
C:Species: Gallus gallus (chicken)
C:Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 03-Nov-2000
C:Accession: JC6200
R:Nomura, O.; Nakabayashi, O.; Nishimori, K.; Mituno, S.
Gene 185, 217-222, 1997
A:Title: The cDNA cloning and transient expression of a chicken gene encoding cytochrome
A:Reference number: JC6200; MUID:97208876
A:Accession: JC6200
A:Molecule type: mRNA
A:Residues: 1-508 <NOM>
A:Cross-references: DDBJ:D49803; NID:q1906770; PIDN:BAI18920.1; PID:q1906771
A:Experimental source: tissue adrenal gland
C:Genetics:
A:Gene: psccl
C:Superfamily: human cytochrome P450 CYP11B1; cytochrome P450 homology
C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase; steroid binding
F:315-474/Domain: cytochrome P450 homology <P45>
F:452/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 52.5%; Score 32; DB 2; Length 508;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 PKPOGF 7
11:111
Db 422 PKPEGF 427

RESULT 136
T34546
hypothetical protein DKFZP434B0328.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 02-Sep-2000
R:Blöcker, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence database, October 1999
A:Reference number: Z21539
A:Accession: T34546
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-513 <BLO>
A:Cross-references: EMBL:AL122051
A:Experimental source: adult testis; clone DKFZP434B0328
C:Genetics:
A:Note: DKFZP434B0328.1
C:Superfamily: protein kinase C zinc-binding repeat homology
F:200-250/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 52.5%; Score 32; DB 2; Length 513;
Best Local Similarity 60.0%; Pred. No. 3.8e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKPOGFGLM 11
11:11111
Db 184 PKPEGFVGM 193

RESULT 137
F70128
transcription termination factor rho - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 26-Aug-1999
C:Accession: F70128; S35618; I40295
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Latifaga, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943
A:Accession: F70128
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-515 <KLE>
A:Cross-references: GB:AE001133; GB:AE000783; NID:g2688120; PIDN:AAAC66619.1; PID:g268
R:Fillis, K.; Campbell, J.
Nucleic Acids Res. 21, 1040, 1993
A:Title: A Borrelia burgdorferi homolog of the Escherichia coli rho gene.
A:Reference number: S35618; MUID:93197131
A:Accession: S35618
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 97-515 <TIL>
A:Cross-references: EMBL:L07656
R:Ojalim, C.; Davidson, B.E.; Saint Girons, I.; Old, I.G.
Microbiology 140, 2931-2940, 1994
A:Title: Conservation of gene arrangement and an unusual organization of rRNA genes i
A:Reference number: I40241; MUID:95111614
A:Accession: I40295
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 142-153, 'H', 155-305, 'D', 307-331 <RES>
A:Cross-references: GB:I46347; NID:9928812; PIDN:AAA73991.1; PID:9928813
C:Genetics:
A:Gene: rho
C:Superfamily: transcription termination factor rho
C:Keywords: ATP; transcription termination
F:264-475/Domain: ATP-binding #status predicted <ATP>

Query Match 52.5%; Score 32; DB 2; Length 515;
Best Local Similarity 71.4%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPQOFG 9
11:11111
Db 391 KPRKFG 397

RESULT 138
T19562
hypothetical protein C29F3.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19562
R:Mathews, L.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19142
A:Accession: T19562
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-518 <WIL>
A:Cross-references: EMBL:281043; PIDN:CAB02803.1; GSPDB:GN00023; CESP:C29F3.7
A:Experimental source: clone C29F3
C:Genetics:
A:Gene: CESP:C29F3.7
A:Map position: 5
A:Introns: 24/1; 76/3; 114/2; 351/2; 456/2

Query Match 52.5%; Score 32; DB 2; Length 518;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 PQOFG 9
11:11111
Db 360 PQEFG 365

RESULT 139

C71346
probable transcription termination factor Rho (rho) - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 15-Oct-1999
C:Accession: C71346
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; Mcd
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A11250; MUID:98332770
A:Accession: C71346
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-519 <COL>
A:Cross-references: GB:AE001207; GB:AE000520; NID:g3322526; PIDN:AC65243.1; PID:g332252
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0254
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 52.5%; Score 32; DB 2; Length 519;
Best Local Similarity 71.4%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPQOFFG 9
||:||||
Db 392 KPQOFFG 398

RESULT 140
T99467
related to COP1-interacting protein CIP8 [imported] - Neurospora crassa
N:Alternate names: protein B14D6.190
C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Sep-2000
C:Accession: T99467
R:Schulte, U.; Align, V.; Hohelsel, J.; Brandt, P.; Farcman, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A:Reference number: 225022
A:Accession: T99467
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-532 <SC>
A:Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.190
A:Experimental source: BAC clone B14D6; strain OR74A
C:Genetics:
A:Gene: NCSP:B14D6.190
A:Map position: 6
C:Superfamily: RING finger homology
P:418-468/Domain: RING finger homology <RRN>

Query Match 52.5%; Score 32; DB 2; Length 532;
Best Local Similarity 66.7%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKQOFFG 10
||:||||
Db 259 PKQOFFG 267

RESULT 141
T08405
hypothetical protein F18B3.120 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 10-Dec-1999
C:Accession: T08405
R:Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salanoub
submitted to the Protein Sequence Database, May 1999
A:Reference number: 216409

A:Accession: T08405
A:Molecule type: DNA
A:Residues: 1-567 <OUE>
A:Cross-references: EMBL:AL049862; GSPDB:GN00061; ATSP:F18B3.120
A:Experimental source: cultivar Columbia; BAC clone F18B3
C:Genetics:
A:Gene: ATSP:F18B3.120
A:Map position: 3
A:Introns: 13/1; 31/3; 406/3
C:Superfamily: Arabidopsis hypothetical protein F19F18.80

Query Match 52.5%; Score 32; DB 2; Length 567;
Best Local Similarity 62.5%; Pred. No. 4.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPQOFFG 10
||:||||
Db 375 KPQOFFG 382

RESULT 142
T35430
probable long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) SC6A5.39 [similarity] - Strep
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Nov-2000
C:Accession: T35430
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parthill, J.; Barrell, B.G.; Rajandream, M.A
submitted to the EMBL Data Library, March 1999
A:Reference number: 221577
A:Accession: T35430
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-612 <OLU>
A:Cross-references: EMBL:AL049485; PIDN:CAB39723.1; GSPDB:GN00070; SC6A5.39
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SC6A5.39
C:Superfamily: synchocystis long-chain-fatty-acid--CoA ligase; acetate--CoA ligase h
C:Keywords: acid-thiol ligase; coenzyme A
P:73-598/Domain: acetate--CoA ligase homology <ACL>

Query Match 52.5%; Score 32; DB 2; Length 612;
Best Local Similarity 62.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPQOFFG 10
||:||||
Db 276 KPQOFFG 283

RESULT 143
T25208
hypothetical protein ZK1067.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T25208; T27687
R:Barlow, K.
submitted to the EMBL Data Library, December 1995
A:Reference number: 219995
A:Accession: T25208
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-614 <WLL>
A:Cross-references: EMBL:Z68319; PIDN:CAA92704.1; GSPDB:GN00020; CESP:ZK1067.6
A:Experimental source: clone T23G7
R:Thomas, K.
submitted to the EMBL Data Library, March 1996
A:Reference number: 220404
A:Accession: T27687
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-614 <MI2>
A:Cross-references: EMBL:270038; PIDN:CAA93887.1; GSPDB:GN00020; CESP:ZK1067.6
A:Experimental source: clone ZK1067
C:Genetics:
A:Gene: CESP:ZK1067.6
A:Map position: 2
A:introns: 146/1; 204/2; 263/1; 318/1; 397/3; 553/3

Query Match 52.5%; Score 32; DB 2; Length 614;
Best Local Similarity 71.4%; Pred. No. 4.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 KPQOFG 8
DB 501 KPQOFG 507

RESULT 144

A:Accession: AB1095
excinnuclease ABC chain C NMA1326 [imported] - Neisseria meningitidis (strain MC58 serogr C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: AB1095
R:Pettilin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; et al. H.; Qin, H.; Yamahayan, J.; Gill, J.; Scarlato, V.; Masiapani, V.; Pizze, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: AB1000; MUID:20175755
A:Accession: AB1095
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-617 <TE>
A:Cross-references: GB:AE002481; GB:AE002098; NID:g7226568; PIDN:AAFA1701.1; PID:g722656 A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMA1326
C:Superfamily: excinnuclease ABC chain C

Query Match 52.5%; Score 32; DB 2; Length 617;
Best Local Similarity 71.4%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPQOFG 9
DB 130 KPQOFG 136

RESULT 145

excinnuclease ABC subunit C NMA1540 [imported] - Neisseria meningitidis (strain Z2491 ser C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: G81845
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel R.; Holtz, S.; Jorgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491. A:Reference number: AB1775; MUID:20222556
A:Accession: G81845
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-628 <PAR>
A:Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84767.1; PID:g738018 A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: UVIC; NMA1540
C:Superfamily: excinnuclease ABC chain C

Query Match 52.5%; Score 32; DB 2; Length 628;
Best Local Similarity 71.4%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPQOFG 9
DB 141 KPQOFG 147

RESULT 146

J50631
alpha-amylase (EC 3.2.1.1) precursor - Pseudomonas sp.
N:Alternate names: maltopentose-forming amylase
C:Species: Pseudomonas sp.
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 07-May-1999
C:Accession: J50631
R:Shida, O.; Takano, T.; Takagi, H.; Kadowaki, K.; Kobayashi, S. Biosci. Biotechnol. Biochem. 56, 76-80, 1992
A:Title: Cloning and nucleotide sequence of the maltopentose-forming amylase gene fr A:Reference number: J50631; MUID:92257012
A:Accession: J50631
A:Molecule type: DNA
A:Residues: 1-632 <SH>
A:Experimental source: strain KO-8940
A:Note: It is uncertain whether ARG for 1-Met or for 19-Met is the initiation codon C:Comment: This enzyme hydrolyzes alpha-1,4-D-glucosidic linkages from the nonreducin C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds A:Pathway: glycogen/starch degradation
C:Superfamily: Thermomonospora curvata alpha-amylase; alpha-amylase core homology C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-44/Domain: signal sequence #status predicted <SLP>
F:45-632/Product: alpha-amylase #status predicted <AMP>
F:197-332/Domain: alpha-amylase core homology <AMP>

Query Match 52.5%; Score 32; DB 2; Length 632;
Best Local Similarity 62.5%; Pred. No. 4.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPQOFG 10
DB 270 QPSQFGL 277

RESULT 147

T00548
hypothetical protein At2g39380 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein F12L6.4
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C:Accession: T00548; F84816
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K submitted to the EMBL Data Library, July 1998
A:Description: Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence. A:Reference number: Z14168
A:Accession: T00548
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-637 <ROU>
A:Cross-references: EMBL:AC004218; NID:g3355463; PID:g3355467
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentli, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Motilal, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A:Reference number: AB4420; MUID:20083487
A:Accession: F84816
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-637 <STO>
A:Cross-references: GB:AE002093; NID:g3355467; PIDN:AC27829.1; GSPDB:GN00139

C:Genetics:
A:Gene: F12L6.4; At2g39380
A:Map position: 2
C:Superfamily: tomato leucine zipper-containing protein

Query Match 52.5%; Score 32; DB 2; Length 637;
Best Local Similarity 45.5%; Pred. No. 4.8e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
| | | | |
Db 302 KPSPERIFRLM 312

RESULT 148
A57542
p96 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996
C:Accession: A57542
R:Yu, X.X.; Yang, W.; Jackowski, S.; Rock, C.O.
J. Biol. Chem. 270, 14184-14191, 1995
A:Title: Cloning of a novel phosphoprotein regulated by colony-stimulating factor 1 shad
A:Reference number: A57542; MUID:95294028
A:Accession: A57542
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-837 <XUA>
A:Cross-references: GB:U18869
A:Note: authors translated the codon GCT for residue 789 as Thr
C:Keywords: alternative splicing; phosphoprotein

Query Match 52.5%; Score 32; DB 2; Length 837;
Best Local Similarity 75.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOFF 8
| | | | |
Db 267 RPKPOASF 274

RESULT 149
I45858
desmocollin - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 21-Jan-2000
C:Accession: I45858
R:Yue, K.K.; Holton, J.L.; Clarke, J.P.; Hyam, J.L.; Hashimoto, T.; Chidgey, M.A.; Garrod
J. Cell Sci. 108, 2163-2173, 1995
A:Title: Characterisation of a desmocollin isoform (bovine DSC3) exclusively expressed in
A:Reference number: I45858; MUID:95403557
A:Accession: I45858
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-896 <YUE>
A:Cross-references: GB:U33774; NID:9914820; PIDN:AAC41625.1; PID:9914821
C:Genetics:
A:Gene: Desc3
A:Introns: 831/3
C:Superfamily: cadherin; cadherin repeat homology
F:137-242/Domain: cadherin repeat homology <CDH>

Query Match 52.5%; Score 32; DB 2; Length 896;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 OFFGIM 11
| | | | |
Db 330 OFFGIM 335

RESULT 150
T22982
hypothetical protein F59B10.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000
C:Accession: T22982; T27953
R:Lloyd, C.
submitted to the EMBL Data Library, March 1995

A:Reference number: Z19646
A:Accession: T22982
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1039 <WIL>
A:Cross-references: EMBL:Z48716; PIDN:CAA88602.2; GSPDB:GN00020; CESP:F59B10.1
A:Experimental source: clone F59B10
R:Wilkinson, J.
submitted to the EMBL Data Library, April 1995
A:Reference number: Z20445
A:Accession: T27953
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1039 <WIL>
A:Cross-references: EMBL:Z49132; PIDN:CAA88990.2; GSPDB:GN00020; CESP:F59B10.1
A:Experimental source: clone ZK666
C:Genetics:
A:Gene: CESP:F59B10.1
A:Map position: 2
A:Introns: 9/1; 73/3; 293/3; 711/1; 754/3; 837/2; 877/3; 927/2
C:Superfamily: Caenorhabditis elegans hypothetical protein F59B10.1

Query Match 52.5%; Score 32; DB 2; Length 1039;
Best Local Similarity 54.5%; Pred. No. 7.8e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
| | | | |
Db 387 RPNPEOKFFLL 397

RESULT 151
S41915
DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Heterosigma carterae chloroplast
C:Species: chloroplast Heterosigma carterae
C:Date: 25-Dec-1994 #sequence_revision 23-Feb-1996 #text_change 18-Jun-1999
C:Accession: S41915
R:Mangahas, J.L.; Cattolico, R.A.; Reynolds, A.E.
submitted to the EMBL Data Library, November 1993
A:Description: Analysis of Heterosigma carterae (chromophyta) chloroplast rpoB gene se
A:Reference number: S41915
A:Accession: S41915
A:Molecule type: DNA
A:Residues: 1-1116 <KAN>
A:Cross-references: EMBL:X75815; NID:9452824; PIDN:CAA53450.1; PID:9452825
C:Genetics:
A:Gene: rpoB
A:Genome: chloroplast
C:Superfamily: DNA-directed RNA polymerase beta chain
C:Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 52.5%; Score 32; DB 2; Length 1116;
Best Local Similarity 50.0%; Pred. No. 8.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOFFGL 10
| | | | |
Db 775 KPKPGKVGCV 784

RESULT 152
D64315

type I restriction enzyme homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 10-Oct-1997
C:Accession: D64315
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
reson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999
A:Accession: D64315
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1163 <BUL>
A:Cross-references: GB:U67469; GB:L77117; NID:g1590890; PID:g1592264; TIGR:M0124; PID:g
C:Genetics:
A:Map position: REV123002-119511
A:Start codon: GTG

Query Match 52.5%; Score 32; DB 2; Length 1163;
Best Local Similarity 54.5%; Pred. No. 8.7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 RPKPOQFGML 11
DB 778 RPKPOQFGML 788

RESULT 153
S24407
formin isoform IV - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S24407
R:Jackson-Grusby, L.; Kuo, A.; Leder, P.
Genes Dev. 6, 29-37, 1992
A:Title: A variant limb deformity transcript expressed in the embryonic mouse limb defin
A:Reference number: S24407; MUID:92112033
A:Accession: S24407
A:Molecule type: mRNA
A:Residues: 1-1206 <JMC>
A:Cross-references: EMBL:X62379; NID:g51552; PIDN:CAA44244.1; PID:g51553

Query Match 52.5%; Score 32; DB 2; Length 1206;
Best Local Similarity 71.4%; Pred. No. 9.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 RPKQOFF 8
DB 1037 RPKQOFF 1043

RESULT 154
A41724
limb deformity (ld) protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 04-Mar-1993 #sequence_revision 15-Aug-1997 #text_change 10-Sep-1997
C:Accession: S24286; S38780; A41724
R:Trump, A.; Blundell, P.A.; de la Pompa, J.L.; Zeller, R.
Genes Dev. 6, 14-28, 1992
A:Title: The chicken limb deformity gene encodes nuclear proteins expressed in specific
A:Reference number: A41724; MUID:92112031
A:Accession: S24286
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1213 <TRU>
A:Cross-references: EMBL:X62681
A:Experimental source: embryo
R:Zeller, R.
submitted to the EMBL Data Library, August 1991

A:Reference number: S38780
A:Accession: S38780
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-885; A', 887-1213 <ZEL>
A:Cross-references: EMBL:X62681; NID:g63567; PID:g63568
C:Comment: Mutations in this gene affect morphogenesis of both limbs and kidneys.
C:Genetics:
A:Gene: ld
C:Keywords: nucleus

Query Match 52.5%; Score 32; DB 2; Length 1213;
Best Local Similarity 71.4%; Pred. No. 9.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 RPKQOFF 8
DB 1044 RPKQOFF 1050

RESULT 155
C83070
conserved hypothetical protein PA4601 [imported] - Pseudomonas aeruginosa (strain PAO
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83070
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laidig, K.; L
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: C83070
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1415 <STO>
A:Cross-references: GB:AE004874; GB:AE004091; NID:g9950849; PIDN:AA07989.1; GSPDB:GN
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA4601

Query Match 52.5%; Score 32; DB 2; Length 1415;
Best Local Similarity 45.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 RPKPOQFGML 11
DB 1393 RPKPOQFGML 1403

RESULT 156
S11515
formin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S11515
R:Woychik, R.P.; Maas, R.L.; Zeller, R.; Vogt, T.F.; Leder, P.
Nature 346, 850-853, 1990
A:Title: 'Formins': proteins deduced from the alternative transcripts of the limb def
A:Reference number: S11515; MUID:90363291
A:Accession: S11515
A:Molecule type: mRNA
A:Residues: 1-1468 <WOY>
A:Cross-references: EMBL:X53599; NID:g52877; PIDN:CAA37668.1; PID:g52878

Query Match 52.5%; Score 32; DB 2; Length 1468;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 RPKQOFF 8

Db 1299 RPKQDF 1305

RESULT 157
B43081

Vitellogenin vit-6 precursor - Caenorhabditis elegans
N:Alternate names: vitellogenin ypl180
N:Contains: vitellogenin ypl15; vitellogenin yp88

C:Species: Caenorhabditis elegans
C>Date: 20-Feb-1995 #sequence_revision 26-Jan-1996 #text_change 08-Dec-2000

C:Accession: B43081; A27271; G3576; T33017; A05154; S24599
R:Spiehl, J.; Nettleton, M.; Zucker-Aprison, E.; Lea, K.; Blumenthal, T.

J. Mol. Evol. 32, 429-438, 1991

A:Title: Vitellogenin motifs conserved in nematodes and vertebrates.
A:Reference number: A43081; MUID:91251142

A:Accession: B43081
A:Molecule type: DNA

A:Residues: 1-1651 <SP11>
A:Cross-references: GB:X56213; NID:g6925; PIDN:CAA39670.1; PID:g6926

R:Spiehl, J.; Blumenthal, T.
Mol. Cell. Biol. 5, 2495-2501, 1985

A:Title: The Caenorhabditis elegans vitellogenin gene family includes a gene encoding a
A:Reference number: A93067; MUID:86284606

A:Accession: A27271
A:Molecule type: DNA

A:Residues: 1-110 <SP12>
A:Cross-references: GB:M1499; NID:g156498; PIDN:AAA28165.1; PID:g552073

R:Spiehl, J.; Dentson, K.; Kirtland, S.; Cane, J.; Blumenthal, T.
Nucleic Acids Res. 13, 5283-5295, 1985

A:Title: The C. elegans vitellogenin genes: short sequence repeats in the promoter region
A:Reference number: A93576; MUID:85269643

A:Accession: C93575
A:Molecule type: DNA

A:Residues: 1-81 <SP13>
A:Cross-references: GB:X02756; NID:g6921

A:Note: The complete nucleotide sequence is not shown
R:Fullton, B.; Hawkins, J.; Gattung, S.; Wohldmann, P.; Elliott, G.

Submitted to the EMBL Data Library, February 1998
A:Description: The sequence of C. elegans cosmid K07H8.

A:Reference number: Z21264
A:Accession: T33017

A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-22, 'N', '24-205, 'E', '207-214, 'F', '216-370, 'A', '372-416, 'A', '418-633, 'N', '635-1622
A:Cross-references: EMBL:AF047559; PIDN:AAC04423.1; GSPDB:GN00022; CESP:K07H8.6

A:Experimental source: strain Bristol N2; clone K07H8
C:Comment: In Caenorhabditis, vitellogenins are synthesized by 32 cells building the int

uently taken up by the gonad.
C:Comment: The vitellogenin 6 precursor (yp180) is cleaved to yield two immunologically

C:Genetics:
A:Gene: vit-6; CESP:K07H8.6

A:Map position: 4
A:Insertions: 32/2; 185/3; 1501/3; 1591/3

C:Superfamily: vitellogenin
C:Keywords: glycoprotein

F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-1651/Product: vitellogenin vit-6 #status predicted <MAT>

F:252,651,1288/Binding site: carbohydrate (asn) (covalent) #status predicted
Query Match 52.5%; Score 32; DB 2; Length 1651;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RPKQDF 8
Db 1234 RPKQDF 1240

RESULT 158
T14603
hypothetical protein - Trypanosoma cruzi

C:Species: Trypanosoma cruzi
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Sep-1999

C:Accession: T14603; T14634
R:Andersson, B.; Aslund, L.; Pettersson, U.

Submitted to the EMBL Data Library, March 1998
A:Description: 93.4 kb of complete sequence from chromosome 3 of Trypanosoma cruzi.

A:Reference number: Z18159
A:Accession: T14603

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-1718 <AND>
A:Cross-references: EMBL:AF052832; NID:g3063540; PID:g3063541; PIDN:AAC14077.1

A:Accession: T14634
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-1718 <AND>

A:Cross-references: EMBL:AF052833; NID:g3063554; PID:g3063567; PIDN:AAC14102.1
C:Genetics:
A:Map position: 3

Query Match 52.5%; Score 32; DB 2; Length 1718;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKQDF 8
Db 142 RPKQDF 149

RESULT 159
T34249

hypothetical protein F31D5.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34249

R:Willcox, L.
Submitted to the EMBL Data Library, June 1995

A:Description: The sequence of C. elegans cosmid F31D5.
A:Reference number: Z21494

A:Accession: T34249
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-1817 <M1D>

A:Cross-references: EMBL:U028941; PIDN:AAC71101.1; GSPDB:GN00020; CESP:F31D5.5
A:Experimental source: strain Bristol N2; clone F31D5

C:Genetics:
A:Gene: CESP:F31D5.5

A:Map position: 2
A:Insertions: 22/2; 107/2; 199/2; 291/2; 384/2; 476/2; 566/2; 648/2; 728/2; 904/2; 1047/

Query Match 52.5%; Score 32; DB 2; Length 1817;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPKQDF 11
Db 1633 RPKQDF 1642

RESULT 160
S61103

SEC16 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein LPTW; protein YL085W

C:Species: Saccharomyces cerevisiae
C>Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 06-Feb-1998

C:Accession: S61103
R:Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.;

submitted to the EMBL Data Library, August 1995
A:Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.

A:Reference number: S59677
A:Accession: S61103

A:Molecule type: DNA
 A:Residues: 1-2195 <HML>
 A:Cross-references: EMBL:U41849; NID:g1147608; PID:g1147609; MIPS:YPL085w
 C:Genetics:
 A:Gene: SGD:SECI6
 A:Cross-references: SGD:S0006006; MIPS:YPL085w
 A:Map position: 16L
 C:Keywords: transmembrane protein
 F:1198-1214/Domain: transmembrane #status predicted <TM1>
 F:1250-1266/Domain: transmembrane #status predicted <TM2>

Query Match 52.5%; Score 32; DB 2; Length 2195;
 Best Local Similarity 85.7%; Pred. No. 1.7e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PPOFGL 10
 Db 582 PPOFGL 588

RESULT 161
 A59156
 gliadin omega-5 - wheat (fragment)
 C:Species: Triticum aestivum (common wheat)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
 C:Accession: A59156
 R:Palosuo, K.; Alenius, H.; Varjonen, E.; Kotyluhta, M.; Mikkola, J.; Keskinen, H.; Kal
 J. Allergy Clin. Immunol. 103, 912-917, 1999
 A:Title: A novel wheat gliadin as a cause of exercise-induced anaphylaxis.
 A:Reference number: A59156; MUID:99262562
 A:Accession: A59156
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-32 <PAL>
 A:Experimental source: strain Tjaive; tissue wheat kernel endosperm
 A:Note: seed storage protein; major allergen in wheat-dependent, exercise-induced anaphy
 C:Superfamily: gliadin
 C:Keywords: seed; storage protein

Query Match 50.8%; Score 31; DB 2; Length 32;
 Best Local Similarity 83.3%; Pred. No. 36;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRPQGF 7
 Db 25 POPQGF 30

RESULT 162
 D69969
 hypothetical protein ygzE - Bacillus subtilis
 C:Species: Bacillus subtilis
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
 C:Accession: D69969
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berten
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulter, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Gall
 lech, J.; Hartwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kunita, K.; Lapidus, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schoeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot
 akouch, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033
 A:Accession: D69969

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-79 <RUN>
 A:Cross-references: GB:299116; GB:AI009126; NID:92634723; PID:CBM14397.1; PID:926349
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: ygzE

Query Match 50.8%; Score 31; DB 2; Length 79;
 Best Local Similarity 50.0%; Pred. No. 89;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRPQPFGLM 11
 Db 38 PVSQWFGIL 47

RESULT 163
 J70703
 ferredoxin--thioredoxin reductase (EC 1.18.-.-) variable chain - maize
 N:Alternate names: ferredoxin:thioredoxin reductase chain A; ferredoxin:thioredoxin r
 C:Species: Zea mays (maize)
 C>Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-1999
 C:Accession: J70703; S74135
 R:Wadate, H.; Tsugita, A.; Kizuki, K.; Schuermann, P.
 Submitted to JIPID, August 1995
 A:Description: Amino acid sequence of maize ferredoxin:thioredoxin reductase variable
 A:Reference number: J70703
 A:Accession: J70703
 A:Molecule type: protein
 A:Residues: 1-97 <IMA>
 R:Wadate, H.; Tsugita, A.; Chow, L.P.; Kizuki, K.; Stritt-Etter, A.L.; Li, J.; Schue
 Eur. J. Biochem. 241, 121-125, 1996
 A:Title: Amino acid sequence of the maize ferredoxin:thioredoxin reductase variable
 A:Reference number: S74135; MUID:97054599
 A:Accession: S74135
 A:Molecule type: protein
 A:Residues: 1-52, 'C', 'S4-97 <IMW>
 A:Experimental source: leaf
 C:Comment: Ferredoxin:thioredoxin reductase is a [4Fe-4S] protein involved in the lig
 ht-generated electron. This enzyme is composed of two dissimilar subunits, a catalyti
 C:Superfamily: ferredoxin--thioredoxin reductase chain A
 C:Keywords: chloroplast; heterodimer; oxidoreductase; photosynthesis

Query Match 50.8%; Score 31; DB 2; Length 97;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQGF 8
 Db 77 QPKPQRF 84

RESULT 164
 S43435
 nuclear receptor protein DR-78 - fruit fly (Drosophila melanogaster) (fragment)
 C:Species: Drosophila melanogaster
 C>Date: 13-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
 C:Accession: S43435; S32723
 R:Martin-Blanco, E.; Kornberg, T.B.
 Blochm. Biophys. Acta 1216, 339-341, 1993
 A:Title: DR-78, a novel Drosophila melanogaster genomic DNA fragment highly homologou
 A:Reference number: S43435; MUID:94060116
 A:Accession: S43435
 A:Molecule type: DNA
 A:Residues: 1-113 <MAP>
 A:Cross-references: EMBL:X73045
 R:Martin-Blanco, E.; Kornberg, T.B.
 Submitted to the EMBL Data Library, April 1993
 A:Description: DR-78, a novel Drosophila melanogaster genomic DNA fragment highly hom

A:Accession: S32723
A:Molecule type: DNA
A:Residues: 1-112, 'K' <MAV>
A:Cross-references: EMBL:X73045
C:Genetics:
A:Gene: FlyBase:Elp78C
A:Cross-references: FlyBase:FBgn0004865
A:Introns: 68/3
C:Superfamily: unassigned: erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; nucleus; transcription regulation; zinc finger
F:45-113/Domain: erba transforming protein homology (fragment) <ERBA>
F:47-67/Region: zinc finger CCCC motif
F:83-107/Region: zinc finger CCCC motif

Query Match 50.8%; Score 31; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQFGL 10
1: ||||
DB 15 PQOQOSYGL 23

RESULT 165

hypothetical protein B1549_F3_106 - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C:Accession: S72785
R:Smith, D.R.; Rcdison, K.
submitted to the EMBL Data Library, November 1993
A:Description: Mycobacterium leprae cosmid B1549.
A:Reference number: S72582
A:Accession: S72785
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-126 <SMT>
A:Cross-references: EMBL:U00014; NID:g466903; PIDN:AAA50903.1; PID:g466928
C:Genetics:
A:Start codon: GTG

Query Match 50.8%; Score 31; DB 2; Length 126;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQO 5
|||||
DB 90 RPKPEQ 95

RESULT 166

conserved hypothetical protein AF0348 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: D69293
R:Klenk, H.P.; Cleyton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Atliach, P.; Kalne, B.P.; Sykes, S.
Smith, H.O.; Moese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea
A:Reference number: A69250; MUID:98049343
A:Accession: D69293
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-126 <KLE>
A:Cross-references: GB:AE001080; GB:AE000782; NID:g2689403; PIDN:AAB90889.1; PID:g265028

Query Match 50.8%; Score 31; DB 2; Length 126;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKPOQF 8
|||||
DB 25 PKPQKLF 31

RESULT 167

hypothetical HIT-family protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C:Accession: T40979
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Voicakeert, G.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z21961
A:Accession: T40979
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-133 <LYN>
A:Cross-references: EMBL:AL031966; PIDN:CAA21448.1; GSPDB:GN00068; SPDB:SPCC1442.14c
C:Genetics:
A:Gene: SPDB:SPCC1442.14c
A:Map position: 3
C:Superfamily: protein kinase C inhibitor; histidine triad homology

Query Match 50.8%; Score 31; DB 2; Length 133;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQFGL 10
|||||
DB 99 RPKNEYGL 107

RESULT 168

hypothetical protein F1P2.200 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 18-Feb-2000
C:Accession: T45725
R:Chisme, N.; Robert, C.; Brothier, P.; Winkler, P.; Cattolico, L.; Artiguenave, F.;
submitted to the protein Sequence Database, November 1999
A:Reference number: Z23010
A:Accession: T45725
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <CHO>
A:Cross-references: EMBL:AL132955
A:Experimental source: cultivar Columbia; BAC clone F1P2
C:Genetics:
A:Map position: 3
A:Introns: 56/3; 79/1; 111/2
A:Note: F1P2.200
C:Superfamily: Arabidopsis thaliana hypothetical protein F1P2.200

Query Match 50.8%; Score 31; DB 2; Length 136;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOQF 8
|||||
DB 23 PKPSHF 29

RESULT 169

chitinase (EC 3.2.1.14) - common sunflower (fragment)
T14185

C:Species: Helianthus annuus (common sunflower)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14185
R:Courbou, I.; Badaoui, S.; Gentzbittel, L.; Mouzeyar, S.; Nicolas, P.
submitted to the EMBL Data Library, April 1997
A:Description: RT-PCR cloning of a sunflower chitinase.
A:Reference number: Z17909
A:Accession: T14185
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-138 <COU>
A:Cross-references: EMBL:U96640; NID:g2098790; PID:g2098791
A:Experimental source: strain RMA266; hypocotyl
C:Function:
A:Description: catalyzes hydrolysis of catalyzes hydrolysis of beta-1,4-linkages of N-A
A:Pathway: polysaccharide degradation
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 50.8%; Score 31; DB 2; Length 138;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 RPKQOFG 9
DB 44 RPKQSYFG 51

RESULT 170
S67619
ribosomal protein S16.e, cytosolic - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D2442; protein YDL083c; protein YMR143w; r
C:Species: Saccharomyces cerevisiae
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 20-Jun-2000
C:Accession: S67619; S69289; S50399; S45510
R:Wambutt, R.; Wedler, H.; Wedler, E.; Scharfe, M.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67608
A:Accession: S67619
A:Molecule type: DNA
A:Residues: 1-143 <WMA>
A:Cross-references: EMBL:Z74131; GSPDB:GN00004; MIPS:YDL083c; NID:g1431105; PIDN:CAA9864
A:Experimental source: strain S288C
A:Genetics: CH4
R:Badcock, K.; Churcher, C.
submitted to the EMBL Data Library, December 1994
A:Reference number: S50388
A:Accession: S69289
A:Molecule type: DNA
A:Residues: 1-143 <BAD>
A:Cross-references: EMBL:Z47071
A:Genetics: CH13
A:Accession: S50399
A:Molecule type: DNA
A:Residues: 1-143 <BAM>
A:Cross-references: EMBL:Z47071; NID:g606429; PIDN:CAA67357.1; PID:g606441; GSPDB:GN0001
A:Genetics: CH13
R:Takahara, H.; Tsunasawa, S.; Miyagi, M.; Warner, J.R.
J. Biol. Chem. 267, 5442-5445, 1992
A:Title: NH2-terminal acetylation of ribosomal proteins of Saccharomyces cerevisiae.
A:Reference number: S45500; MUID:92184799
A:Accession: S45510
A:Molecule type: protein
A:Residues: 2-8, 'A', '10', 'K', '12', 'R', '14', 'V', '16', 'V', '18-20', 'KN', '23-24', 'N', '26 <TAK>
C:Genetics: <CH4>
A:Gene: RPS16B; MIPS:YDL083c
A:Cross-references: MIPS:YDL083c
A:Map position: 4L
A:Introns: 8/3
C:Genetics: <CH13>
A:Gene: RPS16A; MIPS:YMR143w
A:Cross-references: MIPS:YMR143w
A:Map position: 13R

A:Introns: 8/3
C:Superfamily: Escherichia coli ribosomal protein S9
C:Keywords: acetylated amino end; blocked amino end; protein biosynthesis; ribosome
F:2-143/Product: ribosomal protein S16.e #status experimental <MAT>
F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

Query Match 50.8%; Score 31; DB 2; Length 143;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOFG 9
DB 123 RPKPFEG 131

RESULT 171
E81982
probable phosphatase NMA0625 [imported] - Neisseria meningitidis (strain Z2491 serogr
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: E81982
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
: Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: A81775; MUID:2022556
A:Accession: E81982
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-159 <PAR>
A:Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CA883915.1; PID:g737
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA0625

Query Match 50.8%; Score 31; DB 2; Length 159;
Best Local Similarity 40.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOFG 10
DB 82 RPKPMFG 91

RESULT 172
S68232
antimicrobial protein PR-39 precursor, cathelin-associated - pig
N:Alternate names: myeloid antibacterial protein PR-39
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68232; JN0899; I47138; S19563
R:Zhao, C.; Ganz, T.; Lehnert, R.I.
FEBS Lett. 376, 130-134, 1995
A:Title: Structures of genes for two cathelin-associated antimicrobial peptides: prop
A:Reference number: S68232; MUID:96105365
A:Accession: S68232
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-172 <ZHA>
A:Cross-references: EMBL:X89201; NID:g1165150; PIDN:CAA61487.1; PID:g1165151
A:Experimental source: leukocytes
R:Storici, P.; Zanetti, M.
Biochem. Biophys. Res. Commun. 196, 1058-1065, 1993
A:Title: A cDNA derived from pig bone marrow cells predicts a sequence identical to t
A:Reference number: JN0899; MUID:94071853
A:Accession: JN0899
A:Molecule type: mRNA
A:Residues: 1-20, 'A', '22-172 <STO>
A:Cross-references: GB:L23825; NID:g435100; PIDN:AAA31109.1; PID:g435101
A:Experimental source: bone marrow cells
R:Gundmundsson, G.H.; Magnusson, K.P.; Chowdhary, B.P.; Johansson, M.; Andersson, L.;

Proc. Natl. Acad. Sci. U.S.A. 92, 7085-7089, 1995
A:Title: Structure of the gene for porcine peptide antibiotic PR-39, a cathelin gene fam
A:Reference number: 147138; MUID:95350216
A:Accession: 147138
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-23, 'T', 30-89, 'QR', 92-116, 'ND', 120-172 <GND>
A:Cross-references: EMBL:X87236; NID:9829142; PIDN:CAA60682.1; PID:91051298
R:Agarberth, B.; Lee, J.Y.; Bergman, T.; Carlquist, M.; Bowman, H.G.; Mutt, V.; Joernvall
Eur. J. Biochem. 202, 849-854, 1991
A:Title: Amino acid sequence of PR-39, isolation from pig intestine of a new member of t
A:Reference number: S19563; MUID:92111534
A:Accession: S19563
A:Molecule type: protein
A:Residues: 131-169 <AGE>
A:Experimental source: intestine
C:Genetics:
A:Gene: PR39
A:Introns: 66/3; 102/3; 126/3
C:Superfamily: cathelin; cystatin homology
C:Keywords: amidated carboxyl end; antibacterial
F:1-29/Domain: signal sequence <status predicted <SIG>
F:22-129/Domain: cystatin homology <cys>
F:30-139/Domain: propeptide #status predicted <PRO>
F:131-169/Product: antimicrobial protein PR-39 #status experimental <MAT>
F:169/Modified site: amidated carboxyl end (Pro) (amide in mature form from following 91

Query Match 50.8%; Score 31; DB 2; Length 172;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQF 8
111111
DB 141 RRPPEPF 148

RESULT 173
A75624
hypothetical protein DRB0054 - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: A75624
R:Miller, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: A75624
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-176 <WHI>
A:Cross-references: GB:AE001826; NID:96460827; PIDN:AAF12635.1; PID:96460931; TIGR:DRB00
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRB0054
A:Map position: megaplasmid
A:Genome: plasmid
A:Note: plasmid MP1
C:Superfamily: Deinococcus radiodurans hypothetical protein DRB0054

Query Match 50.8%; Score 31; DB 2; Length 176;
Best Local Similarity 60.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFGL 10
111111
DB 119 RPTPOFEGJ 128

RESULT 174

E69296
transcription initiation factor IID homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: E69296
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
., Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kalne, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: E69296
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1183 <KLE>
A:Cross-references: GB:AE001078; GB:AE000782; NID:92689401; PIDN:AAB90862.1; PID:9265
C:Superfamily: transcription initiation factor IID
C:Keywords: transcription initiation

Query Match 50.8%; Score 31; DB 2; Length 183;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOQFGLM 11
111111
DB 36 KPKQFGLV 44

RESULT 175
E96766
hypothetical protein F2P9_24 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: E96766
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hlizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzla
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: E96766
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-193 <STO>
A:Cross-references: GB:AE005173; NID:97109482; PIDN:AAF36746.1; GSPDB:GN00141
C:Genetics:
A:Gene: F2P9_24
A:Map position: 1

Query Match 50.8%; Score 31; DB 2; Length 193;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 KPKQFGL 10
111111
DB 154 PRPSTFGL 162

RESULT 176
F71012
hypothetical protein PH136 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C:Accession: F71012

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatakeyama, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohnuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137
A:Accession: F71012
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-206 <KAM>
A:Cross-references: GB:AP000006; NID:q3236133; PIDN:BAA30502.1; PID:d1031445; PID:q32578
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PHJ396

Query Match 50.8%; Score 31; DB 2; Length 206;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOQFEG 9
Db 76 RPOQFEG 82

RESULT 177

hypothetical protein F49E2.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T22453
R:Stinson, J.
submitted to the EMBL Data Library, October 1994
A:Reference number: Z19566
A:Accession: T22453
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-216 <MIL>
A:Cross-references: EMBL:Z46267; PIDN:CAAB6423.1; GSPDB:GN00028; CESP:F49E2.4
A:Experimental source: clone F49E2
C:Genetics:
A:Gene: CESP:F49E2.4
A:Map position: X
A:introns: 28/2; 74/3; 163/3; 196/1

Query Match 50.8%; Score 31; DB 2; Length 216;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKQOQFGL 10
Db 46 RPKFAEYFGI 55

RESULT 178

phosphoglycolate phosphatase, probable NMB1830 [Imported] - Neisseria meningitidis (stra
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: C81038
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Yamahavean, J.; Gill, J.; Scarlato, V.; Masiugnani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755
A:Accession: C81038
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <TEF>
A:Cross-references: GB:AE002532; GB:AE002098; NID:g7227078; PIDN:AAFA2165.1; PID:g722708

A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1830

Query Match 50.8%; Score 31; DB 2; Length 219;
Best Local Similarity 40.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKQOQFGL 10
Db 142 KPSPEWVFGI 151

RESULT 179

hypothetical protein T05E12.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24530
R:McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19904
A:Accession: T24530
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-226 <MIL>
A:Cross-references: EMBL:Z81585; PIDN:CA804683.1; GSPDB:GN00023; CESP:T05E12.5
A:Experimental source: clone T05E12
C:Genetics:
A:Gene: CESP:T05E12.5
A:Map position: 5
A:introns: 168/2

Query Match 50.8%; Score 31; DB 2; Length 226;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 PPOQFEG 9
Db 70 POKFEG 75

RESULT 180

hypothetical protein ZK632.12 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
C:Accession: S40944
R:Birks, M.
submitted to the EMBL Data Library, February 1993
A:Reference number: S40933
A:Accession: S40944
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-254 <BER>
A:Cross-references: EMBL:Z22181
C:Genetics:
A:introns: 6/1; 137/1; 206/3; 241/3

Query Match 50.8%; Score 31; DB 2; Length 254;
Best Local Similarity 62.5%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKQOQF 8
Db 49 KPKQOQF 56

RESULT 181

WMBVT3

30K protein - tomato mosaic virus (strain L)
C:Species: tomato mosaic virus
A:Note: host (tomato)
C:Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 16-Feb-1997
C:Accession: A04182
R:Takamatsu, N.; Ohno, T.; Meshi, T.; Okada, Y.
Nucleic Acids Res. 11, 3767-3778, 1983
A:Title: Molecular cloning and nucleotide sequence of the 30K and the coat protein cist
A:Reference number: A93473; MUID:83220776
A:Accession: A04182
A:Molecule type: genomic RNA
A:Residues: 1-264 <TAK>
C:Superfamily: tobnavirus 30K protein
C:Keywords: DNA binding

Query Match 50.8%; Score 31; DB 1; Length 264;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQF 7
| | | | |
Db 233 RPKPKSF 239

RESULT 182
WMBVL2
30K protein - tomato mosaic virus (strain LII)
N:Alternate names: transport protein
C:Species: tomato mosaic virus
C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Feb-1997
C:Accession: J01457
R:Calder, V.L.; Palukaitis, P.
J. Gen. Virol. 73, 165-168, 1992
A:Title: Nucleotide sequence analysis of the movement genes of resistance breaking stra
A:Reference number: J01456; MUID:92113565
A:Accession: J01457
A:Molecule type: genomic RNA
A:Residues: 1-264 <CAL>
A:Note: the authors translated the codon TGG for residue 68 as Cys
C:Comment: This protein is involved in cell-to-cell transport of the virus.
C:Superfamily: tobnavirus 30K protein
C:Keywords: DNA binding; transport protein

Query Match 50.8%; Score 31; DB 1; Length 264;
Best Local Similarity 71.4%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQF 7
| | | | |
Db 233 RPKPKSF 239

RESULT 183
E71612
ribosomal protein L7/L12 (O0) PFB0545c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C:Accession: E71612
R:Gardner, M.J.; Tetteelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Perle, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743
A:Accession: E71612
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-266 <GAR>
A:Cross-references: GB:AE001401; GB:AE001362; NID:g3845209; PIDN:AAC71898.1; PID:g384521
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0545c

Query Match 50.8%; Score 31; DB 2; Length 266;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOQFFG 9
| | | | |
Db 136 PPSNFC 143

RESULT 184
A26162
holocytochrome-c synthase (EC 4.4.1.17) CYC3 - yeast (Saccharomyces cerevisiae)
N:Alternate names: cytochrome c heme lyase; protein YAL039C
C:Species: Saccharomyces cerevisiae
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 05-Nov-1999
C:Accession: A26162; S51980
R:Dumont, M.E.; Ernst, J.F.; Hampsey, D.M.; Sherman, F.
EMBO J. 6, 235-241, 1987
A:Title: Identification and sequence of the gene encoding cytochrome c heme lyase in
A:Reference number: A26162; MUID:87218469
A:Accession: A26162
A:Molecule type: DNA
A:Residues: 1-269 <DUM>
A:Cross-references: EMBL:X04776; NID:g3615; PIDN:CAA28470.1; PID:g3616
R:Bussey, H.; Kaback, D.B.; Zhong, W.; Vo, D.T.; Clark, M.W.; Fortin, N.; Hall, J.; O
submitted to the EMBL data library, August 1994
A:Description: The sequence of chromosome 1 of Saccharomyces cerevisiae.
A:Reference number: S51956
A:Accession: S51980
A:Molecule type: DNA
A:Residues: 1-269 <BUS>
A:Cross-references: EMBL:U12980; NID:g1326053; PIDN:AAC04992.1; PID:g595545; GSPDB:GN
C:Genetics:
A:Gene: SGD:CYC3; MIPS:YAL039C
A:Cross-references: MIPS:YAL039C; SGD:S0000037
A:Map position: 1L
A:Genome: nuclear
C:Keywords: carbon-sulfur lyase; mitochondrion

Query Match 50.8%; Score 31; DB 2; Length 269;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PKPOQFFG 11
| | | | |
Db 95 PPSQOMYNA 104

RESULT 185
D75552
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: D75552
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896
A:Accession: D75552
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-271 <WHI>
A:Cross-references: GB:AE001879; GB:AE000513; NID:g6457832; PIDN:AAF09759.1; PID:g645
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0172
A:Map position: 1

Query Match 50.8%; Score 31; DB 2; Length 271;
 Best Local Similarity 55.6%; Pred. No. 3.1e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQF 9
 11:111
 Db 22 RPKPOQF 30

RESULT 186

S48776

hypothetical protein YDR087c - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: hypothetical protein D4478; hypothetical protein YDR554.20C

C:Species: *Saccharomyces cerevisiae*

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-Oct-1999

C/Accession: S48776; S49842; S39583; S55836; S67904

R/Coster, F.; Jonniaux, J.L.; Goffeau, A.

submitted to the EMBL Data Library, October 1994

A:Reference number: S48758

A:Accession: S48776

A:Molecule type: DNA

A:Residues: 1-278 <COS>

A:Cross-references: EMBL:X82086; NID:9558241; PIDN:CAA57616.1; PID:9558260

R:Richards, C.; Harris, D.E.

submitted to the EMBL Data Library, November 1994

A:Reference number: S49823

A:Accession: S49842

A:Molecule type: DNA

A:Residues: 1-278 <RSC>

A:Cross-references: EMBL:Z46796; NID:9577794; PIDN:CAA66809.1; PID:9577814

R:Essault, Y.; Blondel, M.O.; Deshaies, R.J.; Schekman, R.; Kepes, F.

EMBO J. 12, 4083-4093, 1993

A:Title: The yeast SSI1 gene is essential for secretory protein translocation and encode

A:Reference number: S39583; MUID:94038890

A:Accession: S39583

A:Molecule type: translation not shown

A:Residues: 146-278 <ESN>

A:Cross-references: EMBL:X74499; NID:9414690; PIDN:CAA52607.1; PID:9414691

R:Coster, F.; Jonniaux, J.L.; Goffeau, A.

Yeast 11, 673-679, 1995

A:Title: Analysis of a 32.8 kb segment of yeast chromosome IV reveals 21 open reading fr

A:Reference number: S55819; MUID:96093910

A:Accession: S55836

A:Molecule type: DNA

A:Status: nucleic acid sequence not shown; translation not shown

A:Residues: 1-278 <COM>

A:Cross-references: EMBL:X82086; NID:9558241; PIDN:CAA57616.1; PID:9558260

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994

R:Foury, F.; Jonniaux, J.L.; Purnelle, B.; Coster, F.; Goffeau, A.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67889

A:Accession: S67904

A:Molecule type: DNA

A:Residues: 1-278 <FOU>

A:Cross-references: EMBL:Z74383; NID:91431562; PIDN:CAA98907.1; PID:e253404; PID:9143156

A:Experimental source: strain S288C

C:Genetics:

A:Map position: 4R

Query Match 50.8%; Score 31; DB 2; Length 278;
 Best Local Similarity 83.3%; Pred. No. 3.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQ 6
 11:1111
 Db 58 RPKPOQ 63

RESULT 187
 A35935

NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 31K chain precursor - *Neurospora crassa*
 C:Species: *Neurospora crassa*
 C>Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 23-Feb-1997

C/Accession: A35935
 R:Videla, A.; Tropisch, M.; Werner, S.
 Biochem. Biophys. Res. Commun. 171, 1168-1174, 1990

A:Title: Primary structure and expression of a nuclear-coded subunit of complex I hom
 A:Reference number: A35935; MUID:91024977

A:Accession: A35935

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-283 <VID>

C:Keywords: mitochondrion; NAD; oxidoreductase

Query Match 50.8%; Score 31; DB 2; Length 283;
 Best Local Similarity 71.4%; Pred. No. 3.2e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQF 7
 11:111
 Db 40 RPKPOQF 46

RESULT 188

G64175

hypothetical protein H11699 - *Haemophilus influenzae*C:Species: *Haemophilus influenzae*

C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 04-Mar-2000

C/Accession: G64175; S27578

R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage

, D.M.; Brandon, R.C.; Rine, L.D.; Fritchman, J.L.; Geoghagen, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente

A:Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.

A:Reference number: A64000; MUID:95350630

A:Accession: G64175

A:Molecule type: translation not shown

A:Residues: 1-304 <TIGR>

A:Cross-references: GB:U32842; GB:U42023; NID:91574541; PIDN:AA23345.1; PID:91574553

A:Experimental source: strain Rd KW20

R:McLaughlin, R.; Abu Kwaik, Y.; Young, R.; Spicola, S.; Apicella, M.

submitted to the EMBL Data Library, June 1992

A:Description: Characterization and sequence of the *lsg* locus from *Haemophilus influe*

A:Reference number: S27577

A:Accession: S27578

A:Molecule type: DNA

A:Residues: 1-3, 'T', 'S', '69-129', 'D', '131-219', 'C', '221-252', 'K', '254-304 <MCL>

A:Cross-references: EMBL:M94855; NID:9148931; PIDN:AAA24979.1; PID:9148933

A:Experimental source: strain A2

C:Superfamily: *Haemophilus influenzae* hypothetical protein H11699

Query Match 50.8%; Score 31; DB 2; Length 304;
 Best Local Similarity 71.4%; Pred. No. 3.5e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 OOFPGM 11
 111111
 Db 25 OOFPGM 31

RESULT 189

D96750

unknown protein P28P22.22 [imported] - *Arabidopsis thaliana*C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C/Accession: D96750

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiet, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewart,

ansen, N.F.; Hughes, B.; Hultzer, L.

Nature 408, 816-820, 2000
 A:Authors: Hunter, C.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.: Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,
 Rizzo, M.; Rooney, J.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719
 A:Accession: D96750
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1320 <STO>
 A:Cross-references: GB:AE005173; NID:g6648169; PIDN:AAF21169.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F28P22.22
 A:Map position: 1

Query Match 50.8%; Score 31; DB 2; Length 320;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 PKQPF 9
 |||||
 DB 61 PKQPF 66

RESULT 190

PRJHD
 proteinase (EC 3.4.23.-) - squirrel monkey retrovirus SMRV-H

C:Species: squirrel monkey retrovirus SMRV-H
 C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 23-Feb-1997

C:Accession: B31827

R:Oda, T.; Ikeda, S.; Watanabe, S.; Hatushika, M.; Akiyama, K.; Mitsunobu, F.

A:Title: Molecular cloning, complete nucleotide sequence, and gene structure of the pro-

A:Reference number: A31827; MUID:89073750

A:Accession: B31827

A:Molecule type: DNA

A:Residues: 1-323 <ODA>

C:Genetics:

A:Gene: prt

C:Complex: homodimer

C:Superfamily: retroviral proteinase

C:Keywords: aspartic proteinase; homodimer; hydrolase

F:193/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 50.8%; Score 31; DB 1; Length 323;
 Best Local Similarity 60.0%; Pred. No. 3.7e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKQPF 11
 |||||
 DB 82 PKQPF 91

RESULT 191

T19592
 hypothetical protein C30H6.7 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19592

R:Mortimore, B.

A:Reference number: Z19148

A:Accession: T19592

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-337 <WIL>
 A:Cross-references: EMBL:Z81044; PIDN:CAB02813.1; GSPDB:GN00022; CESP:C30H6.7
 A:Experimental source: clone C30H6
 C:Genetics:

A:Gene: CESP:C30H6.7
 A:Map position: 4
 A:Introns: 19/2; 85/3; 120/3; 166/3; 240/2; 286/2

Query Match 50.8%; Score 31; DB 2; Length 337;
 Best Local Similarity 85.7%; Pred. No. 3.8e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOQF 9
 |||||
 DB 230 KPOQF 236

RESULT 192

G69027
 phosphoribosylformylglycinamide cyclo-ligase - *Methanobacterium thermoautotrophicum*

C:Species: *Methanobacterium thermoautotrophicum*

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Jul-1999

C:Accession: G69027

R:Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.

Olui, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Mierzbowski, J.; Gibson, R.; Jiwani,

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: fu

A:Reference number: A69000; MUID:98037514

A:Accession: G69027

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-338 <MTB>

A:Cross-references: GB:AE000888; GB:AE000666; NID:g2622304; PIDN:AA85693.1; PID:g262

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH104

C:Superfamily: phosphoribosylformylglycinamide cyclo-ligase; phosphoribosylformylgl

F:4-317/Domain: phosphoribosylformylglycinamide cyclo-ligase homology <PFL>

Query Match 50.8%; Score 31; DB 2; Length 338;
 Best Local Similarity 71.4%; Pred. No. 3.8e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKQPF 8
 |||||
 DB 264 PKQPF 270

RESULT 193

S75196
 hypothetical protein slr2043 - *Synechocystis* sp. (strain PCC 6803)

C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C:Accession: S75196

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocys*

A:Reference number: S74322; MUID:97061201

A:Accession: S75196

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-338 <KAN>

A:Cross-references: EMBL:D90903; GB:AB001339; NID:g1652127; PIDN:BA17110.1; PID:g165

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: adhesin B

Query Match 50.8%; Score 31; DB 2; Length 338;
 Best Local Similarity 66.7%; Pred. No. 3.8e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKPOOFFGL 10
| | | | |
Db 87 PKPOQLAAL 95

RESULT 194

T24822

hypothetical protein T11A5.3 - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T24822

R:McMurray, A. submitted to the EMBL Data Library, May 1996

A:Reference number: Z19939

A:Accession: T24822

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-355 <MTL>

A:Cross-references: EMBL:Z72515; PIDN:CAA96683.1; GSPDB:GN00023; CESP:T11A5.3

A:Experimental source: clone T11A5

C:Genetics:

A:Gene: CESP:T11A5.3

A:Map position: 5

A:Introns: 74/2; 151/3; 177/3; 252/2; 334/1

Query Match 50.8%; Score 31; DB 2; Length 355;
Best Local Similarity 44.4%; Pred. No. 4e+02;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 3 PKPOFFGLM 11
| | | | |

Db 286 EPYQYFGIL 294

RESULT 195

C72077

conserved hypothetical protein CP0305 [imported] - *Chlamydomonas reinhardtii* (strains CWIC:Species: *Chlamydomonas reinhardtii*

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 28-Jul-2000

C:Accession: C72077; A81592

R:Kalmn, S.; Mitchell, W.; Marathe, R.; Lammell, C.; Fan, J.; Olinger, L.; Grimwood, J.;

Nature Genet. 21, 385-389, 1999

A:Title: Comparative genomes of *Chlamydomonas reinhardtii* and *C. trachomatis*.

A:Reference number: A72000; MUID:99206606

A:Accession: C72077

A:Molecule type: DNA

A:Residues: 1-371 <ARN>

A:Cross-references: GB:AE001628; GB:AE001363; NID:g4376730; PIDN:ADI8592.1; PID:g437673

A:Experimental source: strain CWI029

R:Read, T.D.; Brundham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of *Chlamydomonas reinhardtii* and *Chlamydomonas reinhardtii* AR39.

A:Reference number: A81500; MUID:20150255

A:Accession: A81592

A:Molecule type: DNA

A:Residues: 1-371 <REA>

A:Cross-references: GB:AE002192; GB:AE002161; NID:g7189226; PIDN:AAF38162.1; PID:g718923

A:Experimental source: strain AR39, HL cells

C:Genetics:

A:Gene: YXJG_2; CP0305

C:Superfamily: conserved hypothetical protein CP0630

Query Match 50.8%; Score 31; DB 2; Length 371;
Best Local Similarity 71.4%; Pred. No. 4.2e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOOFF 8
| | | | |

Db 136 PPSQOFF 142

RESULT 196

F86546

hypothetical protein yxjG_2 [imported] - *Chlamydomonas reinhardtii* (strain J138)C:Species: *Chlamydomonas reinhardtii*

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: F86546

R:Shira, M.; Hirakawa, H.; Kinoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;

Nucleic Acids Res. 28, 2311-2314, 2000

A:Title: Comparison of whole genome sequences of *Chlamydomonas reinhardtii* J138.

A:Reference number: A86491; MUID:20330349

A:Accession: F86546

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-371 <STO>

A:Cross-references: GB:BA000008; NID:g8978820; PIDN:BA098656.1; GSPDB:GN00142

A:Experimental source: strain J138

C:Genetics:

A:Gene: YXJG_2

C:Superfamily: conserved hypothetical protein CP0630

Query Match 50.8%; Score 31; DB 2; Length 371;
Best Local Similarity 71.4%; Pred. No. 4.2e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOOFF 8
| | | | |

Db 136 PPSQOFF 142

RESULT 197

T40024

probable cytochrome c heme lyase - fission yeast (*Schizosaccharomyces pombe*)C:Species: *Schizosaccharomyces pombe*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T40024

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.

submitted to the EMBL Data Library, September 1998

A:Reference number: Z21899

A:Accession: T40024

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-377 <MOO>

A:Cross-references: EMBL:AL031743; PIDN:CAA21104.1; GSPDB:GN00067; SPDB:SPBC26H8.12

A:Experimental source: strain 972h-; cosmid c26H8

C:Genetics:

A:Gene: SPDB:SPBC26H8.12

A:Map position: 2

Query Match 50.8%; Score 31; DB 2; Length 377;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 PKPOFFGLM 11
| | | | |

Db 224 PPSQOMYNM 233

RESULT 198

DB3803

rRNA-guanine transglycosylase fgt [imported] - *Bacillus halodurans* (strain C-125)C:Species: *Bacillus halodurans*

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000

C:Accession: DB3803

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.;

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* a

A:Reference number: A83650; MUID:2026314

A:Accession: DB3803

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-379 <STO>
A:Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BA04947.1; GSPDB:GN00
A:Experimental source: strain C-125
C:Genetics:
A:Gene: tgt
C:Superfamily: genuine tRNA-ribosyltransferase

OY 2 PKPQOFF 8
||| ||
Db 4 PKPSHFF 10

Query Match 50.8%; Score 31; DB 2; Length 379;
Best Local Similarity 45.5%; Pred. No. 4.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Search completed: April 1, 2002, 16:19:17
Job time: 108 sec

OY 1 PKPQOFFGIM 11
||:| ||::
Db 180 RPEDQALFGII 190

RESULT 199

G72569
hypothetical protein APE1840 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: G72569
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taken
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A:Reference number: A72450; MIMD:99310339
A:Accession: G72569
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-385 <XAM>
A:Cross-references: DDBJ:AP000062; NID:g5105244; PIDN:BAA80844.1; PID:d1044630; PID:g510
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1840

Query Match 50.8%; Score 31; DB 2; Length 385;
Best Local Similarity 62.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 PKPQOFF 8
||| |:
Db 254 RPKPPQLY 261

RESULT 200

F82369
conserved hypothetical protein VC0047 [imported] - Vibrio cholerae (strain N16961 serogr
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: F82369
R:Heidelberg, J.E.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MIMD:20406833
A:Accession: F82369
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-391 <HEI>
A:Cross-references: GB:AE004096; GB:AE003852; NID:g9654440; PIDN:AAF93225.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0047
A:Map position: 1

Query Match 50.8%; Score 31; DB 2; Length 391;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 1, 2002, 16:17:29 ; Search time 20.12 Seconds
(without alignments)
12.303 Million cell updates/sec

Title: US-09-988-792-1
Perfect score: 61
Sequence: 1 RPKQOFGCLM 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 203

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 50%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
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6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	11	1	US-07-934-553-1 Sequence 1, Appl
2	61	100.0	11	1	US-08-184-935-12 Sequence 12, Appl
3	61	100.0	11	1	US-08-269-288-2 Sequence 2, Appl
4	61	100.0	11	1	US-08-338-484-1 Sequence 1, Appl
5	61	100.0	11	1	US-08-125-432-1 Sequence 1, Appl
6	61	100.0	11	1	US-08-225-474-1 Sequence 1, Appl
7	61	100.0	11	1	US-08-391-910-2 Sequence 2, Appl
8	61	100.0	11	1	US-08-418-994-2 Sequence 2, Appl
9	61	100.0	11	1	US-08-480-505-3 Sequence 3, Appl
10	61	100.0	11	1	US-08-391-814-2 Sequence 2, Appl
11	61	100.0	11	1	US-08-167-870-1 Sequence 1, Appl
12	61	100.0	11	1	US-08-255-272-6 Sequence 6, Appl
13	61	100.0	11	1	US-08-441-591-6 Sequence 6, Appl
14	61	100.0	11	1	US-08-303-362A-6 Sequence 6, Appl
15	61	100.0	11	1	US-08-462-859A-1 Sequence 1, Appl
16	61	100.0	11	1	US-08-123-659A-1 Sequence 1, Appl
17	61	100.0	11	1	US-08-462-415-2 Sequence 2, Appl
18	61	100.0	11	1	US-08-463-874-2 Sequence 2, Appl
19	61	100.0	11	1	US-08-464-247A-1 Sequence 1, Appl
20	61	100.0	11	1	US-08-464-248A-1 Sequence 1, Appl
21	61	100.0	11	1	US-08-444-135-2 Sequence 2, Appl
22	61	100.0	11	1	US-08-318-391-2 Sequence 2, Appl
23	61	100.0	11	2	US-08-796-598-11 Sequence 11, Appl
24	61	100.0	11	2	US-08-447-175A-11 Sequence 11, Appl
25	61	100.0	11	2	US-07-737-371E-77 Sequence 77, Appl
26	61	100.0	11	2	US-08-848-766A-1 Sequence 1, Appl
27	61	100.0	11	3	US-08-927-128-17 Sequence 17, Appl

28	61	100.0	11	4	US-08-257-966-2 Sequence 2, Appl
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55	56	91.8	11	1	US-08-031-325A-26 Sequence 26, Appl
56	56	91.8	11	2	US-07-737-371E-13 Sequence 13, Appl
57	56	91.8	11	2	US-07-737-371E-14 Sequence 14, Appl
58	56	91.8	11	2	US-07-737-371E-16 Sequence 16, Appl
59	56	91.8	11	2	US-07-737-371E-18 Sequence 18, Appl
60	56	91.8	11	2	US-07-737-371E-61 Sequence 61, Appl
61	56	91.8	11	2	US-07-737-371E-63 Sequence 63, Appl
62	56	91.8	11	2	US-07-737-371E-64 Sequence 64, Appl
63	56	91.8	11	2	US-08-747-137-34 Sequence 34, Appl
64	56	91.8	11	2	US-08-505-250-34 Sequence 34, Appl
65	56	91.8	11	1	US-08-428-488-15 Sequence 15, Appl
66	55	90.2	11	2	US-07-737-371E-15 Sequence 15, Appl
67	55	90.2	11	2	US-07-737-371E-17 Sequence 17, Appl
68	55	90.2	11	2	US-07-737-371E-19 Sequence 19, Appl
69	55	90.2	11	2	US-07-737-371E-20 Sequence 20, Appl
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71	54	88.5	11	2	US-07-737-371E-22 Sequence 22, Appl
72	54	88.5	11	2	US-07-737-371E-24 Sequence 24, Appl
73	54	88.5	11	2	US-07-737-371E-26 Sequence 26, Appl
74	54	88.5	11	2	US-07-737-371E-62 Sequence 62, Appl
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79	53	86.9	11	6	5441935-8 Patent No. 5441935
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83	52	85.2	11	2	US-07-737-371E-32 Sequence 32, Appl
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85	50	82.0	22	1	US-07-737-371E-55 Sequence 55, Appl
86	49	80.3	9	2	US-07-737-371E-55 Sequence 55, Appl
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89	49	80.3	11	2	US-07-737-371E-31 Sequence 31, Appl
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96	47	77.0	11	2	US-07-737-371E-54 Sequence 54, Appl
97	47	77.0	11	3	US-08-890-157A-4 Sequence 4, Appl
98	46	75.4	8	2	US-07-737-371E-57 Sequence 57, Appl
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122	36	59.0	12	2	US-08-447-175A-10	Sequence 10, Appl
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131	35	57.4	474	3	US-08-978-741-8	Sequence 8, Appl
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153	33	54.1	324	2	US-08-793-410-30	Sequence 30, Appl
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156	33	54.1	404	2	US-09-143-438-7	Sequence 7, Appl
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165	32	52.5	11	2	US-08-796-598-7	Sequence 7, Appl
166	32	52.5	11	2	US-08-447-175A-7	Sequence 7, Appl
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168	32	52.5	54	3	US-08-967-867-4	Sequence 4, Appl
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171	32	52.5	462	4	US-08-068-392-3	Sequence 3, Appl
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176 <td>32</td> <td>52.5</td> <td>614</td> <td>3</td> <td>US-09-017-706-12</td> <td>Sequence 12, Appl</td>	32	52.5	614	3	US-09-017-706-12	Sequence 12, Appl
177 <td>32</td> <td>52.5</td> <td>614</td> <td>3</td> <td>US-09-017-706-13</td> <td>Sequence 13, Appl</td>	32	52.5	614	3	US-09-017-706-13	Sequence 13, Appl
178 <td>32</td> <td>52.5</td> <td>614</td> <td>3</td> <td>US-09-017-706-14</td> <td>Sequence 14, Appl</td>	32	52.5	614	3	US-09-017-706-14	Sequence 14, Appl
179 <td>31</td> <td>50.8</td> <td>8</td> <td>6</td> <td>5441935-10</td> <td>Patent No. 5441935</td>	31	50.8	8	6	5441935-10	Patent No. 5441935
180 <td>31</td> <td>50.8</td> <td>16</td> <td>4</td> <td>US-09-024-975-3</td> <td>Sequence 3, Appl</td>	31	50.8	16	4	US-09-024-975-3	Sequence 3, Appl
181 <td>31</td> <td>50.8</td> <td>26</td> <td>2</td> <td>US-08-419-066-2</td> <td>Sequence 2, Appl</td>	31	50.8	26	2	US-08-419-066-2	Sequence 2, Appl
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183 <td>31</td> <td>50.8</td> <td>39</td> <td>1</td> <td>US-08-162-052-1</td> <td>Sequence 1, Appl</td>	31	50.8	39	1	US-08-162-052-1	Sequence 1, Appl
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187 <td>31</td> <td>50.8</td> <td>39</td> <td>5</td> <td>US-09-024-975-1</td> <td>Sequence 1, Appl</td>	31	50.8	39	5	US-09-024-975-1	Sequence 1, Appl
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192 <td>31</td> <td>50.8</td> <td>316</td> <td>3</td> <td>US-08-253-682-22</td> <td>Sequence 22, Appl</td>	31	50.8	316	3	US-08-253-682-22	Sequence 22, Appl
193 <td>31</td> <td>50.8</td> <td>316</td> <td>4</td> <td>US-09-527-657-22</td> <td>Sequence 22, Appl</td>	31	50.8	316	4	US-09-527-657-22	Sequence 22, Appl
194 <td>31</td> <td>50.8</td> <td>406</td> <td>6</td> <td>5212296-6</td> <td>Patent No. 5212296</td>	31	50.8	406	6	5212296-6	Patent No. 5212296
195 <td>31</td> <td>50.8</td> <td>566</td> <td>2</td> <td>US-08-533-669A-8</td> <td>Sequence 8, Appl</td>	31	50.8	566	2	US-08-533-669A-8	Sequence 8, Appl
196 <td>31</td> <td>50.8</td> <td>566</td> <td>2</td> <td>US-08-511-872-2</td> <td>Sequence 2, Appl</td>	31	50.8	566	2	US-08-511-872-2	Sequence 2, Appl
197 <td>31</td> <td>50.8</td> <td>631</td> <td>4</td> <td>US-08-448-489-17</td> <td>Sequence 17, Appl</td>	31	50.8	631	4	US-08-448-489-17	Sequence 17, Appl
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200 <td>31</td> <td>50.8</td> <td>3712</td> <td>2</td> <td>US-08-222-617A-4</td> <td>Sequence 4, Appl</td>	31	50.8	3712	2	US-08-222-617A-4	Sequence 4, Appl
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202 <td>30.5</td> <td>50.0</td> <td>1375</td> <td>3</td> <td>US-08-665-259-26</td> <td>Sequence 26, Appl</td>	30.5	50.0	1375	3	US-08-665-259-26	Sequence 26, Appl
203 <td>30.5</td> <td>50.0</td> <td>1375</td> <td>3</td> <td>US-08-762-500-26</td> <td>Sequence 26, Appl</td>	30.5	50.0	1375	3	US-08-762-500-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-07-934-553-1
Sequence 1, Application US/07934553
Patent No. 5314690
GENERAL INFORMATION:
APPLICANT: PATTERSON, ROY
APPLICANT: HARRIS, KATHLEEN E
TITLE OF INVENTION: METHOD AND COMPOSITION FOR REDUCING IGE
TITLE OF INVENTION: ANTIBODIES TO SPECIFIC ALLERGENS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TILTON, FALLON, LUNGKUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,553
FILING DATE: 19920821
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: FENREISS, SUSAN B
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9033CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/456-8000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids

TYPE: AMINO ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-934-553-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
|||||
Db 1 RPKPOQFFGLM 11

RESULT 2
US-08-184-935-12
Sequence 12, Application US/08184935
Patent No. 5476770

GENERAL INFORMATION:
APPLICANT: PRADELES, PHILIPPE
TITLE OF INVENTION: IMMUNOMETRIC DETERMINATION OF AN ANTIGEN
TITLE OF INVENTION: OR HAPTEN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,935
FILING DATE: 24-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NO. 5476770man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 846-286-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /note- "C-terminal amide"
US-08-184-935-12

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
|||||
Db 1 RPKPOQFFGLM 11

RESULT 3

US-08-269-288-2
Sequence 2, Application US/08269288
Patent No. 5491140

GENERAL INFORMATION:
APPLICANT: Bruns, Robert F.
APPLICANT: Gehlert, Donald R.
APPLICANT: Howbert, James J.
APPLICANT: Lunn, William H.W.
TITLE OF INVENTION: NAPHTHYL TACHYKININ RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Eli Lilly and Company
STREET: Lilly Corporate Center/1104
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/269,288
FILING DATE:

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9715
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-269-288-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
|||||
Db 1 RPKPOQFFGLM 11

RESULT 4
US-08-338-484-1
Sequence 1, Application US/08338484
Patent No. 5494926

GENERAL INFORMATION:
APPLICANT: Owens, Andrew P.
APPLICANT: Teall, Martin R.
APPLICANT: Williams, Brian J.
TITLE OF INVENTION: 2/3-(HETEROCYCLIC ALKYL
AMINO)-1-(SUBSTITUTED PHENYL-METHOXY)-ETHANES/PROPANES AS
TACHYKININ RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: Dr. Robert J. No. 5494926th
STREET: 126 E. Lincoln Ave., P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,484
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5494926th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-338-484-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPOFFGLM 11
|||
Db 1 RPKPOFFGLM 11

RESULT 5
US-08-175-432-1
Sequence 1, Application US/08175432
Patent No. 5495047
GENERAL INFORMATION:
APPLICANT: Saarl, Walfred S.
APPLICANT: Van Niel, Monique B.
APPLICANT: Williams, Brian J.
TITLE OF INVENTION: FUSED TRICYCLIC COMPOUNDS.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR USE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: NORTH, ROBERT J.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,432
FILING DATE: 07-JAN-1994
CLASSIFICATION: 560
ATTORNEY/AGENT INFORMATION:
NAME: No. 5495047th, Robert J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1152Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-175-432-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPOFFGLM 11
|||
Db 1 RPKPOFFGLM 11

RESULT 6
US-08-225-474-1
Sequence 1, Application US/08225474
Patent No. 5560915
GENERAL INFORMATION:
APPLICANT: Patterson, Roy
APPLICANT: Harris, Kathleen E.
TITLE OF INVENTION: Method and Composition for Treating
TITLE OF INVENTION: Ige Mediated Allergies
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
STREET: 100 S. Wacker Drive, Suite 960
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,474
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,553
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/705,071
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.
REGISTRATION NUMBER: 16,926
REFERENCE/DOCKET NUMBER: NU 9033-CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)-456-8000
TELEFAX: (312)-456-7776
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-225-474-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RPKPOFFGLM 11
|||
Db 1 RPKPOFFGLM 11

RESULT 7
US-08-391-910-2
; Sequence 2, Application US/08391910
; Patent No. 556313
; GENERAL INFORMATION:
; APPLICANT: Hipskind, Philip A.
; TITLE OF INVENTION: HEXAMETHYLENEMINYL TACHYKININ RECEPTOR
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/391,910
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9979
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-391-910-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 8
US-08-418-994-2
; Sequence 2, Application US/08418994
; Patent No. 5565568
; GENERAL INFORMATION:
; APPLICANT: Cho, Sung-Yong S.
; APPLICANT: Hipskind, Philip A.
; APPLICANT: Howbert, J. J.
; APPLICANT: Muehl, Brian S.
; APPLICANT: Nixon, James A.
; TITLE OF INVENTION: 2-ACETAMINOPROPANAMIDES AS TACHYKININ
; TITLE OF INVENTION: RECEPTOR ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,994
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-8252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-418-994-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 9
US-08-480-505-3
; Sequence 3, Application US/08480505
; Patent No. 5601821
; GENERAL INFORMATION:
; APPLICANT: STANMORTH, DENIS R
; APPLICANT: LEWIN, IAN V
; APPLICANT: NAYYAR, SARITA
; APPLICANT: JONES, VALERIE
; TITLE OF INVENTION: IMMUNOACTIVE PEPTIDES AND ANTIBODIES AND
; TITLE OF INVENTION: THEIR USE IN ANTI-ALLERGY TREATMENT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: NIXON & VANDERHYTE P.C.
; STREET: 14TH FLOOR, 2200 CLARENDON BOULEVARD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-5360
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,505
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,692
; FILING DATE:
; APPLICATION NUMBER: US 07/776,380
; FILING DATE: 26-NOV-1991
; APPLICATION NUMBER: GB 8913737.6
; FILING DATE: 15-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB90/00926
; FILING DATE: 15-JUN-1990
; ATTORNEY/AGENT INFORMATION:

NAME: MITCHARD, LEONARD C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-176
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 875-0400
TELEFAX: (703) 525-3468
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Neuropeptide "Substance P"
US-08-480-505-3

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
Db 1 RPKPOFFGLM 11

RESULT 10
US-08-391-814-2
Sequence 2, Application US/08391814
Patent No. 5607947
GENERAL INFORMATION:
APPLICANT: Hipskind, Philip A.
TITLE OF INVENTION: PYRROLIDINYL TACHYKININ RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,814
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-9965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-391-814-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
Db 1 RPKPOFFGLM 11

RESULT 11
US-08-167-870-1
Sequence 1, Application US/08167870
Patent No. 5610183
GENERAL INFORMATION:
APPLICANT: OWENS, ANDREW P.
TITLE OF INVENTION: AROMATIC COMPOUNDS, COMPOSITIONS
CONTAINING THEM AND THEIR USE IN THERAPY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERT J. NORTH
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,870
FILING DATE: 17-DEC-1993
CLASSIFICATION: 544
ATTORNEY/AGENT INFORMATION:
NAME: NORTH, ROBERT J.
REGISTRATION NUMBER: 27,366
REFERENCE/DOCKET NUMBER: T-1151Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-4720
TELEFAX: (908)594-7262
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-167-870-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
Db 1 RPKPOFFGLM 11

RESULT 12
US-08-255-272-6
Sequence 6, Application US/08255272
Patent No. 5627268
GENERAL INFORMATION:
APPLICANT: Kumar, Ramesh
APPLICANT: Sharma, Ajay
APPLICANT: Khoury-Christianson, Anastasia
APPLICANT: M.
TITLE OF INVENTION: Production of Therapeutic Peptides in
Transgenic Animals as a Fusion with Hemoglobin
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:

ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,272
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 6794-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-255-272-6

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOOFFGLM 11
| | | | | | | | | | | | |
Db 1 RPKPOOFFGLM 11

RESULT 13
US-08-441-591-6
; Sequence 6, Application US/08441591
; Patent No. 5637682
; GENERAL INFORMATION:
; APPLICANT: NIEWLANDT, D., GOLD, L. AND WECKER, M.
; TITLE OF INVENTION: HIGH-AFFINITY
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO THE TACHYKININ
; TITLE OF INVENTION: SUBSTANCE P
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,591
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,362
; FILING DATE: 9-SEPTEMBER-1994
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bairy J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-441-591-6

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOOFFGLM 11
| | | | | | | | | | | | |
Db 1 RPKPOOFFGLM 11

RESULT 14
US-08-303-362A-6
; Sequence 6, Application US/08303362A
; Patent No. 5648214
; GENERAL INFORMATION:
; APPLICANT: NIEWLANDT, D., GOLD, L. AND WECKER, M.
; TITLE OF INVENTION: HIGH-AFFINITY
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO THE TACHYKININ
; TITLE OF INVENTION: SUBSTANCE P
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,362A
; FILING DATE: 9-SEPTEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 11
TYPE: amine acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-303-362A-6

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
Db 1 RPKPOFFGLM 11

RESULT 15
US-08-462-859A-1
Sequence 1, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-462-859A-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
Db 1 RPKPOFFGLM 11

RESULT 16
US-08-123-659A-1
Sequence 1, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
Db 1 RPKPOFFGLM 11

RESULT 17
US-08-462-415-2
Sequence 2, Application US/08462415
Patent No. 5670499
GENERAL INFORMATION:
APPLICANT: Cho, Sung Y.
APPLICANT: Crowell, Thomas A.
APPLICANT: Gitter, Bruce D.

APPLICANT: Hipskind, Philip A.
APPLICANT: Howbert, Jeffery J.
APPLICANT: Krushinski, Joseph H.
APPLICANT: Lobb, Karen L.
APPLICANT: Muehl, Brian S.
APPLICANT: Nixon, James A.
TITLE OF INVENTION: HETEROOCYCIC TACHYKININ RECEPTOR
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,415
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gavlo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X8849B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-0756
TELEFAX: 317-276-3861
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-462-415-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOQFFGLM 11
|||||
Db 1 RPKQOQFFGLM 11

RESULT 18
US-08-463-874-2
Sequence 2, Application US/08463874
Patent No. 5684033
GENERAL INFORMATION:
APPLICANT: Cho, Sung Y.
APPLICANT: Crowell, Thomas A.
APPLICANT: Gitter, Bruce D.
APPLICANT: Hipskind, Philip A.
APPLICANT: Howbert, Jeffery J.
APPLICANT: Krushinski, Joseph H.
APPLICANT: Lobb, Karen L.
APPLICANT: Muehl, Brian S.
APPLICANT: Nixon, James A.
TITLE OF INVENTION: NON-PEPTIDE TACHYKININ RECEPTOR
TITLE OF INVENTION: ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: IN

COUNTRY: US
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,874
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gavlo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X8849C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-0756
TELEFAX: 317-276-3861
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-874-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOQFFGLM 11
|||||
Db 1 RPKQOQFFGLM 11

RESULT 19
US-08-464-247A-1
Sequence 1, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: NO. 5693478el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-4117
TELEFAX: 201-683-2158
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOQFFGLM 11
|||||
DB 1 RRPQOQFFGLM 11

RESULT 20
US-08-464-248A-1
Sequence 1, Application US/08464248A
Patent No. 5703209

GENERAL INFORMATION:
APPLICANT: JACOBSEN, J. S.
APPLICANT: VITEK, M. P.
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-1

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOQFFGLM 11
|||||
DB 1 RRPQOQFFGLM 11

RESULT 21
US-08-444-135-2
Sequence 2, Application US/08444135

Patent No. 5723575
GENERAL INFORMATION:
APPLICANT: Gilson, Chaim
APPLICANT: Zeligler, Zvi
APPLICANT: Byk, Gerardo
TITLE OF INVENTION: Backbone Cyclic Peptides, Processes For
TITLE OF INVENTION: Their Preparation and Pharmaceutical Compositions
TITLE OF INVENTION: Containing Them
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,135
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/955,380
FILING DATE: 01-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jarkovsky, Issac
REGISTRATION NUMBER: 22,713
REFERENCE/DOCKET NUMBER: 7754-003-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-135-2

Query Match 100.0%; Score 61; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOQFFGLM 11
|||||
DB 1 RRPQOQFFGLM 11

RESULT 22
US-08-318-391-2
Sequence 2, Application US/08318391
Patent No. 5744482
GENERAL INFORMATION:
APPLICANT: Cohen, Marlene L.
APPLICANT: Johnson, Kirk W.
APPLICANT: Phebus, Lee A.
TITLE OF INVENTION: USE OF A SEROTONIN AGONIST IN
TITLE OF INVENTION: COMBINATION WITH A TACHYKININ RECEPTOR ANTAGONIST IN THE
TITLE OF INVENTION: TREATMENT OR PREVENTION OF MIGRAINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America

```

;
;   ZIP: 46285
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/318,391
;   FILING DATE:
;   CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Gaylo, Paul J.
;   REGISTRATION NUMBER: 36,808
;   REFERENCE/DOCKET NUMBER: X-9664
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (317) 276-0756
;   TELEFAX: (317) 276-3861
;   INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   US-08-318-391-2

Query Match      100.0%, Score 61, DB 1, Length 11,
Best Local Similarity 100.0%, Pred. No. 7.2e-05,
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 23
US-08-796-598-11
; Sequence 11, Application US/08796598
; Patent No. 5827659
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, DALE H.
; APPLICANT: FARR, GEORGE E.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
; TITLE OF INVENTION: POLYMERS USING MASS SPECTROMETRY.
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Patent Administrator - Testa, Hurwitz &
; STREET: High Street Tower, 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,598
; FILING DATE: 07-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,055
; FILING DATE: 19-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FLYNN ESQ., KERRY A.
; REGISTRATION NUMBER: 33,693
; REFERENCE/DOCKET NUMBER: SYP-115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100

```

```

;
;   INFORMATION FOR SEQ ID NO: 11:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   US-08-796-598-11

Query Match      100.0%, Score 61, DB 2, Length 11,
Best Local Similarity 100.0%, Pred. No. 7.2e-05,
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 24
US-08-447-175A-11
; Sequence 11, Application US/08447175A
; Patent No. 5869240
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, DALE H.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
; TITLE OF INVENTION: POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Patent Administrator - Testa, Hurwitz &
; STREET: High Street Tower, 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,175A
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 422
; ATTORNEY/AGENT INFORMATION:
; NAME: RAUSCHENBACH, Kurt
; REGISTRATION NUMBER: 40,137
; REFERENCE/DOCKET NUMBER: SYP-114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7100
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-447-175A-11

Query Match      100.0%, Score 61, DB 2, Length 11,
Best Local Similarity 100.0%, Pred. No. 7.2e-05,
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 25

```

US-07-737-371E-77
; Sequence 77, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-737-371E-77

Query Match 100.0%; Score 61; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOOFFGLM 11
Db 1 RPKPOOFFGLM 11

RESULT 26
US-08-848-766A-1
; Sequence 1, Application US/08848766A
; Patent No. 5932551
; GENERAL INFORMATION:
; APPLICANT: Caldwell, Charles G.
; APPLICANT: Chapman, Kevin T.
; APPLICANT: Curette, Philippe L.
; APPLICANT: Esser, Craig K.
; APPLICANT: Hagmann, William K.
; APPLICANT: Hopka, Ihor E.
; APPLICANT: Iolo, Scott A.
; APPLICANT: Sahoo, Soumya P.
; TITLE OF INVENTION: SUBSTITUTED N-CARBOXYALKYLPEPTIDYL
; TITLE OF INVENTION: DERIVATIVES AS ANTIDEGENERATIVE ACTIVE AGENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway

STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848,766A
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/873,905
; FILING DATE: 24-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Panzer, Curtis C
; REGISTRATION NUMBER: 33,752
; REFERENCE/DOCKET NUMBER: 183551A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3199
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-848-766A-1

Query Match 100.0%; Score 61; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOOFFGLM 11
Db 1 RPKPOOFFGLM 11

RESULT 27
US-08-927-128-17
; Sequence 17, Application US/08927128
; Patent No. 6127150
; GENERAL INFORMATION:
; APPLICANT: Coolidge, Thomas
; APPLICANT: Wagner, Fred
; APPLICANT: ven Heeke, Gino
; APPLICANT: Schuster, Sheldon
; APPLICANT: Stout, Jay
; APPLICANT: Wylie, Dwane
; TITLE OF INVENTION: PURIFICATION DIRECTED CLOSING OF PEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 6127150west Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,128
; FILING DATE: 05-SEP-1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/680,004

FILING DATE: 15-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.2USD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/332-5300
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-927-128-17

Query Match 100.0%; Score 61; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOQFFGLM 11
1111111111
DB 1 RRPQOQFFGLM 11

RESULT 28
US-08-257-966-2

; Sequence 2, Application US/08257966
; Patent No. 6175013
; GENERAL INFORMATION:
; APPLICANT: Hipskind, Philip A.
; APPLICANT: Howbert, James J.
; APPLICANT: Muehl, Brian S.
; TITLE OF INVENTION: IMIDAZOLINYL TACHYKININ RECEPTOR
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/1104
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentia Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,966
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-9197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-257-966-2

Query Match 100.0%; Score 61; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOQFFGLM 11
1111111111
DB 1 RRPQOQFFGLM 11

RESULT 29
PCT-US95-05600-23

; Sequence 23, Application PC/TUS9505600
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY
; APPLICANT: NIEUWLANDT, DAN
; APPLICANT: WECKER, MATTHEW
; APPLICANT: SCHNEIDER, DANIEL J.
; APPLICANT: FEIGON, JULI
; APPLICANT: ALLEN, PATRICK
; APPLICANT: SULLENGER, BRUCE A.
; APPLICANT: DOUDNA, JENNIFER, A.
; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF
; TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
; TITLE OF INVENTION: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05600
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,863
; FILING DATE: 06-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/248,632
; FILING DATE: 24-MAY-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,362
; FILING DATE: 09-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/361,795
; FILING DATE: 21-DECEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 08-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/536,428
: FILING DATE: 11-JUNE-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Barry J. Swanson
: REGISTRATION NUMBER: 33,215
: REFERENCE/DOCKET NUMBER: NEX17/PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 793-3333
: TELEFAX: (303) 793-3433
: INFORMATION FOR SEQ ID NO: 23:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 11 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: PCT-US95-05600-23

Query Match 100.0%; Score 61; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 30
5441935-1
: Patent No. 5441935
: APPLICANT: Rozenfurt, Enrique; Zachary, Ian; Moll, Penella
: TITLE OF INVENTION: ROTH FACTOR RECEPTORS
: NUMBER OF SEQUENCES: 10
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/939,587
: FILING DATE: 03-SEP-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 814,064
: FILING DATE: 23-DEC-1991
: APPLICATION NUMBER: 411,536
: FILING DATE: 29-NOV-1989
: SEQ ID NO: 1:
: LENGTH: 11
: 5441935-1

Query Match 100.0%; Score 61; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 31
US-08-441-591-7
: Sequence 7, Application US/08441591
: Patent No. 5637682
: GENERAL INFORMATION:
: APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.
: TITLE OF INVENTION: HIGH-AFFINITY
: TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
: TITLE OF INVENTION: TO THE TACHIKININ
: TITLE OF INVENTION: SUBSTANCE P
: NUMBER OF SEQUENCES: 66
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Swanson & Bratschun, L.L.C.
: STREET: 8400 E. Prentice Avenue, Suite 200
: CITY: Englewood
: STATE: Colorado
: COUNTRY: USA

ZIP: 80111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 Inch, 1.44 MG storage
: COMPUTER: IBM compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WordPerfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/441,591
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/303,362
: FILING DATE: 9-SEPTEMBER-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/714,131
: FILING DATE: 10-JUNE-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/931,473
: FILING DATE: 17-AUGUST-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/117,991
: FILING DATE: 8-SEPTEMBER-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/536,428
: FILING DATE: 11-JUNE-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/964,624
: FILING DATE: 21-OCTOBER-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Barry J. Swanson
: REGISTRATION NUMBER: 33,215
: REFERENCE/DOCKET NUMBER: NEX21/C
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 793-3333
: TELEFAX: (303) 793-3433
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 12
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-441-591-7

Query Match 100.0%; Score 61; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 32
US-08-303-362A-7
: Sequence 7, Application US/08303362A
: Patent No. 5648214
: GENERAL INFORMATION:
: APPLICANT: NIEUWLANDT, D., GOLD, L. AND WECKER, M.
: TITLE OF INVENTION: HIGH-AFFINITY
: TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
: TITLE OF INVENTION: TO THE TACHIKININ
: TITLE OF INVENTION: SUBSTANCE P
: NUMBER OF SEQUENCES: 66
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Swanson & Bratschun, L.L.C.
: STREET: 8400 E. Prentice Avenue, Suite 200
: CITY: Englewood
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 Inch, 1.44 MG storage


```
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,362A
FILING DATE: 9-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-303-362A-7

Query Match      100.0%; Score 61; DB 1; Length 12:
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RPKPOQFFGLM 11
        |||||
DB      1 RPKPOQFFGLM 11

RESULT 33
US-08-505-250-27
; Sequence 27, Application US/08505250
; Patent No. 6183983
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; CURRENT FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: PCT/JP95/00298
; EARLIER FILING DATE: 1995-02-27
; EARLIER APPLICATION NUMBER: JP 198187/94
; EARLIER FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-08-505-250-53
```

```
OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
; US-08-505-250-27

Query Match      100.0%; Score 61; DB 4; Length 12:
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RPKPOQFFGLM 11
        |||||
DB      2 RPKPOQFFGLM 12

RESULT 34
US-08-505-250-53
; Sequence 53, Application US/08505250
; Patent No. 6183983
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; CURRENT FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: PCT/JP95/00298
; EARLIER FILING DATE: 1995-02-27
; EARLIER APPLICATION NUMBER: JP 198187/94
; EARLIER FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-08-505-250-53

Query Match      100.0%; Score 61; DB 4; Length 12:
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RPKPOQFFGLM 11
        |||||
DB      2 RPKPOQFFGLM 12

RESULT 35
PCT-US92-06532-4
; Sequence 4, Application PC/TUS9206532
; GENERAL INFORMATION:
; APPLICANT: Krause, James E.
; TITLE OF INVENTION: Human Substance P Receptor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SD
; STREET: 800 N. Lindbergh Blvd.
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: U.S.A
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
```

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/06532
;; FILING DATE: 19920805
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyer, Scott J.
;; REGISTRATION NUMBER: 25,275
;; REFERENCE/DOCKET NUMBER: 07-24(776)A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (314)694-3117
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FEATURE:
;; NAME/KEY: Modified-site
;; LOCATION: 12
;; OTHER INFORMATION: /label= amide
PCT-US92-06532-4

Query Match 100.0%; Score 61; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
Db 2 RPKPQOFFGLM 12

RESULT 36
PCT-US95-05600-24
; Sequence 24, Application PC/TUS9505600
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY
; APPLICANT: NIEUWLANDT, DAN
; APPLICANT: WECKER, MATTHEM
; APPLICANT: SCHNEIDER, DANIEL J.
; APPLICANT: FEIGON, JULI
; APPLICANT: ALLEN, PATRICK
; APPLICANT: SULLINGER, BRUCE A.
; APPLICANT: DOODNA, JENNIFER, A.
; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF
; TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
; TITLE OF INVENTION: P. HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05600
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/238,863
; FILING DATE: 06-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/248,632
; FILING DATE: 24-MAY-1994
; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/303,362
;; FILING DATE: 09-SEPTEMBER-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/361,795
;; FILING DATE: 21-DECEMBER-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/117,991
;; FILING DATE: 08-SEPTEMBER-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/931,473
;; FILING DATE: 17-AUGUST-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/964,624
;; FILING DATE: 21-OCTOBER-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/536,428
;; FILING DATE: 11-JUNE-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/714,131
;; FILING DATE: 10-JUNE-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/536,428
;; FILING DATE: 11-JUNE-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 33,215
;; NAME: Barry J. Swanson
;; REGISTRATION NUMBER: 33,215
;; REFERENCE/DOCKET NUMBER: NEX17/PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (303) 793-3333
;; TELEFAX: (303) 793-3433
;; INFORMATION FOR SEQ ID NO: 24:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
PCT-US95-05600-24

Query Match 100.0%; Score 61; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQOFFGLM 11
Db 1 RPKPQOFFGLM 11

RESULT 37
US-08-890-157A-2
; Sequence 2, Application US/08890157A
; Patent No. 6063758
; GENERAL INFORMATION:
; APPLICANT: Douglas A. Iapri and Ronald G. Wiley
; TITLE OF INVENTION: Substance P-Saporin (SP-SAP) Conjugates And
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,157A
; FILING DATE: 09-JUL-1997
; CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Phillips, Peter J.
REGISTRATION NUMBER: 29,691
REFERENCE/DOCKET NUMBER: 53984
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-157A-2

Query Match 100.0%; Score 61; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
Db 10 RPKPOQFFGLM 20

RESULT 38
US-08-505-250-50
Sequence 50, Application US/08505250
Patent No. 6183983
GENERAL INFORMATION:
APPLICANT: Sato, Haruya
APPLICANT: Yamamoto, Keiji
APPLICANT: Suzuki, Kokichi
APPLICANT: Ikeda, Masahiro
APPLICANT: Sakagami, Masahiro
APPLICANT: Taniguchi, Makoto
TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
FILE REFERENCE: 110-511
CURRENT APPLICATION NUMBER: US/08/505,250
CURRENT FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: PCT/JP95/00298
EARLIER FILING DATE: 1995-02-27
EARLIER APPLICATION NUMBER: JP 198187/94
EARLIER FILING DATE: 1994-08-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 50
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-08-505-250-50

Query Match 100.0%; Score 61; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
Db 2 RPKPOQFFGLM 12

RESULT 39
5268359-5
Patent No. 5268359
APPLICANT: HARMAR, ANTHONY J.;PASCALL, JOHN;MCKEOWN, ANN
TITLE OF INVENTION: HUMAN TACHYKININS AND THEIR PRECURSOR
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/285,964
FILING DATE: 03-JUN-1987
SEQ ID NO: 5:
LENGTH: 126
5268359-5

Query Match 100.0%; Score 61; DB 6; Length 126;
Best Local Similarity 100.0%; Pred. No. 0.00087;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
Db 58 RPKPOQFFGLM 68

RESULT 40
5268359-2
Patent No. 5268359
APPLICANT: HARMAR, ANTHONY J.;PASCALL, JOHN;MCKEOWN, ANN
TITLE OF INVENTION: HUMAN TACHYKININS AND THEIR PRECURSOR
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/285,964
FILING DATE: 03-JUN-1987
SEQ ID NO: 2:
LENGTH: 130
5268359-2

Query Match 100.0%; Score 61; DB 6; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
Db 58 RPKPOQFFGLM 68

RESULT 41
US-08-462-859A-9
Sequence 9, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-9

Query Match 100.0%; Score 61; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOQFFGLM 11
|||||
DB 362 RPKQOQFFGLM 372

RESULT 42

US-08-123-659A-9
Sequence 9, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-9

Query Match 100.0%; Score 61; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOQFFGLM 11
|||||
DB 362 RPKQOQFFGLM 372

RESULT 43
US-08-464-247A-9
Sequence 9, Application US/08464247A

Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-9

Query Match 100.0%; Score 61; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOQFFGLM 11
|||||
DB 362 RPKQOQFFGLM 372

RESULT 44
US-08-464-248A-9
Sequence 9, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
APPLICANT: Vittek, M. P.
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-9

Query Match 100.0%; Score 61; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOOFFGLM 11
|||||
DB 362 RPKPOOFFGLM 372

RESULT 45
US-08-462-859A-7
Sequence 7, Application US/08462859A
Patent No. 5652092
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5652092e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,859A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-859A-7

Query Match 100.0%; Score 61; DB 1; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.0035;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RPKPOOFFGLM 11
|||||
DB 362 RPKPOOFFGLM 372

RESULT 46
US-08-123-659A-7
Sequence 7, Application US/08123659A
Patent No. 5656477
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5656477e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Rosenblum
STREET: 163 Delaware Avenue, Suite 212
CITY: Delmar
STATE: New York
COUNTRY: U.S.A.
ZIP: 12054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,659A
FILING DATE: 20-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenblum, Anne M.
REGISTRATION NUMBER: 30,419
REFERENCE/DOCKET NUMBER: 31,844-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (518)475-0611
TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-7

Query Match 100.0%; Score 61; DB 1; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOOFFGLM 11
|||||
DB 362 RPKPOOFFGLM 372

RESULT 47
US-08-464-247A-7
Sequence 7, Application US/08464247A
Patent No. 5693478
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: No. 5693478e1 Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive

CITY: Parsippany
STATE: New Jersey
COUNTRY: United States
ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-7

Query Match 100.0%; Score 61; DB 1; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 362 RPKPOQFFGLM 372

RESULT 48
US-08-464-248A-7
Sequence 7, Application US/08464248A
Patent No. 5703209
GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.
TITLE OF INVENTION: NO. 5703209el Amyloid Precursor and Method of
TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3505
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-7

Query Match 100.0%; Score 61; DB 1; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 362 RPKPOQFFGLM 372

RESULT 49
US-07-899-205-1
Sequence 1, Application US/07899205
Patent No. 5288730
GENERAL INFORMATION:
APPLICANT: Baker, Raymond
APPLICANT: Teall, Martin R.
APPLICANT: Swain, Christopher J.
APPLICANT: Williams, Brian J.
TITLE OF INVENTION: AZABICYCLIC COMPOUNDS PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS CONTAINING THEM AND THEIR USE IN THERAPY
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/899,205
FILING DATE: 19920616
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Polk, Manfred
REGISTRATION NUMBER: 27,102
REFERENCE/DOCKET NUMBER: T-1106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4285
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-899-205-1

Query Match 95.1%; Score 58; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
|||||
Db 1 RPKPOQFFGLM 11

RESULT 50
US-08-496-118-1

Sequence 1, Application US/08496118
Patent No. 5830854
GENERAL INFORMATION:
APPLICANT: Hargreaves, Richard J.
TITLE OF INVENTION: THERAPEUTIC USE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robert J. No. 5830854th
STREET: 126 E. Lincoln Avenue - P. O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,118
FILING DATE: 27-JUNE-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5830854th, Robert J.
REGISTRATION NUMBER: T-1213CA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-7262
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-496-118-1

Query Match 95.1%; Score 58; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOQFFGLM 11
DB 1 RRPQOQFFGLM 11

RESULT 51
US-07-737-371E-12
Sequence 12, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-12

Query Match 95.1%; Score 58; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRPQOQFFGLM 11
DB 1 RRPQOQFFGLM 11

RESULT 52
US-07-737-371E-25
Sequence 25, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-25

Query Match 95.1%, Score 58; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
|1111111111|
Db 1 RPKPOQFFGLM 11

RESULT 53

PCT-US92-06532-1
Sequence 1, Application PC/TUS9206532
GENERAL INFORMATION:
APPLICANT: Krause, James E.
TITLE OF INVENTION: Human Substance P Receptor
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., ASD
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: U.S.A
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06532
FILING DATE: 19920805
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: 07-24(776)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /Label- amide
PCT-US92-06532-1

Query Match 95.1%; Score 58; DB 5; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00024;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFFGLM 11
|1111111111|
Db 1 RPKPOQFFGLM 11

RESULT 54

US-07-737-371E-9
Sequence 9, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-9

Query Match 91.8%; Score 56; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PKPOQFFGLM 11
|1111111111|
Db 1 PKPOQFFGLM 10

RESULT 55
US-08-031-325A-26
Sequence 26, Application US/08031325A
Patent No. 5369094
GENERAL INFORMATION:
APPLICANT: Schally, Andrew V.
TITLE OF INVENTION: POLYPEPTIDE BOMBESIN ANTAGONISTS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: OMRI M. BEHR, ESO
STREET: 325 PIERSON AVENUE
CITY: EDISON
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 08837
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,325A
FILING DATE: 15-MAR-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/619,747
FILING DATE: 29-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: BEHR, OMRI M.

REGISTRATION NUMBER: 22,940
REFERENCE/DOCKET NUMBER: SHAL3-0-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 494-5240
TELEFAX: (908) 494-04281
TELEX: 511642 BEPATEDIN
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc-feature
LOCATION: 11
OTHER INFORMATION: /note= "Res 11 = Met-NH2"
US-08-031-325A-26

Query Match
Best Local Similarity 91.8%; Score 56; DB 1; Length 11;
Matches 10; Conservative 100.0%; Pred. No. 0.00053;
Indels 0; Gaps 0;

QY 1 RPKPOQFGL 10
DB 1 RPKPOQFGL 10

RESULT 56
US-07-737-371E-13
; Sequence 13, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 11...11

OTHER INFORMATION: where Xaa at position 11 is ethionine
US-07-737-371E-13

Query Match
Best Local Similarity 91.8%; Score 56; DB 2; Length 11;
Matches 10; Conservative 100.0%; Pred. No. 0.00053;
Indels 0; Gaps 0;

QY 1 RPKPOQFGL 10
DB 1 RPKPOQFGL 10

RESULT 57
US-07-737-371E-14
; Sequence 14, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 11...11
; OTHER INFORMATION: where Xaa at position 11 is Nle
US-07-737-371E-14

Query Match
Best Local Similarity 91.8%; Score 56; DB 2; Length 11;
Matches 10; Conservative 100.0%; Pred. No. 0.00053;
Indels 0; Gaps 0;

QY 1 RPKPOQFGL 10
DB 1 RPKPOQFGL 10

RESULT 58
US-07-737-371E-16
; Sequence 16, Application US/07737371E

```
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 1...1
; OTHER INFORMATION: where xaa at position 1 is ethionine
;
US-07-737-371E-16
;
; Query Match
; Best Local Similarity 91.8%; Score 56; DB 2; Length 11;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PKPOQFFGLM 11
;
; DB 2 PKPOQFFGLM 11
;
; RESULT 59
; US-07-737-371E-18
; Sequence 18, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
```

```
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-07-737-371E-18
;
; Query Match
; Best Local Similarity 91.8%; Score 56; DB 2; Length 11;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PKPOQFFGLM 11
;
; DB 2 PKPOQFFGLM 11
;
; RESULT 60
; US-07-737-371E-61
; Sequence 61, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
```

LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 10...10
OTHER INFORMATION: where xaa at location 10 is Me-Leu
US-07-737-371E-61

Query Match 91.8%; Score 56; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFGL 11
|||||
Db 1 RPKPOQFGL 11

RESULT 61
US-07-737-371E-63
Sequence 63, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 11...11
OTHER INFORMATION: where xaa at position 11 is Me-Met
US-07-737-371E-63

Query Match 91.8%; Score 56; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFGL 10
|||||

Db 1 RPKPOQFGL 10

RESULT 62
US-07-737-371E-64
Sequence 64, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-64

Query Match 91.8%; Score 56; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFGL 10
|||||
Db 1 RPKPOQFGL 10

RESULT 63
US-07-737-371E-66
Sequence 66, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 10...10
OTHER INFORMATION: where Xaa at position 10 is Me-Leu
US-07-737-371E-66

Query Match 91.8%; Score 56; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 1; Indels 0;

QY 1 RPKPQOEFGLM 11
|||||
Db 1 RPKPQOEFGLM 11

RESULT 64
US-08-747-137-34
Sequence 34, Application US/08747137
Patent No. 5945033
GENERAL INFORMATION:
APPLICANT: YEN, Richard C.K.
TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
NUMBER OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,137
FILING DATE: 12-NOV-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,546
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,831
FILING DATE: 01-JUN-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/959,560
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/641,720
FILING DATE: 15-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016197-000840US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /product= "Met-Amide"
US-08-747-137-34

Query Match 91.8%; Score 56; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 1 RPKPQOEFGL 10
|||||
Db 1 RPKPQOEFGL 10

RESULT 65
US-08-505-250-34
Sequence 34, Application US/08505250
Patent No. 6183983
GENERAL INFORMATION:
APPLICANT: Sato, Haruya
APPLICANT: Yamamoto, Koji
APPLICANT: Suzuki, Kokiichi
APPLICANT: Ikeda, Masahiro
APPLICANT: Sakagami, Masahiro
APPLICANT: Taniguchi, Makoto
TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
FILE REFERENCE: 110-511
CURRENT APPLICATION NUMBER: US/08/505,250
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: PCT/JP95/00298
EARLIER FILING DATE: 1995-02-27
EARLIER APPLICATION NUMBER: JP 198187/94
EARLIER FILING DATE: 1994-08-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 11
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-08-505-250-34

Query Match 91.8%; Score 56; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 1 RPKPQOEFGL 10
|||||
Db 2 RPKPQOEFGL 11

RESULT 66
US-08-428-488-15
; Sequence 15, Application US/08428488
; Patent No. 5624894
; GENERAL INFORMATION:
; APPLICANT: BODOR, Nicholas S.
; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P. O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/428,488
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Mary Katherine
; REGISTRATION NUMBER: 26,254
; REFERENCE/DOCKET NUMBER: 028724-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "Position 1 = H-Arg."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /note= "Position 5 = Glu-NH2."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 6
; OTHER INFORMATION: /note= "Position 6 = Glu-NH2."
US-08-428-488-15

Query Match 90.2%; Score 55; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.00079;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
DB 1 RPKPEFFGLM 11

RESULT 67
US-07-737-371E-15
; Sequence 15, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ATTORNEY/AGENT INFORMATION:

; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-15

Query Match 90.2%; Score 55; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00079;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
DB 1 RPKPOQFFGLM 11

RESULT 68
US-07-737-371E-17
; Sequence 17, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-17

Query Match 90.2%; Score 55; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00079;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 69
US-07-737-371E-19
Sequence 19, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-19

Query Match 90.2%; Score 55; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00079;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 70
US-07-737-371E-20
Sequence 20, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-20

Query Match 90.2%; Score 55; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00079;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 RPKPOQFFGLM 11

RESULT 71
US-07-737-371E-21
Sequence 21, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston

Query Match 90.2%; Score 55; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.00079;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 9...9
OTHER INFORMATION: where Xaa at position 9 is D-Ala
US-07-737-371E-21

Query Match 88.5%; Score 54; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
||||| 11
DB 1 RPKPOQFFXLM 11

RESULT 72
US-07-737-371E-22
Sequence 22, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:

NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 9...9
OTHER INFORMATION: where Xaa at position 9 is Sar
US-07-737-371E-22

Query Match 88.5%; Score 54; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
||||| 11
DB 1 RPKPOQFFXLM 11

RESULT 73
US-07-737-371E-24
Sequence 24, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 9...9
OTHER INFORMATION: where Xaa at position 9 is D-Pro

US-07-737-371E-24

Query Match 88.5%; Score 54; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
||||| 11
Db 1 RPKPOQFFXLM 11

RESULT 74

US-07-737-371E-26
; Sequence 26, Application US/07737371E
; Patent No. 5876943

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/737,371E

; FILING DATE: 29-JUL-1991

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/559,172

; FILING DATE: 27-JUL-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Freeman, John W.

; REGISTRATION NUMBER: 29,066

; REFERENCE/DOCKET NUMBER: 00108/028002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; LOCATION: 8...8

; OTHER INFORMATION: where Xaa at position 8 is Me-Phe

Query Match 88.5%; Score 54; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
||||| 11
Db 1 RPKPOQFFXGLM 11

RESULT 75

US-07-737-371E-27

; Sequence 27, Application US/07737371E
; Patent No. 5876948

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/737,371E

; FILING DATE: 29-JUL-1991

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/559,172

; FILING DATE: 27-JUL-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Freeman, John W.

; REGISTRATION NUMBER: 29,066

; REFERENCE/DOCKET NUMBER: 00108/028002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; LOCATION: 9...9

; OTHER INFORMATION: where Xaa at position 9 is Me-Gly

Query Match 88.5%; Score 54; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
||||| 11
Db 1 RPKPOQFFXLM 11

RESULT 76

US-07-737-371E-62

; Sequence 62, Application US/07737371E
; Patent No. 5876948

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95


```

; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737.371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-737-371E-62

Query Match      88.5%; Score 54; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RPKPOQFFGLM 11
      ||| ||| ||| |||
Db      1 RPKPOQFFGPM 11

RESULT 77
US-07-737-371E-65
; Sequence 65, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
```

```

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 9...9
; OTHER INFORMATION: where Xaa at position 9 is Me-Gly
; US-07-737-371E-65

Query Match      88.5%; Score 54; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RPKPOQFFGLM 11
      ||| ||| ||| |||
Db      1 RPKPOQFFXLM 11

RESULT 78
US-07-737-371E-23
; Sequence 23, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-737-371E-23

Query Match      86.9%; Score 53; DB 2; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 RPKPOQFFGLM 11
      ||| ||| ||| |||
Db      1 RPKPOQFFPLM 11

RESULT 79
```

5441935-3
Patent No. 5441935
APPLICANT: Rosegurt, Enrique;Zachary, Ian;Woll, Penella
TITLE OF INVENTION: ROTH FACTOR RECEPTORS
NUMBER OF SEQUENCES:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,587
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 814,064
FILING DATE: 23-DEC-1991
APPLICATION NUMBER: 411,536
FILING DATE: 29-NOV-1989
SEQ ID NO:3
LENGTH: 11
5441935-3

Query Match 86.9%; Score 53; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQFGLM 11
||||| 11
Db 1 RPKPOQFGLM 11

RESULT 80
5441935-8
Patent No. 5441935
APPLICANT: Rosegurt, Enrique;Zachary, Ian;Woll, Penella
TITLE OF INVENTION: ROTH FACTOR RECEPTORS
NUMBER OF SEQUENCES:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,587
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 814,064
FILING DATE: 23-DEC-1991
APPLICATION NUMBER: 411,536
FILING DATE: 29-NOV-1989
SEQ ID NO:8
LENGTH: 11
5441935-8

Query Match 86.9%; Score 53; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPKPOQFGLM 11
||||| 11
Db 1 RPKPOQFGLM 11

RESULT 81
US-07-737-371E-11
Sequence 11, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-11

Query Match 85.2%; Score 52; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RPKPOQFG 9
||||| 11
Db 1 RPKPOQFG 9

RESULT 82
US-08-462-413-2
Sequence 2, Application US/08462413
Patent No. 5530009
GENERAL INFORMATION:
APPLICANT: Cho, Sung Y.
APPLICANT: Copp, James D.
APPLICANT: Glnah, Francis O.
APPLICANT: Hansen, Guy J.
APPLICANT: Hipskind, Phillip A.
APPLICANT: Huff, Bret E.
APPLICANT: Martineilli, Michael J.
APPLICANT: Staszak, Michael A.
TITLE OF INVENTION: PROCESS FOR PREPARING NON-PEPTIDYL
TITLE OF INVENTION: TACHYKININ RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,413
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/271,708
FILING DATE:
ATTORNEY/AGENT INFORMATION:


```

; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 5...5
; OTHER INFORMATION: where Xaa at position 5 is homocysteine
; LOCATION: 11...11
; OTHER INFORMATION: where Xaa at position 11 is homocysteine
; US-07-737-371E-32

Query Match      82.0%; Score 50; DB 2; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.0057;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGL 10
    |||||
Db 1 RPKPXQFFGL 10

RESULT 86
US-08-468-514-11
; Sequence 11, Application US/08468514
; Patent No. 5576296
; GENERAL INFORMATION:
; APPLICANT: Barfai, Tamas
; APPLICANT: Hockfelt, Tomas
; APPLICANT: Langel, Uto
; APPLICANT: Ahren, Bo
; APPLICANT: Lindskog, Stefan
; APPLICANT: Consolo, Silvana
; APPLICANT: Land, Tilt
; APPLICANT: Wiesenfeld-Hallin, Zsuzsanna
; TITLE OF INVENTION: GALANIN ANTAGONIST
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
```

```

; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,514
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,139
; FILING DATE: 12-NOV-1993
; APPLICATION NUMBER: PCT/SE92/00316
; FILING DATE: 14-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9101472-0
; FILING DATE: 15-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner Ph.D., Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-354-8113
; TELEFAX: 212-819-8783
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 22
; OTHER INFORMATION: /note="amide"
; US-08-468-514-11

Query Match      82.0%; Score 50; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKPOQFFGLM 11
    ||||||
Db 13 PPQOQFFGLM 22

RESULT 87
US-07-737-371E-60
; Sequence 60, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
```

FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-60

Query Match 80.3%; Score 49; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 RPKQPFGLM 11
DB 1 RPKQPFGLM 9

RESULT 88
US-07-737-371E-55
Sequence 55, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CURRENT APPLICATION DATA:
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

FEATURE:
LOCATION: 9...9
OTHER INFORMATION: where Xaa at position 9 is Sar
LOCATION: 11...11
OTHER INFORMATION: where Xaa at position 11 is Met(O2)
US-07-737-371E-55

Query Match 80.3%; Score 49; DB 2; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.0086;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKQPFGL 10
DB 1 RPKQPFGL 10

RESULT 89
US-07-712-828B-5
Sequence 5, Application US/07712828B
Patent No. 5235039
GENERAL INFORMATION:
APPLICANT: Heath et al.
TITLE OF INVENTION: Assay Method for Hydrolytic
NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
FILING DATE: 19010610
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-712-828B-5

Query Match 80.3%; Score 49; DB 1; Length 13;
Best Local Similarity 81.8%; Pred. No. 0.01;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKQPFGLM 11
DB 1 RPKQPFGLM 11

RESULT 90
US-07-737-371E-29
Sequence 29, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CURRENT APPLICATION DATA:
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-29

STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 5...5
OTHER INFORMATION: where Xaa at position 5 is homocysteine
LOCATION: 9...9
OTHER INFORMATION: where Xaa at position 9 is homocysteine
US-07-737-371E-29

Query Match 78.7%; Score 48; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRPPOOFFGLM 11
||| ||| ||| |||
DB 1 RRPXOFFXLM 11

RESULT 91
US-07-737-371E-31
Sequence 31, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172

FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-31

Query Match 78.7%; Score 48; DB 2; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRPPOOFFGL 10
||| ||| ||| |||
DB 1 RRPPOOFFGL 10

RESULT 92
5441935-5
Patent No. 5441935
APPLICANT: Rozenfurt, Enrique; Zachary, Ian; Moll, Penella
TITLE OF INVENTION: ROWTH FACTOR RECEPTORS
NUMBER OF SEQUENCES:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,587
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 814,064
FILING DATE: 23-DEC-1991
APPLICATION NUMBER: 411,536
FILING DATE: 29-NOV-1989
SEQ ID NO: 5;
LENGTH: 11
5441935-5

Query Match 78.7%; Score 48; DB 6; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRPPOOFFGLM 11
||| ||| ||| |||
DB 1 RRPPOOFFGLM 11

RESULT 93
US-07-737-371E-33
Sequence 33, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 5...5
OTHER INFORMATION: where Xaa at position 5 is D-Cys
US-07-737-371E-33

Query Match 77.0%; Score 47; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPOQFEGLM 11
|||||
Db 1 RPKPXQFCGLM 11

RESULT 94
US-07-737-371E-34
Sequence 34, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070

TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 5...5
OTHER INFORMATION: where Xaa at position 5 is D-Cys
US-07-737-371E-34

Query Match 77.0%; Score 47; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RPKPOQFEGLM 11
|||||
Db 1 RPKPXQFCGLM 11

RESULT 95
US-07-737-371E-35
Sequence 35, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
LOCATION: 3...3
OTHER INFORMATION: where Xaa at position 3 is D-Cys
US-07-737-371E-35

Query Match 77.0%; Score 47; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.019;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
||| |||
Db 1 RPKPCFFGLM 11

RESULT 96
US-07-737-371E-54
; Sequence 54, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 7...7
; OTHER INFORMATION: where Xaa at position 7 is p-Chloro-Phe
; LOCATION: 8...8
; OTHER INFORMATION: where Xaa at position 8 is p-Chloro-Phe
; US-07-737-371E-54

Query Match 77.0%; Score 47; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
||| |||
Db 1 RPKPCFFGLM 11

RESULT 97
US-08-890-157A-4
; Sequence 4, Application US/08890157A
; Patent No. 6063758
; GENERAL INFORMATION:
; APPLICANT: Douglas A. Lappi and Ronald G. Wiley
; TITLE OF INVENTION: Substance P-Saporin (SP-SAP) Conjugates And

NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,157A
; FILING DATE: 09-JUL-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Phillips, Peter J.
; REGISTRATION NUMBER: 29,691
; REFERENCE/DOCKET NUMBER: 53984
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)278-0400
; TELEFAX: (212)391-0526
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-890-157A-4

Query Match 77.0%; Score 47; DB 3; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
||| |||
Db 1 RPKPCFFGLM 11

RESULT 98
US-07-737-371E-57
; Sequence 57, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.

REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-57

Query Match 75.4%; Score 46; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOOFF 8
Db 1 RPKPOOFF 8

RESULT 99
US-08-890-157A-1

Sequence 1, Application US/08890157A
Patent No. 6063758
GENERAL INFORMATION:
APPLICANT: Douglas A. Lappl and Ronald G. Wiley
TITLE OF INVENTION: Substance P-Saporin (SP-SAP) Conjugates And
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,157A
FILING DATE: 09-JUL-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Phillips, Peter J.
REGISTRATION NUMBER: 29,691
REFERENCE/DOCKET NUMBER: 53984
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)278-0400
TELEFAX: (212)391-0526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-890-157A-1

Query Match 75.4%; Score 46; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOOFF 8
Db 10 RPKPOOFF 17

RESULT 100
US-09-168-548-2
Sequence 2, Application US/09168548
Patent No. 6265542
GENERAL INFORMATION:
APPLICANT: Fahner, Robert
TITLE OF INVENTION: PURIFICATION OF MOLECULES
FILE REFERENCE: P10281
CURRENT APPLICATION NUMBER: US/09/168,548
CURRENT FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 2
SEQ ID NO: 2
LENGTH: 10
TYPE: PPT
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: Artificial sequence
LOCATION: 1-10
OTHER INFORMATION: Sequence is synthesized
Patent No. 6265542
US-09-168-548-2

Query Match 74.6%; Score 45.5; DB 4; Length 10;
Best Local Similarity 90.9%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 RPKPOOFFGLM 11
Db 1 RPKP-QFFGLM 10

RESULT 101
5169865-11
Patent No. 5169865
APPLICANT: ANANTHANARAYANAN, V. S.
TITLE OF INVENTION: METHOD AND COMPOSITION FOR CALCIUM
BINDING TRANSLOCATION AND MEDIATING
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/323,421
FILING DATE: 14-MAR-1989
SEQ ID NO: 11
LENGTH: 10
5169865-11

Query Match 74.6%; Score 45.5; DB 6; Length 10;
Best Local Similarity 90.9%; Pred. No. 0.031;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 RPKPOOFFGLM 11
Db 1 RPKP-QFFGLM 10

RESULT 102
US-07-737-371E-36
Sequence 36, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US

```

1 ZIP: 02110-2804
2
3 COMPUTER READABLE FORM:
4
5 MEDIUM TYPE: Diskette
6
7 COMPUTER: IBM Compatible
8
9 OPERATING SYSTEM: Windows95
10
11 SOFTWARE: FastSeq for Windows Version
12
13 CURRENT APPLICATION DATA:
14
15 APPLICATION NUMBER: US/07/737, 371E
16
17 FILING DATE: 29-JUL-1991
18
19 CLASSIFICATION: 536
20
21 PRIOR APPLICATION DATA:
22
23 APPLICATION NUMBER: 07/559, 172
24
25 FILING DATE: 27-JUL-1990
26
27 ATTORNEY/AGENT INFORMATION:
28
29 NAME: Freeman, John W.
30
31 REGISTRATION NUMBER: 29, 066
32
33 REFERENCE/DOCKET NUMBER: 00108/028002
34
35 TELECOMMUNICATION INFORMATION:
36
37 TELEPHONE: 617-542-5070
38
39 TELEFAX: 617-542-8906
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41 TELEX: 200154
42
43 INFORMATION FOR SEQ ID NO: 36:
44
45 SEQUENCE CHARACTERISTICS:
46
47 LENGTH: 11 amino acids
48
49 TYPE: amino acid
50
51 TOPOLOGY: linear
52
53 MOLECULE TYPE: protein
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Query Match	73.8%	Score 45:	DB 2:	length 11:
Best Local Similarity	81.8%	Pred. No.	0.042:	
Matches	9:	Conservative	0:	Indels 0:
		Mismatches	2:	Gaps 0:

RESULT 103
5441935-2
Patent No. 5441935
APPLICANT: Rozeurgurt, Enrique; Zachary, Ian; Woll, Penella
TITLE OF INVENTION: ROTHF FACTOR RECEPTORS
NUMBER OF SEQUENCES: 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,587
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 814,064
FILING DATE: 23-DEC-1991
APPLICATION NUMBER: 411,536
FILING DATE: 28-NOV-1989
SEQ ID NO: 2:
LENGTH: 11
5441935-2

Query Match	73.8%	Score 45	DB 6	Length 11
Best Local Similarity	72.7%	Pred. No. 0.042		
Matches	8	Mismatches	2	Indels 0
				Gaps 0

RESULT 104
US-07-737-371E-10
: Sequence 10, Application US/07737371E
: Patent No. 5876948
: GENERAL INFORMATION:
: APPLICANT: Yankner, Bruce A.

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Query March      72.1%  Score 44;  DB 2;  Length 8;
Best Local Similarity 100.0%  Pred. NO. 1.6e+05;
Matches      8;  Conservative  0;  Mismatches  0;  Indels  0;
QY      4  PQOFFGLM 11
          |||||
db      1  PQOFFGLM 8

```

RESULT 105
 US-08-505-250-29
 Sequence 29, Application US/08505250
 Patent No. 6183983
 GENERAL INFORMATION:
 APPLICANT: Sato, Haruya
 APPLICANT: Yamamoto, Keiji
 APPLICANT: Suzuki, Kokichi
 APPLICANT: Ikeda, Masahiro
 APPLICANT: Sakagami, Masahiro
 APPLICANT: Taniguchi, Makoto
 TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
 FILE REFERENCE: 110-511
 CURRENT APPLICATION NUMBER: US/08/505,250
 CURRENT FILING DATE: 1995-11-29
 EARLIER APPLICATION NUMBER: PCT/JP95/00298
 EARLIER FILING DATE: 1995-02-27
 EARLIER APPLICATION NUMBER: JP 198187/94
 EARLIER FILING DATE: 1994-08-23
 NUMBER OF SEQ ID NOS: 53
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 29
 LENGTH: 9
 TYPE: PPT
 ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: peptide
US-08-505-250-29

Query Match 72.1%; Score 44; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KPOQFFGL 10
|||||
DB 2 KPOQFFGL 9

RESULT 106
US-07-737-371E-28
; Sequence 28, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737, 371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-737-371E-28

Query Match 72.1%; Score 44; DB 2; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.063;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKQOFGGLM 11
|||||
DB 1 RPKQOFGGLM 11

RESULT 107
US-08-468-514-1
; Sequence 1, Application US/08468514
; Patent No. 5576296

GENERAL INFORMATION:
; APPLICANT: Bartfal, Tamas
; APPLICANT: HOKfelt, Tomas
; APPLICANT: Langel, Olo
; APPLICANT: Ahren, Bo
; APPLICANT: Lindskog, Stefan
; APPLICANT: Consolo, Silvana
; APPLICANT: Land, Tilt
; APPLICANT: Wiesenfeld-Hallin, Zsuzsanna
; TITLE OF INVENTION: GALANIN ANTAGONIST
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,514
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,139
; FILING DATE: 12-NOV-1993
; APPLICATION NUMBER: PCT/SE92/00316
; FILING DATE: 14-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9101472-0
; FILING DATE: 15-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Steiner Ph.D., Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-074
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-819-8783
; TELEFAX: 212-354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 20
; OTHER INFORMATION: /note= "amide or free acid"
; US-08-468-514-1

Query Match 72.1%; Score 44; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPOQFGGLM 11
|||||
DB 13 PPOQFGGLM 20

RESULT 108
US-08-088-322-6
; Sequence 6, Application US/08088322
; Patent No. 5413914
; GENERAL INFORMATION:
; APPLICANT: Franzusoff, Alex
; TITLE OF INVENTION: YEAST ASSAY TO IDENTIFY INHIBITORS OF
; DIBASIC AMINO ACID PROCESSING ENDOPEPTIDASES

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/088,322
FILING DATE: 07-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2848-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
TELEX: 467377
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-088-322-6

Query Match
Best Local Similarity 71.3%; Score 43.5; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 RPKQOQFFGLM 11
DB 1 RPK-QOQFFGLM 10

RESULT 109
US-08-437-820-6
Sequence 6, Application US/08437820
Patent No. 5627043
GENERAL INFORMATION:
APPLICANT: Franzusoff, Alex
TITLE OF INVENTION: YEAST STRAINS USED TO IDENTIFY
TITLE OF INVENTION: INHIBITORS OF DIBASIC AMINO ACID PROCESSING ENDOPROTEASES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,820
FILING DATE: 09-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2848-7-1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-437-820-6

Query Match
Best Local Similarity 71.3%; Score 43.5; DB 1; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 RPKQOQFFGLM 11
DB 1 RPK-QOQFFGLM 10

RESULT 110
US-07-737-371E-37
Sequence 37, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-37

Query Match
Best Local Similarity 68.9%; Score 42; DB 2; Length 11;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKQOQFFGLM 11
DB 1 RPKQOQFFGLM 11

RESULT 111
US-07-737-371E-4
; Sequence 4, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-737-371E-4

Query Match 65.6%; Score 40; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOOF 7
DB 1 RPKPOOF 7

RESULT 112
US-08-505-250-37
; Sequence 37, Application US/08505250
; Patent No. 6183983
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kohichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; CURRENT FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: PCT/JP95/00298
; EARLIER FILING DATE: 1995-02-27

EARLIER APPLICATION NUMBER: JP 198187/94
; EARLIER FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-08-505-250-37

Query Match 65.6%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOOF 7
DB 2 RPKPOOF 8

RESULT 113
US-07-737-371E-3
; Sequence 3, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 1...1
; OTHER INFORMATION: where Xaa at position 1 is D-Arg
; LOCATION: 7...7
; OTHER INFORMATION: where Xaa at position 7 is D-Trp
; LOCATION: 9...9
; OTHER INFORMATION: where Xaa at position 9 is D-Trp
US-07-737-371E-3

Query Match 63.9%; Score 39; DB 2; Length 11;
Best Local Similarity 70.0%; Pred. No. 0.46;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPKPOQFFGLM 11
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Db 2 RPKPOQFXFLM 11

RESULT 114

US-07-737-371E-2
; Sequence 2, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; LOCATION: 2...2
; OTHER INFORMATION: where Xaa at position 2 is D-Pro
; LOCATION: 7...7
; OTHER INFORMATION: where Xaa at position 7 is D-Arg
; LOCATION: 9...9
; OTHER INFORMATION: where Xaa at position 9 is D-Trp
US-07-737-371E-2

Query Match 62.3%; Score 38; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.68;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
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Db 1 RPKPOQFXFLM 11

RESULT 115

US-07-737-371E-38
; Sequence 38, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-38

Query Match 62.3%; Score 38; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.68;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
| | | | | | | |
Db 1 RPKPOQFXFLM 11

RESULT 116

US-08-468-514-4
; Sequence 4, Application US/08468514
; Patent No. 5576296
; GENERAL INFORMATION:
; APPLICANT: Bartfal, Tamás
; APPLICANT: Horkfel, Tomas
; APPLICANT: Langel, Ulo
; APPLICANT: Ahren, Bo
; APPLICANT: Lindskog, Stefan
; APPLICANT: Consolo, Silvana
; APPLICANT: Land, Tilt
; APPLICANT: Wiesenfeld-Hallin, Zsuzsanna
; TITLE OF INVENTION: GALANIN ANTAGONIST
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY

COUNTRY: USA
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,514
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,139
FILING DATE: 12-NOV-1993
APPLICATION NUMBER: PCT/SE92/00316
FILING DATE: 14-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9101472-0
FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Sterner Ph.D., Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8783
TELEFAX: 212-354-8113
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: Modified-site
LOCATION: 21
OTHER INFORMATION: /note= "amide or free acid"
US-08-468-514-4

Query Match 62.3%; Score 38; DB 1; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
I I I I I I I I
Db 14 PQOFFGLM 21

RESULT 117
US-07-737-371E-8
Sequence 8, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991

CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-8

Query Match 60.7%; Score 37; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QOFFGLM 11
I I I I I I I I
Db 1 QOFFGLM 7

RESULT 118
US-07-737-371E-56
Sequence 56, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

LOCATION: 1...1
OTHER INFORMATION: where Xaa at position 1 is D-Ala
US-07-737-371E-56

Query Match 60.7%; Score 37; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.0e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 OOFFGLM 11
111111
DB 2 OOFFGLM 8

RESULT 119
US-07-737-371E-39
Sequence 39, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
CLASSIFICATION: 536
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-39

Query Match 59.0%; Score 36; DB 2; Length 11;
Best Local Similarity 63.6%; Pred. No. 1.5;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
111111
DB 1 RPKPOFFGLM 11

RESULT 120
US-08-428-488-18
Sequence 18, Application US/08428488
Patent No. 5624834
GENERAL INFORMATION:

APPLICANT: BODOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: /note="Position 12 = Met-NH2."
US-08-428-488-18

Query Match 59.0%; Score 36; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 PKPOFFGLM 11
111111
DB 3 PKSDOFFGLM 12

RESULT 121
US-08-796-598-10
Sequence 10, Application US/08796598
Patent No. 5827659
GENERAL INFORMATION:
APPLICANT: PATTERSON, DALE H.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS USING MASS SPECTROMETRY.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator - Testa, Hurwitz &
ADDRESS: Philbeault
STREET: High Street Tower, 125 High Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/796,598
;; FILING DATE: 07-FEB-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/446,055
;; FILING DATE: 19-MAY-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: FLYNN Esq., Kerry A.
;; REGISTRATION NUMBER: 33,693
;; REFERENCE/DOCKET NUMBER: SYP-115
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 248-7000
;; TELEFAX: (617) 248-7100
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-796-598-10

Query Match 59.0%; Score 36; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOFFFGIM 11
DB 3 PKSDQFVGIM 12

RESULT 122
US-08-447-175A-10
; Sequence 10, Application US/08447175A
; Patent No. 5869240
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, DALE H.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
; TITLE OF INVENTION: POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Administrator - Testa, Hurwitz &
; ADDRESS: Thibault, LLP
; STREET: High Street Tower, 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,175A
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 422
; ATTORNEY/AGENT INFORMATION:
; NAME: RAUSCHENBACH, Kurt
; REGISTRATION NUMBER: 40,137
; REFERENCE/DOCKET NUMBER: SYP-114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

;; MOLECULE TYPE: peptide
;; US-08-447-175A-10

Query Match 59.0%; Score 36; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOFFFGIM 11
DB 3 PKSDQFVGIM 12

RESULT 123
US-07-737-371E-76
; Sequence 76, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;; US-07-737-371E-76

Query Match 59.0%; Score 36; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PKPOFFFGIM 11
DB 3 PKSDQFVGIM 12

RESULT 124
US-08-503-250-40
; Sequence 40, Application US/08505250
; Patent No. 6183983
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya

APPLICANT: Yamamoto, Keiji
APPLICANT: Suzuki, Kokihiro
APPLICANT: Ikeda, Masahiro
APPLICANT: Sakagami, Masahiro
APPLICANT: Taniguchi, Makoto
TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
FILE REFERENCE: 110-511
CURRENT APPLICATION NUMBER: US/08/505,250
CURRENT FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: PCT/JP95/00298
EARLIER FILING DATE: 1995-02-27
EARLIER APPLICATION NUMBER: JP 198187/94
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 40
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-08-505-250-40

Query Match 57.4%; Score 35; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RPKPOOF 7
111111
Db 2 RPKPOOF 7

RESULT 125
US-08-346-849-7
Sequence 7, Application US/08346849
Patent No. 5670483
GENERAL INFORMATION:
APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (517) 861-9540

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-346-849-7

Query Match 57.4%; Score 35; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOOF 7
111111
Db 1 RPKPOOF 7

RESULT 126
US-08-293-284A-7
Sequence 7, Application US/08293284A
Patent No. 5955343
GENERAL INFORMATION:
APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: DiPersio, C. Michael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,284A
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-284A-7

Query Match 57.4%; Score 35; DB 2; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.6e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOOF 7
111111

Db 1 RPKPOOM 7

RESULT 127

US-07-753-909B-2

; Sequence 2, Application US/07753909B
; Patent No. 5304632

; GENERAL INFORMATION:

; APPLICANT: Vaudry, Hubert

; APPLICANT: Conlon, Michael J.

; TITLE OF INVENTION: Neuropeptides of the Tachykinin Family

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Zarley, McKee, Thomte, Voorhees, and Sease

; STREET: 801 Grand, Suite 3200

; CITY: Des Moines

; STATE: Iowa

; COUNTRY: United States

; ZIP: 50309

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/753,909B

; FILING DATE: 19910903

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 9106759

; FILING DATE: 04-JUN-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Sease, Edmund J.

; REGISTRATION NUMBER: 24,741

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (515)-288-3667

; TELEFAX: (515)-288-1338

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:

; ORGANISM: Rana ridibunda

; DEVELOPMENTAL STAGE: adult

; TISSUE TYPE: brain

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1

; OTHER INFORMATION: /label= peptide

; OTHER INFORMATION: /note= "X in position 1 is a basic type amino

; OTHER INFORMATION: acid, for example Arg, Glu, or Lys."

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 3

; OTHER INFORMATION: /label= peptide

; OTHER INFORMATION: /note= "X in position 3 is Lys, Asx, or Asn."

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 5

; OTHER INFORMATION: /label= peptide

; OTHER INFORMATION: /note= "X in position 5 is Glu, Lys, or Arg."

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 6

; OTHER INFORMATION: /label= peptide

; OTHER INFORMATION: /note= "X in position 6 of the sequence is Glu,

; OTHER INFORMATION: Lys, or Arg."

; US-07-753-909B-2

Query Match 57.4%; Score 35; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.2;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;Qy 2 RPKPOFFGLM 11
| | | | |
Db 2 RPKPOFFGLM 11

RESULT 128

US-07-737-371E-41

; Sequence 41, Application US/07737371E

; Patent No. 5876948

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/737,371E

; FILING DATE: 29-JUL-1991

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/559,172

; FILING DATE: 27-JUL-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Freeman, John W.

; REGISTRATION NUMBER: 29,066

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 41:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-07-737-371E-41

Query Match 57.4%; Score 35; DB 2; Length 11;
Best Local Similarity 63.6%; Pred. No. 2.2;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;Qy 1 RPKPOFFGLM 11
| | | | |
Db 1 RPKPOFFGLM 11

RESULT 129

US-08-833-876-4

; Sequence 4, Application US/08833876

; Patent No. 6270999

; GENERAL INFORMATION:

; APPLICANT: Lawlor, Elizabeth

; TITLE OF INVENTION: NO. 6270999e1 Compounds

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

STREET: 705 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833.876
FILING DATE: 10-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9607991.8
FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P11458-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-876-4

Query Match 57.4% Score 35; DB 4; Length 130;
Best Local Similarity 60.0% Pred. No. 28;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOOFFGL 10
|||:|
DB 45 RPLPEKFGHL 54

RESULT 130
US-09-483-054-4
Sequence 4, Application US/09483054
Patent No. 6303124
GENERAL INFORMATION:
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6303124e1 Compounds
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/483.054
FILING DATE: 13-Jan-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833.876
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Gimm1, Edward R

REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P11458-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-483-054-4

Query Match 57.4% Score 35; DB 4; Length 130;
Best Local Similarity 60.0% Pred. No. 28;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOOFFGL 10
|||:|
DB 45 RPLPEKFGHL 54

RESULT 131
US-08-978-741-8
Sequence 8, Application US/08978741
Patent No. 6100076
GENERAL INFORMATION:
APPLICANT: Yang Wang, Michael W. Spellman
TITLE OF INVENTION: O-Fucosyltransferase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978.741
FILING DATE: 26-No. 6100076-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/792498
FILING DATE: 31
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1041P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 474 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-978-741-8

Query Match 57.4% Score 35; DB 3; Length 474;
Best Local Similarity 55.6% Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PKPOOFFGL 10

Db 457 PRPSAFGL 465

RESULT 132

US-09-333-729A-12
; Sequence 12, Application US/09333729A
; Patent No. 6270987
; GENERAL INFORMATION:
; APPLICANT: Wang, Yang
; APPLICANT: Spelman, Michael W.
; TITLE OF INVENTION: O-Fucosyltransferase
; FILE REFERENCE: P1041PDI-Substitute
; CURRENT APPLICATION NUMBER: US/09/333,729A
; CURRENT FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: US 08/798,741
; PRIOR FILING DATE: 1997-11-26
; NUMBER OF SEQ ID NOS: 21
; SEQ ID NO 12
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Caenorhabditis Elegans
US-09-333-729A-12

Query Match 57.4%; Score 35; DB 4; Length 474;
Best Local Similarity 55.6%; Pred. NO. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RPKPOFFGL 10
Db 457 PRPSAFGL 465

RESULT 133

US-08-833-876-2
; Sequence 2, Application US/08833876
; Patent No. 6270999
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 6270999e1 Compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,876
; FILING DATE: 10-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9607991.8
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31458-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; MOLECULE TYPE: protein
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-833-876-2

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-876-2

Query Match 57.4%; Score 35; DB 4; Length 496;
Best Local Similarity 60.0%; Pred. NO. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOFFGL 10
Db 145 RPLPEKPHGL 154

RESULT 134

US-09-483-054-2
; Sequence 2, Application US/09483054
; Patent No. 6303124
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 6303124e1 Compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/483,054
; FILING DATE: 13-Jan-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/833,876
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimm, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31458-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 496 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-483-054-2

Query Match 57.4%; Score 35; DB 4; Length 496;
Best Local Similarity 60.0%; Pred. NO. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOFFGL 10
Db 145 RPLPEKPHGL 154

RESULT 135
US-07-737-371E-58
; Sequence 58, Application US/07737371E

Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-58

Query Match 55.7%; Score 34; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPOQ 6
DB 1 RPKPOQ 6

RESULT 136
US-07-737-371E-40
Sequence 40, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-40

Query Match 55.7%; Score 34; DB 2; Length 11;
Best Local Similarity 63.6%; Pred. No. 3.3;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
DB 1 RPKPOFFGLM 11

RESULT 137
US-08-457-274A-24
Sequence 24, Application US/08457274A
Patent No. 5734086
GENERAL INFORMATION:
APPLICANT: Scott, Jeffrey G.
TITLE OF INVENTION: Tomita, Takashi
TITLE OF INVENTION: Cytochrome P4501pr Gene and Its Uses
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,274A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: papillio polyxnes
STRAIN:
DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
US-08-457-274A-24

Query Match 55.7%; Score 34; DB 1; Length 498;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOFFG 9
DB 34 PKVPFFG 41

RESULT 138
PCT-US95-05758-24
Sequence 24, Application PC/TUS9505758
GENERAL INFORMATION:
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Cytochrome P4501pr Gene and Its
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05758
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/241 (D-1519)
TELEPHONE: 716-263-1304
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: papillio polyxnes
STRAIN:
DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
PCT-US95-05758-24

Query Match 55.7%; Score 34; DB 5; Length 498;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PKPOFFG 9
DB 34 PKVPFFG 41

DB 34 PKVPFFG 41

RESULT 139
US-08-457-274A-25
Sequence 25, Application US/08457274A
Patent No. 5734086
GENERAL INFORMATION:
APPLICANT: Scott, Jeffrey G.
APPLICANT: Tomita, Takashi
TITLE OF INVENTION: Cytochrome P4501pr Gene and Its Uses
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,274A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
TELEPHONE: 716-263-1600
TELEFAX: 716-263-1304
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rat
STRAIN:
DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
US-08-457-274A-25

Query Match 55.7%; Score 34; DB 1; Length 504;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOFFG 9
DB 41 PKPLPFFG 48

RESULT 140
PCT-US95-05758-25
Sequence 25, Application PC/TUS9505758
GENERAL INFORMATION:
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: Cytochrome P4501pr Gene and Its
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: P.O. Box 1051, Clinton Square

CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05758
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/241 (D-1519)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1304
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rat
STRAIN: Unknown
DEVELOPMENTAL STAGE: Adult
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Unknown
PCT-US95-05758-25

Query Match 55.7%; Score 34; DB 5; Length 504;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PKPODFG 9
Db 41 PKPLPFG 48

RESULT 141
US-08-481-190-19
Sequence 19, Application US/08481190
Patent No. 6160204
GENERAL INFORMATION:
APPLICANT: John C. Steffens
TITLE OF INVENTION: Polyphenol Oxidase cDNA
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481.190
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 203.533

FILING DATE: 02-24-1994
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: UA 816 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-190-19

Query Match 55.7%; Score 34; DB 4; Length 583;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PKPODFG 9
Db 296 PCPSQFG 303

RESULT 142
PCT-US93-00869-19
Sequence 19, Application PC/TUS9300869
GENERAL INFORMATION:
APPLICANT: John C. Steffens
TITLE OF INVENTION: Polyphenol Oxidase cDNAs: Cloning
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00869
FILING DATE: 19930129
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF D-1057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-00869-19

Query Match 55.7%; Score 34; DB 5; Length 583;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PKPODFG 9

Db 296 PCPSQFPG 303

RESULT 143

US-08-481-190-4

Sequence 4, Application US/08481190

Patent No. 6160204

GENERAL INFORMATION:

APPLICANT: John C. Steffens

TITLE OF INVENTION: Polyphenol Oxidase CDNA

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Yahwak & Associates

STREET: 25 Skytop Drive

CITY: Trumbull

STATE: Connecticut

COUNTRY: USA

ZIP: 06611

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: MS-DOS

SOFTWARE: Microsoft Word 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,190

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 203,533

FILING DATE: 02-24-1994

ATTORNEY/AGENT INFORMATION:

NAME: George M. Yahwak

REGISTRATION NUMBER: 26,824

REFERENCE/DOCKET NUMBER: UA 816 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203)268-1951

TELEFAX: (203)268-1951

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 587 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-481-190-4

Query Match 55.7%; Score 34; DB 4; Length 587;

Best Local Similarity 75.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRPOFPG 9

Db 300 PCPSQFPG 307

RESULT 144

PCT-US93-00869-4

Sequence 4, Application PC/TUS9300869

GENERAL INFORMATION:

APPLICANT: John C. Steffens

TITLE OF INVENTION: Polyphenol Oxidase CDNAs: Cloning

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Yahwak & Associates

STREET: 25 Skytop Drive

CITY: Trumbull

STATE: Connecticut

COUNTRY: USA

ZIP: 06611

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: MS-DOS

SOFTWARE: Microsoft Word 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,190

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 203,533

FILING DATE: 02-24-1994

ATTORNEY/AGENT INFORMATION:

NAME: George M. Yahwak

REGISTRATION NUMBER: 26,824

REFERENCE/DOCKET NUMBER: UA 816 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203)268-1951

TELEFAX: (203)268-1951

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 588 amino acids

TYPE: amino acid

STRANDEDNESS: single

MEDIUM TYPE: floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: MS-DOS

SOFTWARE: Microsoft Word 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/00869

FILING DATE: 19930129

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: George M. Yahwak

REGISTRATION NUMBER: 26,824

REFERENCE/DOCKET NUMBER: CRF D-1057

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203)268-1951

TELEFAX: (203)268-1951

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 587 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US93-00869-4

Query Match 55.7%; Score 34; DB 5; Length 587;

Best Local Similarity 75.0%; Pred. No. 1.9e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRPOFPG 9

Db 300 PCPSQFPG 307

RESULT 145

US-08-481-190-16

Sequence 16, Application US/08481190

Patent No. 6160204

GENERAL INFORMATION:

APPLICANT: John C. Steffens

TITLE OF INVENTION: Polyphenol Oxidase CDNA

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Yahwak & Associates

STREET: 25 Skytop Drive

CITY: Trumbull

STATE: Connecticut

COUNTRY: USA

ZIP: 06611

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: MS-DOS

SOFTWARE: Microsoft Word 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,190

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 203,533

FILING DATE: 02-24-1994

ATTORNEY/AGENT INFORMATION:

NAME: George M. Yahwak

REGISTRATION NUMBER: 26,824

REFERENCE/DOCKET NUMBER: UA 816 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203)268-1951

TELEFAX: (203)268-1951

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 588 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-190-16

Query Match 55.7%; Score 34; DB 4; Length 588;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOFFG 9
| | | | |
Db 301 PCPSOFFG 308

RESULT 146
PCT-US93-00869-16
Sequence 16, Application PC/TUS9300869
GENERAL INFORMATION:
APPLICANT: John C. Steffens
TITLE OF INVENTION: Polyphenol Oxidase cDNAs: Cloning
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
CITY: Trumbull
STATE: Connecticut
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00869
FILING DATE: 19930129
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF D-1057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 588 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-00869-16

Query Match 55.7%; Score 34; DB 5; Length 588;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOFFG 9
| | | | |
Db 301 PCPSOFFG 308

RESULT 147
US-08-346-849-6
Sequence 6, Application US/08346849
Patent No. 5670483
GENERAL INFORMATION:
APPLICANT: Zhang, Shuguang
APPLICANT: Lockshin, Curtis
APPLICANT: Rich, Alexander
APPLICANT: Holmes, Todd

TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentia Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,849
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28 DECEMBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-346-849-6

Query Match 54.1%; Score 33; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KPOFFGLM 11
| | | | |
Db 1 RPKOFGLM 9

RESULT 148
US-08-293-284A-6
Sequence 6, Application US/08293284A
Patent No. 5955343
GENERAL INFORMATION:
APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuguang
APPLICANT: Rich, Alexander
APPLICANT: DiPersio, C. Michael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,284A
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: BROOK, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-284A-6

Query Match 54.1%; Score 33; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.6e+05;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PQOFFGLM 11
Db 1 RPKQOFFGLM 9

RESULT 149
US-08-053-451B-159
Sequence 159, Application US/08053451B
Patent No. 5955584
GENERAL INFORMATION:
APPLICANT: Chen, Francis W.
APPLICANT: Dittlow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-053-451B-159

Query Match 54.1%; Score 33; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 5;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
Db 4 PQOFFGL 11

RESULT 150
US-08-480-434-63
Sequence 63, Application US/08480434
Patent No. 5811248
GENERAL INFORMATION:
APPLICANT: Charles C. Dittlow, et al.
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
TITLE OF INVENTION: ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,434
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOHETICAL: N
ANTI-SENSE: N
US-08-480-434-63

Query Match 54.1%; Score 33; DB 2; Length 138;
Best Local Similarity 62.5%; Pred. No. 66;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQOFFGLM 11
Db 4 PQOFFGL 11

RESULT 151
US-08-053-451B-63
Sequence 63, Application US/08053451B
Patent No. 5955584
GENERAL INFORMATION:

APPLICANT: Cien, Francis W.
APPLICANT: Dittlow, Charles C.
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
TITLE OF INVENTION: ANTIGENS, ANTIBODIES THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 176
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,451B
FILING DATE: 26-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 7606-033-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA
HYPOTHETICAL: N
ANTI-SENSE: N
US-08-053-451B-63

Query Match 54.1%; Score 33; DB 2; Length 138;
Best Local Similarity 62.5%; Pred. No. 66;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PPOPFGLM 11
DB 4 PPOPFGL 11

RESULT 152
US-09-129-030-56
Sequence 56, Application US/09129030A
Patent No. 6242221
GENERAL INFORMATION:
APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
TITLE OF INVENTION: GENOMIC PRO CLONES
FILE REFERENCE: 57072-PCT-US
CURRENT APPLICATION NUMBER: US/09/129,030A
CURRENT FILING DATE: 1998-08-04
EARLIER APPLICATION NUMBER: AU PN7856
EARLIER FILING DATE: 1996-02-05
EARLIER APPLICATION NUMBER: AU PO2361
EARLIER FILING DATE: 1996-09-16
EARLIER APPLICATION NUMBER: PCT/AU97/00041
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56
LENGTH: 171
TYPE: PRT
ORGANISM: POTATO

US-09-129-030-56

Query Match 54.1%; Score 33; DB 4; Length 171;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKPOFFG 9
DB 73 PKPOFFG 80

RESULT 153
US-08-793-410-30
Sequence 30, Application US/08793410
Patent No. 5955650
GENERAL INFORMATION:
APPLICANT: HITZ, WILLIAM DEAN
TITLE OF INVENTION: NOCOTENIDE SEQUENCES OF CANOLA
TITLE OF INVENTION: AND SOYBEAN PALMITOYL-ACP THIO-
TITLE OF INVENTION: ESTERASE GENES AND THEIR USE IN
TITLE OF INVENTION: THE REGULATION OF FATTY ACID
TITLE OF INVENTION: CONTENT OF THE OILS OF SOYBEAN
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,410
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10627
FILING DATE: AUGUST 25, 1995
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNN M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: CR-9567-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-773-0164
TELEFAX: 302-992-5481
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-793-410-30

Query Match 54.1%; Score 33; DB 2; Length 324;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOFFGLM 11
DB 306 RPKPVNNGGV 316

RESULT 154
US-08-793-410-7

; Sequence 7, Application US/08793410
; Patent No. 5955650
; GENERAL INFORMATION:
; APPLICANT: HITZ, WILLIAM DEAN
; TITLE OF INVENTION: NOCLOTEIDE SEQUENCES OF CANOLA
; TITLE OF INVENTION: AND SOYBEAN PALMITOYL-ACP THIO-
; TITLE OF INVENTION: ESTERASE GENES AND THEIR USE IN
; TITLE OF INVENTION: THE REGULATION OF FATY ACID
; TITLE OF INVENTION: CONTENT OF THE OILS OF SOYBEAN
; TITLE OF INVENTION: AND CANOLA PLANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,410
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10627
; FILING DATE: AUGUST 25, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CHRISTENBURY, LYNNE M.
; REGISTRATION NUMBER: 30,971
; REFERENCE/DOCKET NUMBER: CR-9567-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-773-0164
; TELEFAX: 302-992-5481
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; US-08-793-410-7

Query Match 54.1%; Score 33; DB 2; Length 328;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 RPKPOQFGLM 11
DB 310 RPKPVNFGV 320

RESULT 155
US-08-666-367B-7
; Sequence 7, Application US/08666367B
; Patent No. 5854042
; GENERAL INFORMATION:
; APPLICANT: Shuichi TSUI et al.
; TITLE OF INVENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR
; TITLE OF INVENTION: PRODUCING THE SAME
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/666,367B
; FILING DATE: August 19, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 404 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: G. gallus (chicken)
; US-08-666-367B-7

Query Match 54.1%; Score 33; DB 2; Length 404;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOQFGL 10
DB 288 EPQKRFGL 295

RESULT 156
US-09-143-438-7
; Sequence 7, Application US/09143438
; Patent No. 6218161
; GENERAL INFORMATION:
; APPLICANT: Shuichi TSUI et al.
; TITLE OF INVENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR
; TITLE OF INVENTION: PRODUCING THE SAME
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., #800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/143,438
; FILING DATE: August 28, 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/666,367
; FILING DATE: August 19, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: G. gallus (chicken)
US-09-143-438-7

Query Match 54.1%; Score 33; DB 4; Length 404;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 3 PQQFFGL 10
Db 288 EPQKYFGL 295

RESULT 157
US-08-222-616-20
Sequence 20, Application US/08222616
Patent No. 5635177
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
NUMBER OF SEQUENCES: 42
TITLE OF INVENTION: ANTIBODIES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222, 616
FILING DATE: 4-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00586
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 821P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-222-616-20

Query Match 54.1%; Score 33; DB 1; Length 505;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQQFFGLM 11
Db 459 PQQFYNNM 466

RESULT 158
PCT-US95-04228-20
Sequence 20, Application PC/TUS9504228
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 505 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-04228-20

Query Match 54.1%; Score 33; DB 5; Length 505;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PQQFFGLM 11
Db 459 PQQFYNNM 466

RESULT 159
PCT-US95-05008-6
Sequence 6, Application PC/TUS9505008
GENERAL INFORMATION:
APPLICANT: Sugen, Inc.

```

: APPLICANT: 515 Galveston Drive
: APPLICANT: Redwood City, California 94063-4720
: APPLICANT: United States of America
: APPLICANT: Wissenschaften E.V.
: APPLICANT: Hofgarten Str. 2
: APPLICANT: Munchen 80539
: APPLICANT: Germany
: TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
: TITLE OF INVENTION: Kinases
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESS: Pennle & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/05008
: FILING DATE: 24-APR-1995
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/232,545
: FILING DATE: 22-APR-1994
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7683-074
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212)790-9090
: TELEFAX: (212)869-9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 511 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: PCT-US95-05008-6

Query Match          54.1%; Score 33; DB 5; Length 511;
Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 PQQFFGLM 11
      11111:11
DB 465 PQQFFYIM 472

RESULT 160
US-08-949-588-2
: Sequence 2, Application US/08949588
: Patent No. 6025156
: GENERAL INFORMATION:
: APPLICANT: Gwynn, Michael
: APPLICANT: Kallendar, Howard
: APPLICANT: Palmer, Leslie
: TITLE OF INVENTION: No. 6025156e1 Topoisomerase III
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA

```

```

: ZIP: 19406-0939
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/949,588
: FILING DATE: 14-OCT-1997
: CLASSIFICATION: 424
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: 60/028,417
: FILING DATE: 15-OCT-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Gimm, Edward R.
: REGISTRATION NUMBER: 38,891
: REFERENCE/DOCKET NUMBER: P50567
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-270-4478
: TELEFAX: 610-270-5090
: TELEX:
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 711 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-949-588-2

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```

Query Match          54.1%; Score 33; DB 3; Length 711;
Best Local Similarity 75.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 3 KPQQFFGL 10
      11111:11
DB 209 KPQQFFTL 216

```

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RESULT 161
US-09-108-020-49
: Sequence 49, Application US/09108020A
: Patent No. 6143561
: GENERAL INFORMATION:
: APPLICANT: Randall, Douglas D.
: APPLICANT: Johnston, Mark L.
: APPLICANT: Miernyk, Jan A.
: APPLICANT: Luehly, Michael H.
: APPLICANT: Mooney, Brian P.
: TITLE OF INVENTION: USE OF DNA ENCODING PLASTID PYRUVATE DEHYDROGENASE AND
: TITLE OF INVENTION: BRANCHED CHAIN OXOACID DEHYDROGENASE COMPONENTS TO
: TITLE OF INVENTION: ENHANCE POLYHYDROXYALKANOATE BIOSYNTHESIS IN PLANTS
: FILE REFERENCE: UMO 1482
: CURRENT APPLICATION NUMBER: US/09/108,020A
: EARLIER FILING DATE: 1998-06-30
: EARLIER APPLICATION NUMBER: 60/051,291
: EARLIER FILING DATE: 1997-06-30
: EARLIER APPLICATION NUMBER: 60/055,255
: EARLIER FILING DATE: 1997-08-01
: EARLIER APPLICATION NUMBER: 60/076,544
: EARLIER FILING DATE: 1998-03-02
: NUMBER OF SEQ ID NOS: 54
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 49
: LENGTH: 325
: TYPE: PRT
: ORGANISM: B. subtilis
: US-09-108-020-49

```

```

Query Match          53.3%; Score 32.5; DB 4; Length 325;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;

```


TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "Position 1 = p-Glu."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /note= "Position 11 = Met-NH2."
US-08-428-488-16

Query Match 52.5%; Score 32; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 7.4;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
1 : : : : :
DB 4 PNKFYGLM 11

RESULT 165
US-08-796-598-7
Sequence 7, Application US/08796598
Patent No. 5827659
GENERAL INFORMATION:
APPLICANT: PATTERSON, DALE H.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS USING MASS SPECTROMETRY.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator - Testa, Hurwitz &
ADDRESS: Thibault
STREET: High Street Tower, 125 High Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,598
FILING DATE: 07-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,055
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FLYNN Esq., Kerry A.
REGISTRATION NUMBER: 33,693
REFERENCE/DOCKET NUMBER: SYP-115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-796-598-7

Query Match 52.5%; Score 32; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 7.4;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
1 : : : : :
DB 4 PNKFYGLM 11

RESULT 166
US-08-447-175A-7
Sequence 7, Application US/08447175A
Patent No. 5869240
GENERAL INFORMATION:
APPLICANT: PATTERSON, DALE H.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator - Testa, Hurwitz &
ADDRESS: Thibault, LLP
STREET: High Street Tower, 125 High Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,175A
FILING DATE: 19-MAY-1995
CLASSIFICATION: 422
ATTORNEY/AGENT INFORMATION:
NAME: RAUSCHENBACH, Kurt
REGISTRATION NUMBER: 40,137
REFERENCE/DOCKET NUMBER: SYP-114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-447-175A-7

Query Match 52.5%; Score 32; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 7.4;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
1 : : : : :
DB 4 PNKFYGLM 11

RESULT 167
US-09-214-614-1
Sequence 1, Application US/09214614
Patent No. 6225100
GENERAL INFORMATION:
APPLICANT: Grund, Alan D.
APPLICANT: Maurina-Brunker, Julie
TITLE OF INVENTION: NOVEL ARYLSULFOTRANSFERASE
NUMBER OF SEQUENCES: 10

CITY: Portland
STATE: Oregon
COUNTRY: United States of America
ZIP: 97204
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,578
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,409
FILING DATE: February 18, 1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Alan E. Dow, Ph.D.
REGISTRATION NUMBER: 35,123
REFERENCE/DOCKET NUMBER: 4630-49462/AED
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acid residues
TYPE: amino acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
US-09-025-578-2

Query Match 52.5%; Score 32; DB 4; Length 402;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 QOFFGL 11
DB 266 PLSFGLM 273

RESULT 171
US-08-068-392-3
Sequence 3, Application US/08068392
Patent No. 6150152
GENERAL INFORMATION:
APPLICANT: Shapiro, Steven M.
TITLE OF INVENTION: Human Macrophage Metalloprotease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/068,392
FILING DATE: 19930528
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25275
REFERENCE/DOCKET NUMBER: 07-24(12406)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
TELEFAX: (314)694-5435

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-068-392-3

Query Match 52.5%; Score 32; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QOFFGL 10
DB 61 QOFFGL 66

RESULT 172
US-08-396-988-3
Sequence 3, Application US/08396988
Patent No. 6204043
GENERAL INFORMATION:
APPLICANT: Shapiro, Steven M.
TITLE OF INVENTION: Human Macrophage Metalloprotease
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM
STREET: 800 N. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,988
FILING DATE: 01-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,392
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25275
REFERENCE/DOCKET NUMBER: 07-24(12406)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
TELEFAX: (314)694-5435
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-396-988-3

Query Match 52.5%; Score 32; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QOFFGL 10
DB 61 QOFFGL 66

RESULT 173
US-09-017-706-9
Sequence 9, Application US/09017706A

; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTASE, VECTOR CONTAINING SAID GENE AND
; TITLE OF INVENTION: TRANSFORMANT
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 614
; TYPE: PRF
; ORGANISM: Pseudomonas sp., Strain KO-8940
US-09-017-706-9

Query Match 52.5%; Score 32; DB 3; Length 614;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOFFGL 10
:1:1:111
Db 252 QPSQYFGL 259

RESULT 174
US-09-017-706-10
; Sequence 10, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTASE, VECTOR CONTAINING SAID GENE AND
; TITLE OF INVENTION: TRANSFORMANT
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 614
; TYPE: PRF
; ORGANISM: Pseudomonas sp., Strain KO-8940
US-09-017-706-10

Query Match 52.5%; Score 32; DB 3; Length 614;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOFFGL 10
:1:1:111
Db 252 QPSQYFGL 259

RESULT 175
US-09-017-706-11
; Sequence 11, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTASE, VECTOR CONTAINING SAID GENE AND
; TITLE OF INVENTION: TRANSFORMANT
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05

; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 614
; TYPE: PRF
; ORGANISM: Pseudomonas sp., Strain KO-8940
US-09-017-706-11

Query Match 52.5%; Score 32; DB 3; Length 614;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOFFGL 10
:1:1:111
Db 252 QPSQYFGL 259

RESULT 176
US-09-017-706-12
; Sequence 12, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTASE, VECTOR CONTAINING SAID GENE AND
; TITLE OF INVENTION: TRANSFORMANT
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 614
; TYPE: PRF
; ORGANISM: Pseudomonas sp., Strain KO-8940
US-09-017-706-12

Query Match 52.5%; Score 32; DB 3; Length 614;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOFFGL 10
:1:1:111
Db 252 QPSQYFGL 259

RESULT 177
US-09-017-706-13
; Sequence 13, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOPEPTASE, VECTOR CONTAINING SAID GENE AND
; TITLE OF INVENTION: TRANSFORMANT
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 614
; TYPE: PRF
; ORGANISM: Pseudomonas sp., Strain KO-8940
US-09-017-706-13

Query Match 52.5%; Score 32; DB 3; Length 614;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOOFFGL 10
:1:1:1:1
DB 252 QPSQYFGL 259

RESULT 178
US-09-017-706-14

; Sequence 14, Application US/09017706A
; Patent No. 6087147
; GENERAL INFORMATION:
; APPLICANT: ITO, YOSHIFUMI
; TITLE OF INVENTION: A-AMYLASE GENE HAVING ABILITY FOR HIGHLY PRODUCING
; TITLE OF INVENTION: MALTOBENTAOSE, VECTOR CONTAINING SAID GENE AND
; TITLE OF INVENTION: TRANSFORMANT
; FILE REFERENCE: 8361-0003-0
; CURRENT APPLICATION NUMBER: US/09/017,706A
; CURRENT FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: JP 305071/1997
; EARLIER FILING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Pseudomonas sp., Strain KO-8940
US-09-017-706-14

Query Match 52.5%; Score 32; DB 3; Length 614;
Best Local Similarity 62.5%; Pred. No. 4.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOOFFGL 10
:1:1:1:1
DB 252 QPSQYFGL 259

RESULT 179
5441935-10
; Patent No. 5441935
; APPLICANT: Rozenqurt, Enrique; Zachary, Ian; Woll, Penella
; TITLE OF INVENTION: ROTH FACTOR RECEPTORS
; NUMBER OF SEQUENCES:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,587
; FILING DATE: 03-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 814,064
; FILING DATE: 23-DEC-1991
; APPLICATION NUMBER: 411,536
; FILING DATE: 29-NOV-1989
; SEQ ID NO:10:
; LENGTH: 8
5441935-10

Query Match 50.8%; Score 31; DB 6; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 POOFFGLM 11
:1:1:1:1
DB 1 POOMFWLM 8

RESULT 180
US-09-024-975-3

; Sequence 3, Application US/09024975
; Patent No. 6133233

; GENERAL INFORMATION:
; APPLICANT: ROSS, CHRISTOPHER R.
; APPLICANT: BLECHA, FRANK
; APPLICANT: SHI, JISHU
; TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
; STREET: 2405 GRAND BLVD., SUITE 400
; CITY: KANSAS CITY
; STATE: MO
; COUNTRY: USA
; ZIP: 64108

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,975
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/802,306
; FILING DATE: 18-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COLLINS, JOHN M.
; REGISTRATION NUMBER: 26,262
; REFERENCE/DOCKET NUMBER: 25585-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 816/474-9050
; TELEFAX: 816/474-9057

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-024-975-3

Query Match 50.8%; Score 31; DB 4; Length 16;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPPPOOFF 8
:1:1:1:1
DB 1 RRPPEPFF 8

RESULT 181
US-08-419-066-2

; Sequence 2, Application US/08419066
; Patent No. 5830993
; GENERAL INFORMATION:
; APPLICANT: Blecha, Frank
; APPLICANT: Shi, Jishu
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John M. Collins, Hovey, Williams, Timmons &
; ADDRESSEE: Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,066
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 23625
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-419-066-2

Query Match 50.8%; Score 31; DB 2; Length 26;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFF 8
11:111
DB 11 RRPPEFF 18

RESULT 182
US-09-024-975-2
Sequence 2, Application US/09024975
Patent No. 613323
GENERAL INFORMATION:
APPLICANT: ROSS, CHRISTOPHER R.
APPLICANT: BLECHA, FRANK
APPLICANT: SHI, JISHU
TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MO
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,975
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/802,306
FILING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 23585-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9057
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-975-2

Query Match 50.8%; Score 31; DB 4; Length 26;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFF 8
11:111
DB 11 RRPPEFF 18

RESULT 183
US-08-162-052-1
Sequence 1, Application US/08162052
Patent No. 5489575
GENERAL INFORMATION:
APPLICANT: LEE, Jong-Youn
APPLICANT: BOMAN, Hans G
APPLICANT: MUTT, Viktor
APPLICANT: JORNVALL, Hans
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND THEIR USE
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,052
FILING DATE: 02-JUN-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9101838-2
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92-22578
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 003300-299
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-162-052-1

Query Match 50.8%; Score 31; DB 1; Length 39;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPOQFF 8
11:111
DB 11 RRPPEFF 18

RESULT 184
US-08-310-722-1
; Sequence 1, Application US/08310722
; Patent No. 5654273
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,722
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: CMCC379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-815-6508
; TELEFAX: (404)-815-6555
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; PUBLICATION INFORMATION:
; AUTHORS: Lee, Jong-Youn
; AUTHORS: Boman, Hans G.
; AUTHORS: Muhl, Viktor
; AUTHORS: Jorvall, Hans
; TITLE: No. 5654273el Polypeptides And Their Use
; JOURNAL: PCT WO 92/22578
; DATE: 12/23/92
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-08-310-722-1

Query Match 50.8%; Score 31; DB 1; Length 39;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPRPOOFF 8
11:11
DB 11 RPRPPPF 18

ADDRESSEE: Collins
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: Missouri
COUNTRY: U.S.A.
ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,066
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Collins, John M.
; REGISTRATION NUMBER: 26262
; REFERENCE/DOCKET NUMBER: 23625
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (816) 474-9050
; TELEFAX: (816) 474-9057
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-419-066-1

Query Match 50.8%; Score 31; DB 2; Length 39;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPRPOOFF 8
11:11
DB 11 RPRPPPF 18

RESULT 186
US-08-728-333-1
; Sequence 1, Application US/08728333
; Patent No. 5863897
; GENERAL INFORMATION:
; APPLICANT: Gallo, Richard L.
; APPLICANT: Klagsbrun, Michael
; TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,333
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/310,722
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: CMCC379
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Lee, Jong-Youn
AUTHORS: Boman, Hans G.
AUTHORS: Mutt, Viktor
AUTHORS: Jorntvall, Hans
TITLE: No. 5863897e1 Polypeptides And Their Use
JOURNAL: PCT WO 92/22578
DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
US-08-728-333-1

Query Match 50.8%; Score 31; DB 2; Length 39;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOFF 8
11:11
Db 11 RPRPPFF 18

RESULT 187
US-09-024-975-1
Sequence 1, Application US/09024975
Patent No. 6133233
GENERAL INFORMATION:
APPLICANT: HOSS, CHRISTOPHER R.
APPLICANT: HLECHA, FRANK
TITLE OF INVENTION: PEPTIDE MODULATION OF REPERFUSION INJURY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MO
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,975
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/802,306
FILING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 25585-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-975-1

Query Match 50.8%; Score 31; DB 4; Length 39;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOFF 8
11:11
Db 11 RPRPPFF 18

RESULT 188
PCT-US95-12080-1
Sequence 1, Application PC/TUS9512080
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
TITLE OF INVENTION: Synuclein Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12080
FILING DATE:
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-815-8795
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
PUBLICATION INFORMATION:
AUTHORS: Lee, Jong-Youn
AUTHORS: Boman, Hans G.
AUTHORS: Mutt, Viktor
AUTHORS: Jorntvall, Hans
TITLE: Novel Polypeptides And Their Use
JOURNAL: PCT WO 92/22578
DATE: 12/23/92
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 39
PCT-US95-12080-1

Query Match 50.8%; Score 31; DB 5; Length 39;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOFF 8
11:11
Db 11 RPRPPFF 18

RESULT 189

US-08-553-619B-7
; Sequence 7, Application US/08553619B
; Patent No. 5919705
; GENERAL INFORMATION:
; APPLICANT: Dehaan, Petrus T.
; TITLE OF INVENTION: Virus Resistant Plants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5919705artis Crop Protection
; STREET: 975 California Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,619B
; FILING DATE: December 1, 1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Marcus-Wyner, Lynn
; REGISTRATION NUMBER: 34,869
; REFERENCE/DOCKET NUMBER: 137-1082/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/354-3588
; TELEFAX: 415/857-1125
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 264 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-553-619B-7

Query Match 50.8%; Score 31; DB 2; Length 264;
Best local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOOF 7
; 11111
; DB 233 RPKPKSF 239

RESULT 190
US-08-414-926A-22
; Sequence 22, Application US/08414926A
; Patent No. 5721354
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard
; APPLICANT: Cha, Tai-An
; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,926A
; FILING DATE: March 31, 1995
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-011/OOUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-494-7622
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: tol.16
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..316
; OTHER INFORMATION: /label= UL148
; US-08-414-926A-22

Query Match 50.8%; Score 31; DB 1; Length 316;
Best local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KPOOFF 8
; 11111
; DB 136 RPKPOFF 141

RESULT 191
US-08-926-922-22
; Sequence 22, Application US/08926922
; Patent No. 5925751
; GENERAL INFORMATION:
; APPLICANT: Spaete, Richard
; APPLICANT: Cha, Tai-An
; TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Luann Cserr Attorney at Law
; STREET: 750 Arlino Avenue
; CITY: Oakland
; STATE: CA
; COUNTRY: USA
; ZIP: 94610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,922
; FILING DATE: September 10, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Cserr, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR 11A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-834-1448
; TELEFAX: 510-839-7810
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: tol.16
; FEATURE:
; NAME/KEY: Protein

LOCATION: 1..316
OTHER INFORMATION: /label= U1148
US-08-926-922-22

Query Match 50.8%; Score 31; DB 2; Length 316;
Best Local Similarity 83.3%; Pred. NO. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOOF 3
:|||||
Db 136 RPOOF 141

RESULT 192
US-09-253-682-22
Sequence 22, Application US/09253682
Patent No. 6040170

GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Luann Cseerr Attorney at Law
STREET: 750 Arimo Avenue
CITY: Oakland
STATE: CA
COUNTRY: USA
ZIP: 94610

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253.682
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/926.922
FILING DATE: September 10, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Cseerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR 11A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-834-1448
TELEFAX: 510-839-7810

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: tol.16
FEATURE:
NAME/KEY: Protein
LOCATION: 1..316
OTHER INFORMATION: /label= U1148

US-09-253-682-22

Query Match 50.8%; Score 31; DB 3; Length 316;
Best Local Similarity 83.3%; Pred. NO. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOOF 8
:|||||
Db 136 RPOOF 141

RESULT 193
US-09-527-657-22
Sequence 22, Application US/09527657
Patent No. 6291236

GENERAL INFORMATION:
APPLICANT: Spaete, Richard
APPLICANT: Cha, Tai-An
TITLE OF INVENTION: NOVEL HUMAN CYTOMEGALOVIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Luann Cseerr Attorney at Law
STREET: 750 Arimo Avenue
CITY: Oakland
STATE: CA
COUNTRY: USA
ZIP: 94610

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/527.657
FILING DATE: 17-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/926.922
FILING DATE: September 10, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Cseerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: AVIR 11A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-834-1448
TELEFAX: 510-839-7810

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: tol.16
FEATURE:
NAME/KEY: Protein
LOCATION: 1..316
OTHER INFORMATION: /label= U1148

US-09-527-657-22

Query Match 50.8%; Score 31; DB 4; Length 316;
Best Local Similarity 83.3%; Pred. NO. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPOOF 8
:|||||
Db 136 RPOOF 141

RESULT 194
US-09-527-657-22

Patent No. 5212296
APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LERO, KENNETH
J.; O'KEEFE, DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES A.
TEPPERMAN, JAMES M.
TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
CYTOCHROMES
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/569.781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:

US-09-527-657-22

APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
SEQ ID NO: 6
LENGTH: 406
5212296-6

Query Match 50.8%; Score 31; DB 6; Length 406;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RPKPOQFFGL 10
DB 89 RSPQAFGL 98

RESULT 195
US-08-533-669A-8
Sequence 8, Application US/08533669A
Patent No. 5834592

GENERAL INFORMATION:
APPLICANT: Corixa Corporation
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,669A
FILING DATE: 22-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 566 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-533-669A-8

Query Match 50.8%; Score 31; DB 2; Length 566;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFFGL 10
DB 355 RPLRPFIFGM 364

RESULT 196
US-08-511-872-2
Sequence 2, Application US/08511872
Patent No. 5965142
GENERAL INFORMATION:

APPLICANT: Dillon, Davin C.
APPLICANT: Reed, Steven G.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: POLYPEPTIDES AND METHODS FOR THE
TITLE OF INVENTION: DETECTION OF L. tropica INFECTION
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,872
FILING DATE: 04-AUG-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5965142tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 210121.405
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANDBERRY

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 566 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-511-872-2

Query Match 50.8%; Score 31; DB 2; Length 566;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RPKPOQFFGL 10
DB 355 RPLRPFIFGM 364

RESULT 197
US-08-448-489-17
Sequence 17, Application US/08448489
Patent No. 6184022
GENERAL INFORMATION:
APPLICANT: SEIKI, Motoharu
APPLICANT: SATO, Hiroshi
APPLICANT: SHINAGAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/08/448,489.
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 17
LENGTH: 631
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Known Member of
US-08-448-489-17

Query Match 50.8%; Score 31; DB 4; Length 631;

Best Local Similarity 75.0%; Pred. No. 6.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOQFFGL 10
11111111
Db 47 KMOKEFFGL 54

RESULT 198

US-08-704-711A-18
; Sequence 18, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
; US-08-704-711A-18

Query Match 50.8%; Score 31; DB 3; Length 660;
Best Local Similarity 75.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KPOQFFGL 10
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Db 76 KMOKEFFGL 83

RESULT 199
US-08-222-617A-13
; Sequence 13, Application US/08222617A
; Patent No. 5882879

GENERAL INFORMATION:
; APPLICANT: Veenstra, Annemarie E.
; APPLICANT: Martin, Juan F.
; APPLICANT: Garcia, Bruno D.
; APPLICANT: Gutierrez, Sanliago
; APPLICANT: Barredo, Jose L.
; APPLICANT: Von Doehren, Hans
; APPLICANT: Palissa, Harriet
; APPLICANT: Van Liempt, Henk
; APPLICANT: Montenegro, Eduardo P.
; TITLE OF INVENTION: A Method for Influencing Beta-Lactam
; TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,617A
; FILING DATE: 04-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 97,157
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3665 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Acremonium chrysogenum
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..3665
; OTHER INFORMATION: /label= ACVS
; OTHER INFORMATION: /note= "ACV Synthetase from Acremonium
; US-08-222-617A-13

Query Match 50.8%; Score 31; DB 2; Length 3665;
Best Local Similarity 71.4%; Pred. No. 4.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQF 7
11111111
Db 2189 RRPQAF 2195

RESULT 200

US-08-222-617A-4
; Sequence 4, Application US/08222617A
; Patent No. 5882879
; GENERAL INFORMATION:
; APPLICANT: Veenstra, Annemarie E.
; APPLICANT: Martin, Juan F.
; APPLICANT: Garcia, Bruno D.
; APPLICANT: Gutierrez, Sanliago
; APPLICANT: Barredo, Jose L.
; APPLICANT: Von Doehren, Hans
; APPLICANT: Palissa, Harriet

APPLICANT: Van Liempt, Henk
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of Acv Synthetase
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3712 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2555
OTHER INFORMATION:
OTHER INFORMATION: /note= "Xaa-Ala or Ser"
US-08-222-617A-4

Query Match 50.8%; Score 31; DB 2; Length 3712;
Best Local Similarity 71.4%; Pred. No. 4.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPOQF 7
11:111
DB 2189 RRPRAQF 2195

Search completed: April 1, 2002, 16:18:44
Job time: 75 sec


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11AA SEQUENCE 1.0
ID AAP30142 Standard; Protein: 11 AA.
AC ACP90442
XX
XX
DE Sequence of peptides with substance P inhibiting activity.
DT 14-JUN-1992 (first entry)
XX
XX
KW Substance P antagonist; pain therapy; hypertension.
XX
FH Key Location/Qualifiers
FT Modified-site 2 /label=D-P
FT Modified-site 7 /label=D-P
FT Modified-site 7 /label=D-W
FT Misc-difference 8 /label=F,I
FT Modified-site 9 /label=D-W
FT Modified-site 11 /label=M,I
FT Modified-site 11 /note="bonded to NH2"
XX
XX
PN W08301251-A.
XX
PD 14-APR-1983.
XX
PE 09-OCT-1981; 81WO-DE00171.
XX
PR 09-OCT-1981; 81WO-DE00171.
PR 09-OCT-1981; 81EP-0902802.
XX
XX
PA (FERR ) FERRING ARZNEIMITTE.
PA (HORL/) HORIG J.
XX
XX
PI Horig J;
XX
DR WPI; 1983-39155K/16 (39155K).
XX
PT Undeca:peptide derivs. with substance P inhibiting activity -
PT useful for treating pain and hypertension
XX
XX
Claim 2; Page 18; 25pp; German.
XX
XX
CC The peptides of the invention are powerful antagonists of Substance
CC P and so are useful in human and veterinary medicine, for treating
CC pain and hypertension (esp.) chronic conditions. A 10 microm concn.
CC of the peptide produced about 50% inhibition at a Substance P concn.
CC 7.5-20 nanom.
XX
XX
SQ Sequence 11 AA:
XX
AAP30142 Length: 45 April 1, 2002 16:31 Type: P Check: 2107 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVYSOOT HERS$PKPOQ:WQWLM
11AA SEQUENCE 1.0
ID AAP40479 standard; peptide: 11 AA.
AC AAP40479;
XX
XX
DE Substance P analogue.
DT 27-NOV-1991 (first entry)
XX
XX
KW Substance P; analogue; antiinflammatory agent; analgesic.
XX
XX
PN USA481139-A.
XX
PD 06-NOV-1984.
XX
PE 13-APR-1983; 83US-0484646.

```

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PR 13-APR-1983: 83US-0484646.
XX (UYTE-) UNIVERSITY OF TEXAS SYSTEM.
XX
XX PI Folkers K, Ji-Cheng X;
XX DR WPI: 1984-294258/47.
XX
XX PT Peptide analogues of substance P - useful as antagonists, e.g. as
XX antiinflammatory agents and analgesics.
XX PS Claim 1; page 5; 5pp; English.
XX
XX CC The peptide is a D-Arg1, D-Trp7, D-Trp9, Ieu11 analogue of substance
CC P. The peptide is a substance P antagonist with higher activity than
CC known substance P analogues. It may be used as a biological
CC research tool, ophthalmological antiinflammatory agent and analgesic.
XX
XX SO Sequence 11 AA;

AAP40479 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRKPOQ WFWLL

11AA_SEQUENCE 1.0
ID AAP40481 standard; Protein; 11 AA.
XX
XX AC AAP40481;
XX
XX DT 27-NOV-1991 (first entry)
XX
XX DE Substance P analogue.
XX
XX KW Substance P; analogue; antiinflammatory agent; analgesic.
XX
XX PN US4481139-A.
XX
XX PD 06-NOV-1984.
XX
XX PE 13-APR-1983; 83US-0484646.
XX
XX PR 13-APR-1983; 83US-0484646.
XX
XX PA (UYTE-) UNIVERSITY OF TEXAS SYSTEM.
XX
XX PI Folkers K, Ji-Cheng X;
XX
XX DR WPI: 1984-294258/47.
XX
XX PT Peptide analogues of substance P - useful as antagonists, e.g. as
XX antiinflammatory agents and analgesics.
XX PS Claim 4; page 5; 5pp; English.
XX
XX CC The peptide is a D-Arg1, D-Pro2, D-Phe 5, D-Trp7, D-Trp9, Ieu11
XX analogue of substance P. The peptide is a substance P antagonist
XX with higher activity than known substance P analogues. It may be
XX used as a biological research tool, ophthalmological antiinflammatory
XX agent and analgesic.
XX
XX SO Sequence 11 AA;

AAP40481 Length: 45 April 1, 2002 16:31 Type: P Check: 1633 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRKPOQ WFWLL

11AA_SEQUENCE 1.0
ID AAP61480 standard; peptide; 11 AA.
XX
XX AC AAP61480;
XX
XX DT 22-AUG-1991 (first entry)

```

XX DE Sequence of undeca peptide substance P1.
 XX KM Hypertension therapy; sleep disorder; anti-stress agent.
 XX FH Key Location/Qualifiers
 FT MISC-difference 11
 FT /label= Met-NH2
 XX PN DD29593-A.
 XX PD 13-NOV-1985.
 XX PF 28-NOV-1984; 84DD-0269954.
 XX PR 28-NOV-1984; 84DD-0269954.
 XX PA (DEAK) AKAD WISSENSCHAFT DDR.
 XX PI Oehme P, Hecht K, Wachtel E, Roske I, Kolometsewa IA;
 PI Alirapetjan M, Blenert M, Vogt WE, Hlase H, Gores E, Poppel M;
 PI Nieber K, Bergmann J;
 XX DR WPI; 1986-069387/11.
 XX PS Cpds. having N-terminal sequences of undeca:peptide substance P -
 PT are medicinal agents with anti-stress activity
 XX CC Claim 1; Page 1; 15pp; German.
 XX CC The inventors claim an antistress compound which contains the N-
 CC terminal SQ of AAP61480, pref. Arg-Pro-Lys-Pro-X (X= COOH or NH2).
 CC Compared with the full undecapeptide they have much reduced
 CC side effects (acute hypotension, spastic effects on the ileum and
 CC histamine release from peritoneal mast cells).
 XX SQ Sequence 11 AA;
 AAP61480 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
 1 SQARNBQCE ZGHSQILKMF PSTWVSGOT HERSRPRPQ FPGLM
 11AA_SEQUENCE 1.0
 ID AAP70431 standard; protein; 129 AA.
 XX AC AAP70431;
 XX DT 17-JAN-1991 (first entry)
 XX DE Human beta-preprotachykinin.
 XX KW Preprotachykinin; substance P; neurokinin A; tachykinin;
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Region 20..56
 FT /label=claimed polypeptide
 FT Region 1..126
 FT /label=claimed polypeptide
 FT Region 111..126
 FT /label=claimed polypeptide
 XX PN W08707643-A.
 XX PD 17-DEC-1987.
 XX PF 03-JUN-1987; 87WO-GB00382.
 XX PR 03-JUN-1986; 86GB-0013431.
 XX PA (RESE) RESEARCH CORPORATION LTD.
 XX

PI Harnar AJ, Pascall J, Mckeown A;
 XX DR WPI: 1987-362730/51.
 XX DR N-PSDB: AAN70688.
 XX XX New DNA sequence coding for the new polypeptide preprotachykinin -
 PT a precursor for substance P, etc., useful as neurotransmitters,
 PT diagnostic reagents, etc.
 XX PS Claim 1; page 15; 25pp; English.
 XX CC Beta-preprotachykinin includes sequences identical to tachykinins, eg
 CC substance P, neurokinin A, or other biologically active peptides, eg
 CC neuropeptide K. These peptides are, eg neurotransmitters, hormones,
 CC analgesics and anti-inflammatory. The polypeptides can be used
 CC as reagents in RIA, eg to monitor or diagnose carcinoid syndrome.
 XX SQ Sequence 129 AA;
 AAP70431 Length: 163 April 1, 2002 16:31 Type: P Check: 5532 ..
 1 SQARNBQCE ZGHSQILKMF PSTWVSGOT HERSMKTLVA LAVFLVSTO
 51 LFAEITGAND DLNWSWDYD SDQIKELPE PEPHLLQRIA RRPKQOEFQ
 101 LMGKRDADSS IEQVALLKA LYGHQISHK RHRTDSFVGL MGKRALNSVA
 151 YERSAMQWYE RRR
 11AA_SEQUENCE 1.0
 ID AAP80312 standard; protein; 11 AA.
 XX AC AAP80312;
 XX DT 14-SEP-1990 (first entry)
 XX DE Sequence of neuropeptide substance P which binds with polypeptide
 DE receptor for bombesin type polypeptides.
 XX KW Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
 KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
 KW substance P.
 XX OS Swiss 3T3 cells.
 XX FH Key Location/Qualifiers
 FT MISC-difference 11
 FT /label=OTHER
 FT /note="Met-NH2"
 XX PN W08807551-A.
 XX PD 06-OCT-1988.
 XX PF 31-MAR-1988; 88WO-GB00255.
 XX PR 25-NOV-1987; 87GB-0027638.
 XX PA (IMCR) IMPERIAL CANCER RES.
 XX PI Rosengurt E, Zachary I, Woll P;
 XX DR WPI; 1988-292842/41.
 XX PT New polypeptide receptor for bombesin type polypeptide(s) -
 PT is isolated from surface of Swiss 3T3 cells, and antibodies and
 XX antagonists are useful for treating uncontrolled cell proliferation
 PS Disclosure; Table 2; 42pp; English.
 XX CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
 CC cells which binds selectively with polypeptides of the bombesin type and
 CC binds with antagonist A and antagonist D. Antagonist A is a

CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX

SO Sequence 11 AA;

AAP80312 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRKPQO FFGILM

!!AA_SEQUENCE 1.0

ID AAP80313 standard; protein; 11 AA.

AC AAP80313;

DT 14-SEP-1990 (first entry)

DE Sequence of neuropeptide antagonist A which binds with polypeptide
DE receptor for bombesin type polypeptides.

XX Spantide; neuropeptide; polypeptide receptor; bombesin; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
XX antagonist A.

OS Swiss 3T3 cells.

XX Key Location/Qualifiers

FT Misc-difference 1 /label=OTHER

FT /note="DArg"

FT Misc-difference 2 /label=OTHER

FT /note="DPro"

FT Misc-difference 7 /label=OTHER

FT /note="DTrp"

FT Misc-difference 9 /label=OTHER

FT /label=OTHER

FT /note="DTrp"

FT Misc-difference 11 /label=OTHER

FT /note="Leu-NH2"

FT

XX W08807551-A.

PN

XX 06-OCT-1988.

PD

XX 31-MAR-1988; 88WO-GB00255.

PF

XX 25-NOV-1987; 87GB-0027638.

PR

XX (IMCR) IMPERIAL CANCER RES.

XX

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XX

CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX

SO Sequence 11 AA;

AAP80313 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRKPQO WFWLL

!!AA_SEQUENCE 1.0

ID AAP80314 standard; protein; 11 AA.

AC AAP80314;

DT 14-SEP-1990 (first entry)

DE Sequence of neuropeptide antagonist B which binds with polypeptide
DE receptor for bombesin type polypeptides.

XX Spantide; neuropeptide; polypeptide receptor; bombesin; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
XX antagonist B.

OS Swiss 3T3 cells.

XX Key Location/Qualifiers

FT Misc-difference 1 /label=OTHER

FT /note="DArg"

FT Misc-difference 7 /label=OTHER

FT /note="DTrp"

FT Misc-difference 1 /label=OTHER

FT /label=OTHER

FT /note="DTrp"

FT Misc-difference 14 /label=OTHER

FT /note="Leu-NH2"

FT

XX W08807551-A.

PN

XX 06-OCT-1988.

PD

XX 31-MAR-1988; 88WO-GB00255.

PF

XX 25-NOV-1987; 87GB-0027638.

PR

XX (IMCR) IMPERIAL CANCER RES.

XX

XX

XX

XX

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XX

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XX

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XX

New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation

XX Disclosure; Table 2; 42pp; English.

XX

CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC (D-Arg1, D-Pro2, D-Trp7,9, Leu11) substance P. It is also known as
CC (D-Pro2) spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as (D-Phe5) spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.

XX Sequence 11 AA;

AAP80314 Length: 45 Apr11 1, 2002 16:31 Type: P Check: 2062 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRPQQ WFWLL

!!AA_SEQUENCE 1.0

ID AAP80315 standard; protein; 11 AA.

XX AC AAP80315;

XX DT 14-SEP-1990 (first entry)

XX DE Sequence of neuropeptide antagonist C which binds with polypeptide
DE receptor for bombesin type polypeptides.

XX KW Spantide: neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
XX antagonist C.

XX OS Swiss 3T3 cells.

XX FH Key Location/Qualifiers

FT Misc-difference 2 /label=OTHER

FT FT /note="DPro"

FT Misc-difference 7 /label=OTHER

FT FT /note="DPhe"

FT Misc-difference 1 /label=OTHER

FT FT /note="DTrp"

FT Misc-difference 11 /label=OTHER

FT FT /note="Met-NH2"

XX PN WO8807551-A.

XX PD 06-OCT-1988.

XX PF 31-MAR-1988; 88WO-GB00255.

XX PR 25-NOV-1987; 87GB-0027638.

XX PA (IMCR) IMPERIAL CANCER RES.

XX PI Rosengurt E, Zachary I, Woll P;

XX DR WPI; 1988-292842/41.

XX PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
XX antagonists are useful for treating uncontrolled cell proliferation
XX PS Disclosure; Table 2; 42pp; English.

CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC (D-Arg1, D-Pro2, D-Trp7,9, Leu11) substance P. It is also known as
CC (D-Pro2) spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as (D-Phe5) spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.

XX Sequence 11 AA;

AAP80315 Length: 45 Apr11 1, 2002 16:31 Type: P Check: 1410 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRPQQ FFWLM

!!AA_SEQUENCE 1.0

ID AAP80316 standard; protein; 11 AA.

XX AC AAP80316;

XX DT 14-SEP-1990 (first entry)

XX DE Sequence of neuropeptide antagonist D which binds with polypeptide
DE receptor for bombesin type polypeptides.

XX KW Spantide: neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides.

XX OS Swiss 3T3 cells.

XX FH Key Location/Qualifiers

FT Misc-difference 1 /label=OTHER

FT FT /note="DArg"

FT Misc-difference 5 /label=OTHER

FT FT /note="DPhe"

FT Misc-difference 7 /label=OTHER

FT FT /note="DTrp"

FT Misc-difference 9 /label=OTHER

FT FT /note="DTrp"

FT Misc-difference 11 /label=OTHER

FT FT /note="Leu-NH2"

XX PN WO8807551-A.

XX PD 06-OCT-1988.

XX PF 31-MAR-1988; 88WO-GB00255.

XX PR 25-NOV-1987; 87GB-0027638.

XX PA (IMCR) IMPERIAL CANCER RES.

XX PI Rosengurt E, Zachary I, Woll P;

XX DR WPI; 1988-292842/41.

XX PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
XX antagonists are useful for treating uncontrolled cell proliferation

PS Disclosure; Table 2; 42pp; English.
XX
CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX
SQ Sequence 11 AA;

AAP80316 Length: 45 April 1, 2002 16:31 Type: P Check: 1633 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRKPFPQ WFWLL

!!AA_SEQUENCE 1.0
ID AAP80317 standard; protein: 11 AA.

AC AAP80317;

DT 14-SEP-1990 (first entry)

DE Sequence of neuropeptide antagonist E which binds with polypeptide
DE receptor for bombesin type polypeptides.

KW Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist E.

OS Swiss 3T3 cells.

FH Key Location/Qualifiers

FT Misc-difference 2 /label=OTHER

FT /note="DPro"

FT Misc-difference 7 /label=OTHER

FT /note="DTrp"

FT Misc-difference 9 /label=OTHER

FT /note="DTrp"

FT Misc-difference 11 /label=OTHER

FT /note="Met-NH2"

PN W08807551-A.

PD 06-OCT-1988.

PF 31-MAR-1988; 88WO-GB00255.

PR 25-NOV-1987; 87GB-0027638.

PA (IMCR) IMPERIAL CANCER RES.

PI Rosengurt E, Zachary I, Woll P;

DR WPI. 1988-292842/41.

PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
XX

PS Disclosure; Table 2; 42pp; English.
XX
CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX
SQ Sequence 11 AA;

AAP80317 Length: 45 April 1, 2002 16:31 Type: P Check: 2107 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRKPFPQ WFWLL

!!AA_SEQUENCE 1.0
ID AAP80320 standard; protein: 11 AA.

AC AAP80320;

DT 14-SEP-1990 (first entry)

DE Sequence of neuropeptide antagonist H which binds with polypeptide
DE receptor for bombesin type polypeptides.

KW Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist H.

OS Swiss 3T3 cells.

FH Key Location/Qualifiers

FT Misc-difference 1 /label=OTHER

FT /note="DArg"

FT Misc-difference 2 /label=OTHER

FT /note="DPro"

FT Misc-difference 7 /label=OTHER

FT /note="DPhe"

FT Misc-difference 9 /label=OTHER

FT /note="DHIS"

FT Misc-difference 11 /label=OTHER

FT /note="Met-NH2"

PN W08807551-A.

PD 06-OCT-1988.

PF 31-MAR-1988; 88WO-GB00255.

PR 25-NOV-1987; 87GB-0027638.

PA (IMCR) IMPERIAL CANCER RES.

PI Rosengurt E, Zachary I, Woll P;

DR WPI. 1988-292842/41.

PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
XX

PT is isolated from surface of Swiss 3T3 cells, and antibodies and
 PT antagonists are useful for treating uncontrolled cell proliferation
 XX
 PS Disclosure; Table 2; 42pp; English.

CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
 CC cells which binds selectively with polypeptides of the bombesin type and
 CC binds with antagonist A and antagonist D. Antagonist A is a
 CC commercially available structural variant of substance P, known as
 CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
 CC [D-Pro2] spantide. Antagonist B is also commercially available structural
 CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
 CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
 CC substance P antagonists (see AAP80313-80322) were tested for their
 CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
 CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
 CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
 CC potent than either A or D. Spantide (B) had no antagonist activity even
 CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
 CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
 CC growth is associated with disorders of proteins of the bombesin family.

XX Sequence 11 AA;

AAP80320 Length: 45 April 1, 2002 16:31 Type: P Check: 765 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FPHLM

11AA_SEQUENCE 1.0

ID AAR05856 standard; protein; 11 AA.

AC AAR05856;

DT 07-SEP-1990 (first entry)

DE D-arginine 1, D-proline 2, D-tyrtycophan 7,9, Leucine 11,
 DE -substance P angiotensin antagonist.

KW Angiotensin; ectopic hormone; mas oncogene; cancer;
 KW neuroblastoma; neuroendocrine.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 1 /label-Dextrorotatory form.

FT Modified-site 2 /label-Dextrorotatory form.

FT Modified-site 7 /label-Dextrorotatory form.

FT Modified-site 9 /label-Dextrorotatory form.

XX Modified-site /label-Dextrorotatory form.

PN WO9003181-A.

PD 05-APR-1990.

PF 22-SEP-1989; 89WO-0001121.

PR 24-SEP-1988; 88GB-0022483.

PA (MED1-) MED RES COUNCIL.

PI Hanley MR, Joedert M;

DR WPI; 1990-132106/17.

XX Use of substances which block the activity of angiotensin
 PT for the treatment or prevention of tumour development or ectopic
 PT hormone prodn.

PS Claim 8; Page 19; 23pp; English.

CC Peptide blocks biological activity of angiotensin and is active
 CC against the mas oncogene, retarding tumour growth, esp
 CC neuroendocrine and neuroblastoma tumours.

XX Sequence 11 AA;

AAR05856 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPPQO WWLL

11AA_SEQUENCE 1.0

ID AAR13162 standard; Protein; 11 AA.

AC AAR13162;

DT 10-OCT-1991 (first entry)

DE Static acid-bonded polypeptide (2).

KW Static acid; cataract; immune disorder.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminally glycosylated by 5-acetamido-

FT 2,4,7,8,9-penta-O-acetyl-1,3,5-deoxy-beta-

FT D-glycero-D-galactono-1,4-lactone" /note= "N-terminally glycosylated by 5-acetamido-

PN JP03151398-A.

PD 27-JUN-1991.

PF 06-NOV-1989; 89JP-0288560.

PR 06-NOV-1989; 89JP-0288560.

PA (MECT-) MECT KK.

DR WPI; 1991-233839/32.

PT New static acid derivs. bonded to physiologically active

PT polypeptide - for treatment of cataracts, immune disorders etc.

PS Example 4; Page 6; 7pp; Japanese.

CC The prod. has prolonged half-life and is used as a pharmaceutical

CC for treatment of various diseases, such as cataract and immune

CC disorders. It comprises a peptide, N-terminally glycosylated by

CC (opt. acetylated) static acid.

XX See also AAR12932, AAR13162 and AAR13201.

XX Sequence 11 AA;

AAR13162 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FPGLM

11AA_SEQUENCE 1.0

ID AAR11144 standard; Protein; 11 AA.

AC AAR11144;

DT 21-MAY-1991 (first entry)

DE Substance P analogue.

KW Anti-proliferation agent; neurogenetic inflammation; fibroblasts;

XX agonist.

XX Synthetic.

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FH Key Location/Qualifiers
FT Modified-site 1
FT /label= D-Arg
FT Modified-site 7
FT /label= D-Trp
FT Modified-site 9
FT /label= D-Trp
FT Modified-site 9..10
FT /label= non-peptide bond
FT /note= "Trp-L[CH2NH]-Trp"
FT Modified-site 11
FT /label= Nle

XX WO9102745-A.
XX 07-MAR-1991.
XX
XX 16-AUG-1990; 90WO-US04633.
XX
XX 16-AUG-1989; 89US-0394727.
XX
XX (TULA ) TULANE E FUND ADMINISTRA.
XX
XX Coy DH, Moreau JP;
XX
XX WPI; 1991-087240/12.
XX
XX Modified linear peptide analogue of natural substance P - acts as
XX competitive inhibitor of substance P and is used for treating
XX neuro genetic inflammation and as anti-proliferative agent.
XX
XX Claim 11; Page 34; 40pp; English.
XX
XX The peptide has a non-peptide bond introduced between Trp9 and
XX Leu10. This may alternatively be positioned between Leu10 and
XX Nle11. For prepn., a benzhydrylamine resin was coupled to Boc-Leu.
XX Boc-Leu aldehyde was dissolved in 5 ml DMF and added to the resin
XX FFA salt suspension followed by addn. of NaCNBH3 and stirring for
XX one hour. The remaining amino acids were then coupled successively.
XX In tests the peptide inhibited P-stimulated amylase release from
XX pancreatic acini.
XX See also AAR1143.
XX
XX Sequence 11 AA;
SQ
AAR1144 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..
1 SQARNDBCOE ZGHSQILKMF PSTWYSQOT HERSRPPQO WFWLL
!!AA_SEQUENCE 1.0
ID AAR1854 standard; peptide; 11 AA.
XX
XX AAR1854;
AC
XX
XX 09-JUL-1991 (first entry)
XX
XX Undecapeptide substance P.
DE
XX Undecapeptide; pharmaceutical; stress; sleep.
XX
XX Synthetic.
XX
XX DD285097-A.
XX
XX 05-DEC-1990.
XX
XX 21-JUN-1989; 89DD-0329831.
XX
XX 21-JUN-1989; 89DD-0329831.
XX
XX (DEAK ) INST WIRKSTOFF AKAD.
XX (PARF ) VEB CHEM BITTERFELD.
XX

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PI Beyermann M, Bienenert M, Egler H, Haupke K, Krause E;
PI Schwarz J, Walz H;
XX
XX WPI; 1991-133498/19.
XX
XX Undeca-peptide substance pharmaceutical intermediate prepn. - by
XX forming di:peptide between nitro-arginine and proline and
XX reacting with polymer-bound non-peptide
XX
XX Calim 1; Page 1; 8pp; German.
XX
XX The peptide is prepared by solid phase synthesis.
XX It can be used in the preparation of pharmaceuticals which can be
XX used to treat certain stress-induced disturbances of the sleep
XX profile.
XX
XX Sequence 11 AA;
SQ
AAR1854 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBCOE ZGHSQILKMF PSTWYSQOT HERSRPPQO FFGLM
!!AA_SEQUENCE 1.0
ID AAR21966 standard; peptide; 11 AA.
XX
XX AAR21966;
AC
XX
XX 25-JUN-1992 (first entry)
XX
XX Cyclic substance P [D Cys 5, hCys 10].
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Disulfide-bond 5..10
XX Misc-difference 10
XX /label= homocysteine
XX Modified-site 5
XX /note="D form"
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 11; Page 22; 35pp; English.
XX
XX The peptide is the tachykinin agonist substance P with a D Cys
XX residue substituted at position 5 and a homocys at position 9,
XX with a disulphide bond formed between them, making the peptide
XX cyclic. The peptide was synthesised by standard solid phase
XX synthesis. Neuronal accumulation of beta-amyloid may be treated
XX by administration of tachykinin agonists. The peptide can reduce
XX the neurotoxic effects of a beta-amyloid related polypeptide on
XX cultured neurons. The peptide and its analogues are useful for
XX controlling diseases characterised by beta amyloid accumulation
XX in the brain such as Alzheimer's disease and Down's syndrome.
XX

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CC See also AAR21932-75.
XX
SQ Sequence 11 AA;

AAR21966 Length: 45 April 1, 2002 16:31 Type: P Check: 704 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRPCQ FFCXM

11AA_SEQUENCE 1.0
ID AAR21965 standard; Peptide; 11 AA.

XX
AC AAR21965;

XX
DT 25-JUN-1992 (first entry)

XX
DE Cyclic substance P [Cys 5,9].

XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
syndrome; hereditary cerebral haemorrhage.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Disulfide-bond 5..9

XX
PN WO9202248-A.

XX
PD 20-FEB-1992.

XX
PE 29-JUL-1991; 91WO-US05323.

XX
PR 27-JUL-1990; 90US-0559173.

XX
PA (CHIL-) CHILDRENS MED CENT.

XX
PI Yankner BA;

XX
DR WPI; 1992-079804/10.

XX
PT Treatment of neuronal accumulation of beta-amyloid - using
tachykinin agonists e.g. substance P, physalaemin and neurokinin
B, for treating Alzheimer's disease, Downs syndrome, etc.

XX
PS Claim 11; Page 22; 35pp; English.

XX
CC The peptide is the tachykinin agonist substance P with Cys
residues substituted at positions 5 and 9, with a disulphide bond
formed between them, making the peptide cyclic. The peptide was
synthesised by standard solid phase synthesis. Neuronal accumu-
lation of beta-amyloid may be treated by administration of tachykinin
agonists. The peptide can reduce the neurotoxic effects of a beta-
amyloid related polypeptide on cultured neurons. The peptide and
its analogues are useful for controlling diseases characterised by
beta amyloid accumulation in the brain such as Alzheimer's disease
and Down's syndrome.
See also AAR21932-75.

XX
SQ Sequence 11 AA;

AAR21965 Length: 45 April 1, 2002 16:31 Type: P Check: 4 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRPCQ FFCXM

11AA_SEQUENCE 1.0

ID AAR21967 standard; Peptide; 11 AA.

XX
AC AAR21967;

XX
DT 25-JUN-1992 (first entry)

XX
DE Cyclic substance P [Cys 5,11].

XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;

KW syndrome; hereditary cerebral haemorrhage.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers
FT Disulfide-bond 5..11

XX
PN WO9202248-A.

XX
PD 20-FEB-1992.

XX
PE 29-JUL-1991; 91WO-US05323.

XX
PR 27-JUL-1990; 90US-0559173.

XX
PA (CHIL-) CHILDRENS MED CENT.

XX
PI Yankner BA;

XX
DR WPI; 1992-079804/10.

XX
PT Treatment of neuronal accumulation of beta-amyloid - using
tachykinin agonists e.g. substance P, physalaemin and neurokinin
B, for treating Alzheimer's disease, Downs syndrome, etc.

XX
PS Claim 11; Page 22; 35pp; English.

XX
CC The peptide is the tachykinin agonist substance P with Cys
residues substituted at positions 5 and 11, with a disulphide bond
formed between them, making the peptide cyclic. The peptide was
synthesised by standard solid phase synthesis. Neuronal accumu-
lation of beta-amyloid may be treated by administration of tachykinin
agonists. The peptide can reduce the neurotoxic effects of a beta-
amyloid related polypeptide on cultured neurons. The peptide and
its analogues are useful for controlling diseases characterised by
beta amyloid accumulation in the brain such as Alzheimer's disease
and Down's syndrome.
See also AAR21932-75.

XX
SQ Sequence 11 AA;

AAR21967 Length: 45 April 1, 2002 16:31 Type: P Check: 9726 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRPCQ FFCXM

11AA_SEQUENCE 1.0

ID AAR21960 standard; Peptide; 11 AA.

XX
AC AAR21960;

XX
DT 25-JUN-1992 (first entry)

XX
DE Cyclic substance P [hcys 5,9].

XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
syndrome; hereditary cerebral haemorrhage.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers

FT MISC-difference 5 /label= OTHER

FT MISC-difference 9 /note= "OTHER = homocysteine"

FT MISC-difference 9 /label= OTHER

XX
PN WO9202248-A.

XX
PD 20-FEB-1992.

XX
PE 29-JUL-1991; 91WO-US05323.

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PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 11; Page 22; 35pp; English.
XX
XX The peptide is the tachykinin agonist, substance P with
CC homocysteine substituted at positions 5 and 9, with a disulphide
CC bond formed between them making the peptide cyclic. The
CC peptide was synthesised by standard solid phase synthesis.
CC Neuronal accumulation of beta-amyloid may be treated by administ-
CC ration of tachykinin agonists. The peptide can reduce the neuro-
CC toxic effects of a beta-amyloid related polypeptide on cultured
CC neurons. The peptide and its analogues are useful for controlling
CC diseases characterised by beta amyloid accumulation in the brain
CC such as Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
XX Sequence 11 AA;
SQ
AAR21960 Length: 45 April 1, 2002 16:31 Type: P Check: 1726 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRKPXQ FFXLM
!!AA_SEQUENCE 1.0
ID AAR21961 standard; peptide; 11 AA.
XX
XX AAR21961;
XX
XX 25-JUN-1992 (first entry)
XX
XX Cyclic substance P [Hcys 5,11].
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 5 //label= OTHER
XX //note= "OTHER = homocysteine"
XX
XX Misc-difference 11 //label= OTHER
XX //note= "OTHER = homocysteine"
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 11; Page 22; 35pp; English.

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XX
XX The peptide is the tachykinin agonist, substance P with
CC homocysteine substituted at positions 5 and 11, with a disulphide
CC bond formed between them making the peptide cyclic. The
CC peptide was synthesised by standard solid phase synthesis.
CC Neuronal accumulation of beta-amyloid may be treated by administ-
CC ration of tachykinin agonists. The peptide can reduce the neuro-
CC toxic effects of a beta-amyloid related polypeptide on cultured
CC neurons. The peptide and its analogues are useful for controlling
CC diseases characterised by beta amyloid accumulation in the brain
CC such as Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
XX Sequence 11 AA;
SQ
AAR21961 Length: 45 April 1, 2002 16:31 Type: P Check: 1490 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRKPXQ FFXLM
!!AA_SEQUENCE 1.0
ID AAR21932 standard; peptide; 9 AA.
XX
XX AAR21932;
XX
XX 25-JUN-1992 (first entry)
XX
XX Substance P (1-9) fragment.
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 9; Page 21; 35pp; English.
XX
XX The peptide is a tachykinin agonist consisting of residues 1-9 of
CC substance P. The peptide was synthesised by standard solid phase
CC synthesis. Analogues of the peptide, with C-terminal deletions down
CC to substance P (1-4) were also synthesised. Neuronal accumulation of
CC beta-amyloid may be treated by administration of these tachykinin
CC agonists. The peptides reduce the neurotoxic effects of a beta-
CC amyloid related polypeptide on cultured neurons. The peptide and
CC its analogues are useful for controlling diseases characterised by
CC beta amyloid accumulation in the brain such as Alzheimer's disease
CC and Down's syndrome.
CC See also AAR21933-75.
XX
XX Sequence 9 AA;
SQ
AAR21932 Length: 43 April 1, 2002 16:31 Type: P Check: 3913 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRKPXQ FFXLM
!!AA_SEQUENCE 1.0
ID AAR21934 standard; Protein; 11 AA.

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XX AC AAR21934:
XX DT 25-JUN-1992 (first entry)
XX DE Substance P [Tyr7] and fragment (7-11) [Tyr 7].
XX DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX DE syndrome; hereditary cerebral haemorrhage.
XX OS Synthetic.
XX PN WO9202248-A.
XX PD 20-FEB-1992.
XX PF 29-JUL-1991: 91WO-US05323.
XX PR 27-JUL-1990: 90US-0559173.
XX PA (CHIL-) CHILDRENS MED CENT.
XX PI Yankner BA;
XX DR WPI; 1992-079804/10.
XX PT Treatment of neuronal accumulation of beta-amyloid - using
XX PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX PS Claim 10; Page 21; 35pp; English.
XX CC The peptide is the tachykinin agonist substance P with a Tyr
XX CC residue substituted at position 7. The peptide was synthesised
XX CC by standard solid phase synthesis. A N-terminal deleted peptide
XX CC (7-11) with the Tyr substitution was also synthesised. Neuronal
XX CC accumulation of beta-amyloid may be treated by administration
XX CC of tachykinin agonists. The peptides can reduce the neurotoxic
XX CC effects of a beta-amyloid related polypeptide on cultured neurons.
XX CC The peptide and its analogues are useful for controlling diseases
XX CC characterised by beta amyloid accumulation in the brain such as
XX CC Alzheimer's disease and Down's syndrome.
XX CC See also AAR21932-75.
XX SQ Sequence 11 AA;
AAR21934 Length: 45 April 1, 2002 16:31 Type: P Check: 1501 ..
1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO YFGLM
11AA_SEQUENCE 1.0
ID AAR21935 standard; Protein; 11 AA.
XX AC AAR21935;
XX DT 25-JUN-1992 (first entry)
XX DE Substance P [Pro 9] or [D-Pro 9].
XX DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX DE syndrome; hereditary cerebral haemorrhage.
XX OS Synthetic.
XX PN WO9202248-A.
XX PD 20-FEB-1992.
XX PF 29-JUL-1991: 91WO-US05323.
XX FT Modified-site 9 Location/Qualifiers
XX FT /note= "either L or D form"
XX PN WO9202248-A.
XX PD 20-FEB-1992.
XX PF 29-JUL-1991: 91WO-US05323.

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XX PR 27-JUL-1990: 90US-0559173.
XX PA (CHIL-) CHILDRENS MED CENT.
XX PI Yankner BA;
XX DR WPI; 1992-079804/10.
XX PT Treatment of neuronal accumulation of beta-amyloid - using
XX PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX PS Claim 10; Page 21; 35pp; English.
XX CC The peptide is the tachykinin agonist substance P with a Pro (D/L)
XX CC residue substituted at position 9. The peptide was synthesised
XX CC by standard solid phase synthesis. Neuronal accumulation of
XX CC beta-amyloid may be treated by administration of tachykinin
XX CC agonists. The peptide can reduce the neurotoxic effects of a beta-
XX CC amyloid related polypeptide on cultured neurons. The peptide and
XX CC its analogues are useful for controlling diseases characterised by
XX CC beta amyloid accumulation in the brain such as Alzheimer's disease
XX CC and Down's syndrome.
XX CC See also AAR21932-75.
XX SQ Sequence 11 AA;
AAR21935 Length: 45 April 1, 2002 16:31 Type: P Check: 1109 ..
1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FPLM
11AA_SEQUENCE 1.0
ID AAR21936 standard; Protein; 11 AA.
XX AC AAR21936;
XX DT 25-JUN-1992 (first entry)
XX DE Substance P or (7-11) [Ethionine 11].
XX DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX DE syndrome; hereditary cerebral haemorrhage.
XX OS Synthetic.
XX PN WO9202248-A.
XX PD 20-FEB-1992.
XX PF 29-JUL-1991: 91WO-US05323.
XX PR 27-JUL-1990: 90US-0559173.
XX PA (CHIL-) CHILDRENS MED CENT.
XX PI Yankner BA;
XX DR WPI; 1992-079804/10.
XX PT Treatment of neuronal accumulation of beta-amyloid - using
XX PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX PS Claim 10; Page 21; 35pp; English.
XX CC The peptide is the tachykinin agonist substance P with an Ethionine
XX CC residue substituted at position 11. The peptide was synthesised

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CC by standard solid phase synthesis. An N-terminal deleted peptide
CC (7-11) with the same substitution was also synthesised. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptides can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA;

AAR21936 Length: 45 April 1, 2002 16:31 Type: P Check: 1217 ..

1 SQARNDBCOE ZGHSQILKMF PSTWYSQOT HERSRKPQO FFGIX

!!AA_SEQUENCE 1.0
ID AAR21937 standard; Protein; 11 AA.
XX
AC AAR21937;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P or (7-11) [Norleucine 11].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KM syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 11 /label= OTHER
FT /note= "OTHER = Nle"
XX
PM WO9202248-A.
XX
PD 20-FEB-1992.
XX
PF 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
DR WPI; 1992-079804/10.
XX
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX
PS Claim 10; Page 21; 35pp; English.
XX
XX
CC The peptide is the tachykinin agonist substance P with a Norleucine
CC residue substituted at position 11. The peptide was synthesised
CC by standard solid phase synthesis. An N-terminal deleted peptide
CC (7-11) with the same substitution was also synthesised. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptides can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA;

AAR21937 Length: 45 April 1, 2002 16:31 Type: P Check: 677 ..

1 SQARNDBCOE ZGHSQILKMF PSTWYSQOT HERSRKPQO FFGIL

!!AA_SEQUENCE 1.0
ID AAR21938 standard; Protein; 11 AA.
XX
AC AAR21938;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [Me-Leu 10].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KM syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 10 /label= OTHER
FT /note= "OTHER = Me-Leu"
XX
PM WO9202248-A.
XX
PD 20-FEB-1992.
XX
PF 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
DR WPI; 1992-079804/10.
XX
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX
PS Claim 10; Page 21; 35pp; English.
XX
XX
CC The peptide is the tachykinin agonist substance P with Me-Leu
CC substituted at position 10. The peptide was synthesised
CC by standard solid phase synthesis. Neuronal accumulation of
CC beta-amyloid may be treated by administration of tachykinin
CC agonists. The peptides can reduce the neurotoxic effects of a
CC beta-amyloid related polypeptide on cultured neurons. The peptide
CC and its analogues are useful for controlling diseases characterised
CC by beta amyloid accumulation in the brain such as Alzheimer's
CC disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA;

AAR21938 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCOE ZGHSQILKMF PSTWYSQOT HERSRKPQO FFGIM

!!AA_SEQUENCE 1.0
ID AAR21940 standard; Protein; 11 AA.
XX
AC AAR21940;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [Pro 10].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KM syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
PM WO9202248-A.
XX
PD 20-FEB-1992.

XX 29-JUL-1991: 91WO-US05323.
XX
XX 27-JUL-1990: 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX
XX Claim 10: Page 21: 35pp; English.
XX
XX The peptide is the tachykinin agonist substance P with a Proline
XX residue substituted at position 10. The peptide was
XX synthesised by standard solid phase synthesis. Neuronal
XX accumulation of beta-amyloid may be treated by administration of
XX tachykinin agonists. The peptide can reduce the neurotoxic effects
XX of a beta-amyloid related polypeptide on cultured neurons. The
XX peptide and its analogues are useful for controlling diseases
XX characterised by beta amyloid accumulation in the brain such as
XX Alzheimer's disease and Down's syndrome.
XX See also AAR21932-75.
XX
XX Sequence 11 AA;
XX
XX AAR21940 Length: 45 April 1, 2002 16:31 Type: P Check: 898 ..
XX
XX 1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGPM
XX
XX !!AA_SEQUENCE 1.0
XX ID AAR21942 standard; Protein; 11 AA.
XX
XX AAR21942;
XX
XX 25-JUN-1992 (first entry)
XX
XX Substance P [Memet 11].
XX
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX
XX Location/Qualifiers
XX FT Misc-difference 11
XX FT /label= OTHER
XX FT /note= "OTHER = Methyl Methionine"
XX
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX
XX
XX 29-JUL-1991: 91WO-US05323.
XX
XX 27-JUL-1990: 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10: Page 21: 35pp; English.
XX

CC The peptide is the tachykinin agonist substance P with a methyl
CC methionine residue substituted at position 11. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
XX Sequence 11 AA;
XX
XX AAR21942 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
XX
XX 1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLM
XX
XX !!AA_SEQUENCE 1.0
XX ID AAR21944 standard; Protein; 11 AA.
XX
XX AAR21944;
XX
XX 25-JUN-1992 (first entry)
XX
XX Substance P [Pro 11].
XX
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX WO9202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991: 91WO-US05323.
XX
XX 27-JUL-1990: 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10: Page 21: 35pp; English.
XX
XX
XX The peptide is the tachykinin agonist substance P with a Proline
XX residue substituted at position 11. The peptide was
XX synthesised by standard solid phase synthesis. Neuronal
XX accumulation of beta-amyloid may be treated by administration of
XX tachykinin agonists. The peptide can reduce the neurotoxic effects
XX of a beta-amyloid related polypeptide on cultured neurons. The
XX peptide and its analogues are useful for controlling diseases
XX characterised by beta amyloid accumulation in the brain such as
XX Alzheimer's disease and Down's syndrome.
XX See also AAR21932-75.
XX
XX Sequence 11 AA;
XX
XX AAR21944 Length: 45 April 1, 2002 16:31 Type: P Check: 857 ..
XX
XX 1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLP
XX
XX !!AA_SEQUENCE 1.0
XX ID AAR21946 standard; Protein; 11 AA.
XX
XX AAR21946;
XX

DT 25-JUN-1992 (first entry)
 XX
 DE Substance P [Me-Phe 8].
 XX
 KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Misc-difference 8 Location/Qualifiers
 FT /label= OTHER
 FT /note= "OTHER = Methyl phenylalanine"
 XX
 PN W09202248-A.
 PD 20-FEB-1992.
 XX
 XX 29-JUL-1991; 91WO-US05323.
 PF
 XX 27-JUL-1990; 90US-0559173.
 PR
 XX (CHIL-) CHILDRENS MED CENT.
 PA
 XX Yankner BA;
 PI
 XX WPI, 1992-079804/10.
 DR
 XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 XX
 PS Claim 10; Page 21; 35pp; English.
 XX
 CC The peptide is the tachykinin agonist substance P with a methyl
 CC phenylalanine residue substituted at position 8. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC tachykinin agonists. The peptide can reduce the neurotoxic effects
 CC of a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.
 CC
 CC Sequence 11 AA;
 SQ
 AAR21946 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
 1 SQARNDBCOE ZGHSQILKMF PSTWYSQOT HERSRPKPOQ FFGLM
 !!AA_SEQUENCE 1.0
 ID AAR21951 standard; Peptide; 11 AA.
 XX
 AC AAR21951;
 XX
 DF 25-JUN-1992 (first entry)
 XX
 DE Substance P [Glu 3].
 XX
 XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 XX
 PN W09202248-A.
 PD 20-FEB-1992.
 XX
 XX 29-JUL-1991; 91WO-US05323.
 PF
 XX 27-JUL-1990; 90US-0559173.
 PR

PA (CHIL-) CHILDRENS MED CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI, 1992-079804/10.
 XX
 XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 XX
 PS Claim 10; Page 21; 35pp; English.
 XX
 CC The peptide is the tachykinin agonist substance P with a glutamic
 CC acid residue substituted at position 5. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC tachykinin agonists. The peptide can reduce the neurotoxic effects
 CC of a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.
 CC
 CC Sequence 11 AA;
 SQ
 AAR21951 Length: 45 April 1, 2002 16:31 Type: P Check: 254 ..
 1 SQARNDBCOE ZGHSQILKMF PSTWYSQOT HERSRPKPOQ FFGLM
 !!AA_SEQUENCE 1.0
 ID AAR21954 standard; Protein; 11 AA.
 XX
 AC AAR21954;
 XX
 DT 25-JUN-1992 (first entry)
 XX
 DE Substance P [Me-Gly 9].
 XX
 KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Misc-difference 9 Location/Qualifiers
 FT /label= OTHER
 FT /note= "OTHER = Methyl glycine"
 XX
 PN W09202248-A.
 PD 20-FEB-1992.
 XX
 XX 29-JUL-1991; 91WO-US05323.
 PF
 XX 27-JUL-1990; 90US-0559173.
 PR
 XX (CHIL-) CHILDRENS MED CENT.
 PA
 XX Yankner BA;
 PI
 XX WPI, 1992-079804/10.
 DR
 XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 XX
 PS Claim 10; Page 22; 35pp; English.
 XX
 CC The peptide is the tachykinin agonist substance P with a methyl
 CC glycine residue substituted at position 9. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC tachykinin agonists. The peptide can reduce the neurotoxic effects

FT /note= "OTHER = p-Chloro-phenylalanine"
 XX WO9202248-A.
 XX 20-FEB-1992.
 PD
 XX 29-JUL-1991; 91WO-US05323.
 PF
 XX 27-JUL-1990; 90US-0559173.
 PR
 XX (CHIL-) CHILDRENS MED CENT.
 PA
 XX Yankner BA;
 PI
 XX WPI: 1992-079804/10.
 DR
 XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.
 XX
 PS Claim 10; Page 22; 35pp: English.
 CC The peptide is the tachykinin agonist, substance P fragment
 CC with p-Chloro-phenylalanine residues substituted at positions 7 and
 CC 8. The peptide was synthesised by standard solid phase synthesis.
 CC Neuronal accumulation of beta-amyloid may be reduced by administ-
 CC ration of tachykinin agonists. The peptide can be treated by neuro-
 CC toxic effects of a beta-amyloid related polypeptide on cultured
 CC neurons. The peptide and its analogues are useful for controlling
 CC diseases characterised by beta amyloid accumulation in the brain
 CC such as Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.
 XX
 SQ Sequence 11 AA;
 AAR21963 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPKPQO FFGLM

!!AA_SEQUENCE 1.0
 ID AAR28442 standard; peptide: 11 AA.
 AC AAR28442;
 XX
 DT 22-MAR-1993 (first entry)
 XX
 DE Substance P.
 XX
 KW NK1 receptor; tumour; malignant glioma; pheochromocytoma;
 KW paraganglia; small cell lung cancer; nerve regeneration; lymphoma;
 KW granuloma; Crohn's disease.
 XX
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 11
 FT /note= "amdated"
 FT
 XX WO9218536-A.
 PM
 XX 29-OCT-1992.
 PD
 XX 22-APR-1992; 92MO-US03307.
 PF
 XX 22-APR-1991; 91EP-0200955.
 PR
 XX (MLCW) MALLINCKRODT MEDICAL INC.
 PA
 XX Bakker WH, Hagen PM, Krenning EP, Lamberts SWJ, Visser TJ;
 PI
 XX WPI: 1992-382047/46.
 DR
 XX Detection and localisation of tissues with neurokinine-1 receptors
 PT

PT - for detecting and treating tumours having neurokinine-1
 PT receptors e.g. malignant glioma, small cell lung cancer etc.
 XX
 PS Disclosure; Page 4; 22pp; English.
 XX
 CC Substance P or its Tyr0 deriv. is a preferred peptide having a
 CC selective affinity to neurokinine-1 receptors which (when
 CC labelled with a radioactive isotope) can be used in imaging methods.
 CC A generic formula for preferred peptides is AAR28441. Such peptides
 CC are thus useful in diagnosis and treatment of conditions that are
 CC related to NK1 receptors and in visualising NK1 receptors on certain
 CC tissues. See also AAR28443-R28446.
 CC
 SQ Sequence 11 AA;
 AAR28442 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPKPQO FFGLM

!!AA_SEQUENCE 1.0
 ID AAR28443 standard; peptide: 11 AA.
 AC AAR28443;
 XX
 DT 22-MAR-1993 (first entry)
 XX
 DE Neurokinine 1 ligand #1.
 XX
 KW NK1 receptor; tumour; malignant glioma; pheochromocytoma;
 KW paraganglia; small cell lung cancer; nerve regeneration; lymphoma;
 KW granuloma; Crohn's disease.
 XX
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 9
 FT /label= Megly
 FT Modified-site 11
 FT /label= OTHER
 FT /note= "Met(O)2-NH2"
 FT
 XX WO9218536-A.
 PM
 XX 29-OCT-1992.
 PD
 XX 22-APR-1992; 92MO-US03307.
 PF
 XX 22-APR-1991; 91EP-0200955.
 PR
 XX (MLCW) MALLINCKRODT MEDICAL INC.
 PA
 XX Bakker WH, Hagen PM, Krenning EP, Lamberts SWJ, Visser TJ;
 PI
 XX WPI: 1992-382047/46.
 DR
 XX Detection and localisation of tissues with neurokinine-1 receptors
 PT - for detecting and treating tumours having neurokinine-1
 PT receptors e.g. malignant glioma, small cell lung cancer etc.
 XX
 PS Disclosure; Page 4; 22pp; English.
 XX
 CC This peptide or its Tyr0 deriv. is a preferred peptide having a
 CC selective affinity to neurokinine-1 receptors which (when
 CC labelled with a radioactive isotope) can be used in imaging methods.
 CC A generic formula for preferred peptides is AAR28441. Such peptides
 CC are thus useful in diagnosis and treatment of conditions that are
 CC related to NK1 receptors and in visualising NK1 receptors on certain
 CC tissues. See AAR28442-R28446.
 CC
 SQ Sequence 11 AA;
 AAR28443 Length: 45 April 1, 2002 16:31 Type: P Check: 980 ..

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1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRKPOQ FFMML
!!AA_SEQUENCE 1.0
ID AAR28445 standard; peptide: 11 AA.
XX
AC AAR28445;
XX
DT 22-MAR-1993 (first entry)
XX
DE Neurokinine 1 ligand #3.
XX
KW NK1 receptor; tumour; malignant glioma; pheochromocytoma;
KW paraganglioma; small cell lung cancer; nerve regeneration; lymphoma;
KW granuloma; Crohn's disease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 11
FT /note= "amidated"
XX
PN W09218536-A.
XX
PD 29-OCT-1992.
XX
PF 22-APR-1992; 92WO-US03307.
XX
PR 22-APR-1991; 91EP-0200955.
XX
PA (MLCW ) MALLINCKRODT MEDICAL INC.
XX
PI Bakker WH, Hagen PM, Krenning EP, Lamberts SWJ, Visser TJ;
DR WPI; 1992-382047/46.
XX
PT Detection and localisation of tissues with neurokinine-1 receptors
PT - for detecting and treating tumours having neurokinine-1
PT receptors e.g. malignant glioma, small cell lung cancer etc.
XX
PS Disclosure: Page 4; 22pp; English.
XX
CC This peptide or its Tyro deriv. is a preferred peptide having a
CC selective affinity to neurokinine-1 receptors which (when
CC labelled with a radioactive isotope) can be used in imaging methods.
CC A generic formula for preferred peptides is AAR28441. Such peptides
CC are thus useful in diagnosis and treatment of conditions that are
CC related to NK1 receptors and in visualising NK1 receptors on certain
CC tissues. See AAR28442-R28446.
XX
SQ Sequence 11 AA;
AAR28445 Length: 45 April 1, 2002 16:31 Type: P Check: 1520 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRKPOQ FYGLM
!!AA_SEQUENCE 1.0
ID AAR28680 standard; Protein; 24 AA.
XX
AC AAR28680;
XX
DT 22-MAR-1993 (first entry)
XX
DE Galanin(1-12)-Pro-Spanide amide (C7).
XX
KW Receptor; Substance P; insulin; growth hormone;
KW acetylcholine; dopamine; somatostatin; noradrenaline;
KW endocrinology; food intake; neurology; psychiatry;
KW Alzheimer-type senile dementia; schizophrenia;
KW intestinal diseases.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers

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FT Misc-difference 14
FT /note= "D-form residue"
FT Misc-difference 20
FT /note= "D-form residue"
FT Misc-difference 22
FT /note= "D-form residue"
FT Peptide 1..12
FT /label= galanin(1-12)
FT Peptide 14..24
FT /label= spanide
XX
PN EP514361-A.
XX
PD 19-NOV-1992.
XX
PF 14-MAY-1992; 92EP-0850108.
XX
PR 15-MAY-1991; 91SE-0001472.
XX
PA (ASTRA ) ASTRA AB.
XX
PI Ahren B, Bartfal T, Consolo S, Hoekfelt T, Land T;
PI Langel U, Lindskog S, Wiesenfeld-Hallin Z;
DR WPI; 1992-384184/47.
XX
PT New galanin antagonist peptide(s) - used for treating
PT Alzheimer's-type senile dementia, schizophrenia, analgesia and
PT intestinal diseases
XX
PS Disclosure: Page 7; 21pp; English.
XX
CC The C-terminal of this peptide is amidated. MW= 2827; IC50= 0.2nM.
CC The peptides given in AAR28679-90 are used to treat disorders in
CC mammals caused by the function of galanin at its receptor. The
CC peptides may be useful in the regulation of insulin release, growth
CC hormone release, acetylcholine release, dopamine release, substance
CC P release, somatostatin release and noradrenaline release. They are
CC useful in endocrinology, food intake, neurology and psychiatry, and
CC to treat Alzheimer-type senile dementia, schizophrenia, intestinal
CC diseases, and in analgesia. Dosage is 0.01-1000, pref. 0.1-1000
CC microg/kg body wt.
XX
SQ Sequence 24 AA;
AAR28680 Length: 58 April 1, 2002 16:31 Type: P Check: 344 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSGWTLSN AGYLLGPRPK
51 PQQWFML
!!AA_SEQUENCE 1.0
ID AAR28392 standard; peptide: 11 AA.
XX
AC AAR28392;
XX
DT 18-MAR-1993 (first entry)
XX
DE Bradykinin receptor antagonist CT-0008.
XX
KW Bradykinin receptor antagonist; heterodimer; higher oligomer;
KW potency; duration; CP-0088; burns; migraine; shock CNS injury;
KW rhinitis; premature labour; inflammatory arthritis; homodimer;
KW inflammatory bowel disease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "D-form residue"
FT Misc-difference 2
FT /note= "D-form residue"
FT Misc-difference 7

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PT /note= "D-form residue"
 FT Misc-difference 9
 FT /note= "D-form residue"
 FT Modified-site 11
 FT /label= Nle
 PN WO9217201-A.
 PD 15-OCT-1992.
 XX
 PF 30-MAR-1992; 92MO-US02431.
 XX
 PR 01-APR-1991; 91US-0677391.
 PR 27-MAR-1992; 92US-0859582.
 XX
 PA (CORT-) CORTECH INC.
 XX
 PI Allen LG, Blodgett JK, Cheronis JC, Eubanks SR, Nguyen KT,
 PI Whalley ET;
 XX
 DR WPI: 1992-365995/44.
 XX
 PT Bradykinin antagonists comprising linked bradykinin antagonist
 PT chains - are for treatment of post-operative pain, asthma and
 PT aseptic shock
 XX
 PS Disclosure: Page 76; 109pp; English.
 XX
 CC The sequence given is a bradykinin receptor antagonist which can form
 CC homo- or heterodimers or higher oligomers. It demonstrates greater
 CC potency and/or duration of action than the parent peptide itself.
 CC Bradykinin receptors antagonists such as this can be used in the
 CC treatment of burns, perioperative pain, migraine and other forms of
 CC pain, shock CNS injury, asthma, rhinitis, premature labour,
 CC inflammatory arthritis, inflammatory bowel disease etc.
 CC
 SQ Sequence 11 AA;
 AAR28392 Length: 45 April 1, 2002 16:31 Type: P Check: 1785 ..
 1 SQARNDBCE ZGHSQILKMF PSTWYVSQOT HERSRPRKPN FFWLX
 !!AA_SEQUENCE 1.0
 ID AAR45229 standard; Protein; 492 AA.
 XX
 AC AAR45229;
 XX
 DT 20-JUN-1994 (first entry)
 XX
 DE APP-REP 751 amyloid precursor protein/reporter protein.
 XX
 KW Amyloid precursor protein; APP; beta amyloid protein; BAP;
 KW detection; Alzheimer's disease; Down's syndrome.
 XX
 OS Homo sapiens.
 OS
 PN AU9338358-A.
 PD 04-NOV-1993.
 XX
 PF 03-MAY-1993; 93AU-0038358.
 XX
 PR 01-MAY-1992; 92US-0877675.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Jacobsen JS, Vitek MP;
 XX
 DR WPI: 1993-406194/51.
 DR N-PSDB; AA054257.
 XX
 PT New mutant forms of amyloid precursor protein - for detecting
 PT cpds. that modify activity of enzymes involved in precursor

PT cleavage, also new nucleic acid encoding them
 XX
 PS Claim 5; Figure 7; 66pp; English.
 XX
 CC This mutant form of amyloid precursor protein comprises from the 5'
 CC to the 3' end a sequence encoding a marker and either (1) a
 CC sequence encoding the N-terminus of an amyloid precursor protein
 CC (APP) up to, but not including, the nucleotides encoding the beta
 CC amyloid protein (BAP) domain or (2) the BAP domain. Recombinant
 CC polypeptides generated from this proteins coding sequence can be
 CC used to detect drugs or compounds that inhibit/augment the
 CC activity of proteolytic enzymes which cleave APP to generate BAP
 CC fragments (deposition of which occurs in patients with Alzheimers
 CC disease and Down's syndrome).
 XX
 SQ Sequence 492 AA;
 AAR45229 Length: 526 April 1, 2002 16:31 Type: P Check: 2172 ..
 1 SQARNDBCE ZGHSQILKMF PSTWYVSQOT HERSMLPGLA LLLAAWTAR
 51 ALEVPIDGNA GLAEPQIAM FCGRLNMHMN VQNGKWDSDP SGTKICIDRK
 101 EGILQYCOEV YPELQITNVV EANOPTVION WCKRGRKCK TDPHFVTPYR
 151 CLVGEFVSDA LLVPDKCKFL HQERNDVOCET HLHWHYAKE TCSEKSTNLH
 201 DYGLMLPCGI DKFRGYEFCV CPLAESDNV DSADAEEDSD DVMWGCADTD
 251 YADGSEDKV EVAEEBEVAE VEEBEADDE DDEGDGEVEE EAEPEYEAT
 301 ERTTSIATTT TTTESVVEV VREVCSEQA TGPCRAMISR WYEDVTEGKC
 351 APFFYGGCGG NNNNDTEY CMAVCGSAIP TTAASTPDAY DYLEPKRQ
 401 QPFGLMGSLT NIKTEISEV KMDAEFRHS GYEVHOKLV FPAEDVGSNK
 451 GAILGLMWG VVIATYIVIT LVMLKKKQYT SIHNGVEVD AAVTPERHL
 501 SKMQNGYEN PTYKFEQMO NYGCFM
 !!AA_SEQUENCE 1.0
 ID AAR32798 standard; peptide; 12 AA.
 XX
 AC AAR32798;
 XX
 DT 17-JUN-1993 (first entry)
 XX
 DE Tyr-1 substance P used for binding assay.
 XX
 KW human substance P receptor protein; SP; neurotransmitter;
 KW neuromodulator; central nervous system; peripheral nervous system;
 KW gastrointestinal disorders; Inflammation; Immune disease.
 XX
 OS Homo sapiens.
 OS
 PN WO9303137-A.
 PD 18-FEB-1993.
 XX
 PF 05-AUG-1992; 92MO-US06532.
 XX
 PR 07-AUG-1991; 91US-0741200.
 XX
 PA (UNIV) UNIV WASHINGTON.
 XX
 PI Krause JE;
 XX
 DR WPI: 1993-076495/09.
 XX
 PT New human substance P receptor protein and DNA encoding it - used
 PT e.g. for screening substance P antagonists

PS Example; Page 8; 40pp; English.

CC This sequence represents Tyr-1 substance P and was used in its
CC 125-Iodinated form in a ligand binding assay of COS-7 cells
CC transfected with substance P receptor coding plasmids (see AA037210).

XX Sequence 12 AA;

AA037298 Length: 46 April 1, 2002 16:31 Type: P Check: 4680 ..

1 SQARNDBQCE ZGHSQILKMF PSTWVVSQOT HERSRPRPQO QRFGLM

!!AA_SEQUENCE 1.0
ID AAR42646 standard; peptide; 11 AA.

XX AAR42646;

DT 19-APR-1994 (first entry)

XX Neurokinin 1 receptor affinity-contg. peptide (Substance P).

XX Neurokinin 1; somatostatin; receptor; cytokine; growth factor;

KM hormone; intra-operativ; tumour; low energy gamma photon;

XX radionuclide.

XX Synthetic.

OS Synthetic.

XX Key

FT Modified-site

FT /note= "the C-terminal is amidated"

XX W09318797-A.

XX 30-SEP-1993.

XX 24-MAR-1993; 93WO-US02772.

XX 25-MAR-1992; 92EP-0200848.

XX (MLCW) MALLINCKRODT MEDICAL INC.

XX Doedens BJ, Ensing GJ, Panek KJ;

XX WPI; 1993-320461/40.

XX Intra-operatively detecting and locating tumour tissues - using

PT specific peptide(s) labelled with low energy gamma photon

PT emitting radionuclide

XX Disclosure; Page 4; 31pp; English.

XX The method of intraoperatively detecting and locating tumoral

CC tissues makes use of peptides having selective neurokinin 1

CC receptor affinity (AAR42644; generic formula: AAR42646-R42650;

CC specific examples), peptides having selective somatostatin

CC receptor affinity (AAR42645; generic formula: AAR42651-R42660;

CC specific examples), and peptides selected from cytokines,

CC growth factors and hormones.

XX Sequence 11 AA;

AA042646 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBQCE ZGHSQILKMF PSTWVVSQOT HERSRPRPQO FFXGLM

!!AA_SEQUENCE 1.0

ID AAR42647 standard; peptide; 11 AA.

XX AAR42647;

DT 19-APR-1994 (first entry)

XX Neurokinin 1 receptor affinity-contg. peptide.

XX Neurokinin 1; somatostatin; receptor; cytokine; growth factor;

KM hormone; intra-operativ; tumour; low energy gamma photon;

XX radionuclide.

XX Synthetic.

OS Synthetic.

XX Key

FT Modified-site

FT /label= Megly

FT Modified-site

FT /note= "Met is Met(O2); the C-terminal is amidated"

XX W09318797-A.

XX 30-SEP-1993.

XX 24-MAR-1993; 93WO-US02772.

XX 25-MAR-1992; 92EP-0200848.

XX (MLCW) MALLINCKRODT MEDICAL INC.

XX Doedens BJ, Ensing GJ, Panek KJ;

XX WPI; 1993-320461/40.

XX Intra-operatively detecting and locating tumour tissues - using

PT specific peptide(s) labelled with low energy gamma photon

PT emitting radionuclide

XX Disclosure; Page 5; 31pp; English.

XX The method of intraoperatively detecting and locating tumoral

CC tissues makes use of peptides having selective neurokinin 1

CC receptor affinity (AAR42644; generic formula: AAR42646-R42650;

CC specific examples), peptides having selective somatostatin

CC receptor affinity (AAR42645; generic formula: AAR42651-R42660;

CC specific examples), and peptides selected from cytokines,

CC growth factors and hormones.

XX Sequence 11 AA;

AA042647 Length: 45 April 1, 2002 16:31 Type: P Check: 1453 ..

1 SQARNDBQCE ZGHSQILKMF PSTWVVSQOT HERSRPRPQO FFXGLM

!!AA_SEQUENCE 1.0

ID AAR42649 standard; peptide; 11 AA.

XX AAR42649;

DT 19-APR-1994 (first entry)

XX Neurokinin 1 receptor affinity-contg. peptide.

XX Neurokinin 1; somatostatin; receptor; cytokine; growth factor;

KM hormone; intra-operativ; tumour; low energy gamma photon;

XX radionuclide.

XX Synthetic.

OS Synthetic.

XX Key

FT Modified-site

FT /note= "the C-terminal is amidated"

XX W09318797-A.

XX 30-SEP-1993.

XX 24-MAR-1993; 93WO-US02772.

XX 25-MAR-1992; 92EP-0200848.


```
XX (MLCW ) MALLINCKRODT MEDICAL INC.
PA
XX Doedens BJ, Ensing GJ, Panek KT;
PI
XX WPI; 1993-320461/40.
DR
XX Intra-operatively detecting and locating tumour tissues - using
PT specific peptides) labelled with low energy gamma photon
PT emitting radionuclide
PS
XX Disclosure; Page 5; 31pp; English.
PS
XX The method of intraoperatively detecting and locating tumoral
CC tissues makes use of peptides having selective neurokinin 1
CC receptor affinity (AAR42644: generic formula; AAR42646-R42650:
CC specific examples), peptides having selective somatostatin
CC receptor affinity (AAR42645: generic formula; AAR42651-R42660:
CC specific examples), and peptides selected from cytokines,
CC growth factors and hormones.
CC
XX Sequence 11 AA:
SQ
AAR42649 Length: 45 April 1, 2002 16:31 Type: P Check: 1520 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRKPQO FYGLM
!!AA_SEQUENCE 1.0
ID AAR85243 standard; peptide; 11 AA.
AC AAR85243;
XX
DT 18-AUG-1997 (first entry)
DE
XX Substance P peptide.
DE
XX
XX Ligand; antibody; receptor; SELEX; random library; amplification; PCR;
KW Systematic Evolution of Ligands by EXponential enrichment; primer;
KW polymerase chain reaction; structure; mimicry; substance P; tachykinin;
KW neuropeptide; rheumatoid arthritis; atherosclerosis; cancer;
KW diabetic retinopathy.
XX
OS Synthetic.
OS
FH Key Location/Qualifiers
FT Modified-site 11 /note= "contains C-terminal NH2 group"
FT
XX W09530775-A1.
PN
XX 16-NOV-1995.
PD
XX
XX 03-MAY-1995; 95WO-US05600.
PF
XX
XX 21-DEC-1994; 94US-0361795.
PR 06-MAY-1994; 94US-0238863.
PR 24-MAY-1994; 94US-0248632.
PR 09-SEP-1994; 94US-0303362.
PR 11-JUN-1990; 90US-0536428.
PR 10-JUN-1991; 91US-0714131.
PR 21-OCT-1992; 92US-0964624.
XX
XX (UYRE-) UNIV RES CORP.
PA
XX Allen P, Doudna JA, Feigon J, Gold L, Nieuwlandt D;
PI Schneider DJ, Sullenger BA, Wecker M;
XX
XX WPI; 1995-404132/51.
DR
XX Systematic evolution of ligands by exponential enrichment - for
PT identifying nucleic acid ligands used in the treatment of, e.g. type
PT B insulin resistance and HIV
XX
```

```
PS Example 10; Fig 8; 209pp; English.
XX
XX The invention relates to a novel method of isolating ligands that bind
CC to target proteins e.g. antibodies or receptors, which bind other
CC proteins or ligands. The method, designated Systematic Evolution of
CC Ligands by EXponential enrichment (SELEX), comprises generating a library
CC of random oligonucleotide sequences, about 40-60 nucleotides in length,
CC and binding these sequences to the target proteins. After removal of
CC unbound material, the remaining bound nucleotides sequences are amplified
CC e.g. by PCR, and the newly amplified material is bound again with the
CC target protein. This cycle continues until a sufficiently pure
CC oligonucleotide sequence is isolated. The method allows the isolation of
CC oligonucleotide sequences which structurally mimic the target protein's
CC ligand. Ligands AAT06098-130 are examples of nucleic acid ligands which
CC bind the tachykinin-family neuropeptide Substance P (this sequence). The
CC new ligands were split into 2 groups based on their affinities for
CC Substance P. Class 1 ligands had binding affinities up to 2 micromolar
CC whereas class 2 ligands bound at above 2 micromolar. This sequence
CC represents the consensus of the class 1 ligands. The ligands can be
CC used to block the activity of Substance P and is useful in the treatment
CC of e.g. rheumatoid arthritis, atherosclerosis, diabetic retinopathy or
CC cancer.
CC
XX Sequence 11 AA:
SQ
AAR85243 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRKPQO FYGLM
!!AA_SEQUENCE 1.0
ID AAR85244 standard; peptide; 12 AA.
AC AAR85244;
XX
DT 18-AUG-1997 (first entry)
DE
XX Substance P analogue peptide Cys-SP.
DE
XX
XX Ligand; antibody; receptor; SELEX; random library; amplification; PCR;
KW Systematic Evolution of Ligands by EXponential enrichment; primer;
KW polymerase chain reaction; structure; mimicry; substance P; tachykinin;
KW neuropeptide; rheumatoid arthritis; atherosclerosis; cancer;
KW diabetic retinopathy.
XX
OS Synthetic.
OS
FH Key Location/Qualifiers
FT Modified-site 1 /note= "Ac-Arg"
FT
XX W09530775-A1.
PN
XX 16-NOV-1995.
PD
XX
XX 03-MAY-1995; 95WO-US05600.
PF
XX
XX 21-DEC-1994; 94US-0361795.
PR 06-MAY-1994; 94US-0238863.
PR 24-MAY-1994; 94US-0248632.
PR 09-SEP-1994; 94US-0303362.
PR 11-JUN-1990; 90US-0536428.
PR 10-JUN-1991; 91US-0714131.
PR 21-OCT-1992; 92US-0964624.
XX
XX (UYRE-) UNIV RES CORP.
PA
XX Allen P, Doudna JA, Feigon J, Gold L, Nieuwlandt D;
PI Schneider DJ, Sullenger BA, Wecker M;
XX
XX WPI; 1995-404132/51.
DR
XX Systematic evolution of ligands by exponential enrichment - for
PT identifying nucleic acid ligands used in the treatment of, e.g. type
PT
```

PT B Insulin resistance and HIV
 XX
 PS Example 11; Fig 8; 209pp; English.
 XX
 CC The invention relates to a novel method of isolating ligands that bind
 CC to target proteins e.g. antibodies or receptors, which bind other
 CC proteins or ligands. The method, designated Systematic Evolution of
 CC Ligands by Exponential enrichment (SELEX), comprises generating a library
 CC of random oligonucleotide sequences, about 40-60 nucleotides in length,
 CC and binding these sequences to the target proteins. After removal of
 CC unbound material, the remaining bound nucleotides sequences are amplified
 CC e.g. by PCR, and the newly amplified material is bound again with the
 CC target protein. This cycle continues until a sufficiently pure
 CC oligonucleotide sequence is isolated. The method allows the isolation of
 CC oligonucleotide sequences which structurally mimic the target protein's
 CC ligand. This peptide represents an analogue of Substance P (AAR85243) in
 CC which the N-terminal amine has been acylated in order to determine
 CC whether this functional group interacts with nucleic acid ligands binding
 CC substance P (see AAR06098-130). The ligands can be used to block the
 CC activity of substance P and is useful in the treatment of e.g. rheumatoid
 CC arthritis, atherosclerosis, diabetic retinopathy or cancer.
 CC
 SO Sequence 12 AA;
 AAR85244 Length: 46 April 1, 2002 16:31 Type: P Check: 3804 ..
 1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRPQQ FGLMCG
 !!AA_SEQUENCE 1.0
 ID AAW09003 standard; peptide; 11 AA.
 XX
 AC AAW09003;
 DT
 XX 03-MAR-1997 (first entry)
 DE Substance P analogue, acts as substance P antagonist.
 XX
 XX Analogue; substance P; spantide; non-peptide bond;
 KW competitive inhibitor; receptor; neurogenic inflammation;
 KW rheumatoid arthritis; ulcerative colitis; eczema; Crohn's disease;
 KW anti-proliferative agent; small cell lung carcinoma; fibroblast.
 XX
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Modified-site 6..7 /label= Gln-psi[CH2-NH]-Phe
 FT /note= "Opt. non-peptide linkage"
 FT 7..8 /label= Phe-psi[CH2-NH]-Phe
 FT /note= "Opt. non-peptide linkage"
 FT 8..9 /label= Phe-psi[CH2-NH]-Gly
 FT /note= "Opt. non-peptide linkage"
 FT Modified-site 9..10 /label= Gly-psi[CH2-NH]-Leu
 FT /note= "Opt. non-peptide linkage"
 FT 10..11 /label= Leu-psi[CH2-NH]-Leu
 FT /note= "Position of claimed non-peptide linkage"
 FT 11 /note= "Amidated C-terminal"
 FT
 FT
 XX US5410019-A.
 PN
 XX
 PD 25-APR-1995.
 XX
 XX 24-SEP-1987; 87US-0100571.
 PF
 XX 30-MAR-1992; 92US-0860675.
 PR 24-SEP-1987; 87US-0100571.
 PR 25-MAR-1988; 88US-0173311.
 PR 08-JUN-1988; 88US-0204171.

PR 16-JUN-1988; 88US-0207759.
 PR 23-SEP-1988; 88US-0248771.
 PR 14-OCT-1988; 88US-0257998.
 PR 09-DEC-1988; 88US-0282328.
 PR 02-MAR-1989; 89US-0317941.
 PR 16-AUG-1989; 89US-0394727.
 XX
 PA (TULANE) TULANE EDUCATIONAL FUND.
 XX
 PI Coy DH, Moreau J;
 XX
 DR WPI: 1995-169633/22.
 XX
 PT Novel linear peptide substance P analogues - useful as substance P
 CC antagonists, for treating neurogenic inflammation
 CC
 PS Claim 3; Column 19, 16pp; English.
 XX
 XX The sequences given in AAW09003-04 represent analogues of substance P
 CC and spantide, respectively. These analogues comprise a non-peptide
 CC bond between an amino acid residue of the active site, which occurs
 CC in the C-terminal half of the peptide, and an adjacent amino acid
 CC residue. They act as competitive inhibitors of the naturally
 CC occurring peptide by binding to its receptor. These peptides may be
 CC used in the treatment of diseases involving neurogenic inflammation,
 CC e.g. rheumatoid arthritis, ulcerative colitis, eczema and Crohn's
 CC disease. They are also useful as anti-proliferative agents, in
 CC the treatment of small cell lung carcinoma or disorders involving the
 CC proliferation of fibroblasts.
 CC
 SO Sequence 11 AA;
 AAW09003 Length: 45 April 1, 2002 16:31 Type: P Check: 677 ..
 1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRPQQ FGLL
 !!AA_SEQUENCE 1.0
 ID AAW09004 standard; peptide; 11 AA.
 XX
 AC AAW09004;
 DT
 XX 03-MAR-1997 (first entry)
 DE Spantide analogue, acts as substance P antagonist.
 XX
 XX Analogue; substance P; spantide; non-peptide bond;
 KW competitive inhibitor; receptor; neurogenic inflammation;
 KW rheumatoid arthritis; ulcerative colitis; eczema; Crohn's disease;
 KW anti-proliferative agent; small cell lung carcinoma; fibroblast.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Modified-site 6..7 /label= Gln-psi[CH2-NH]-Trp
 FT /note= "Opt. non-peptide bond, Claim 7"
 FT Misc-difference 7 /note= "D-form residue"
 FT Modified-site 7..8 /label= Trp-psi[CH2-NH]-Phe
 FT /note= "Opt. non-peptide bond, Claim 6"
 FT 8..9 /label= Phe-psi[CH2-NH]-Trp
 FT /note= "Opt. non-peptide bond"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 9..10 /label= Trp-psi[CH2-NH]-Leu
 FT /note= "Opt. non-peptide bond, Claim 4"
 FT 10..11 /label= Leu-psi[CH2-NH]-Nle
 FT Modified-site

FT Modified-site /note="Opt. non-peptide bond, Claim 5"
 FT 11
 FT /label=Nle
 FT /note="Amidated C-terminal"
 XX US5410019-A.
 PN
 XX 25-APR-1995.
 PD
 XX
 PF 24-SEP-1987; 87US-0100571.
 XX
 PR 30-MAR-1992; 92US-0860675.
 PR 24-SEP-1987; 87US-0100571.
 PR 25-MAR-1988; 88US-0173311.
 PR 08-JUN-1988; 88US-0204171.
 PR 16-JUN-1988; 88US-0207759.
 PR 23-SEP-1988; 88US-0248771.
 PR 14-OCT-1988; 88US-0257998.
 PR 09-DEC-1988; 88US-0282328.
 PR 02-MAR-1989; 89US-0317941.
 PR 16-AUG-1989; 89US-0394727.
 XX
 PA (TULA) TULANE EDUCATIONAL FUND.
 XX
 PI Coy DH, Moreau J;
 XX WPI: 1995-169633/22.
 DR
 XX Novel linear peptide substance P analogues - useful as substance P
 PT antagonists, for treating neurogenic inflammation
 PS
 XX Claim 4-7; Column 20; 16pp: English.
 CC The sequences given in AAM09003-04 represent analogues of substance P
 CC and spantide, respectively. These analogues comprise a non-peptide
 CC bond between an amino acid residue of the active site, which occurs
 CC in the C-terminal half of the peptide, and an adjacent amino acid
 CC residue. They act as competitive inhibitors of the naturally
 CC occurring peptide by binding to its receptor. These peptides may be
 CC used in the treatment of diseases involving neurogenic inflammation,
 CC e.g. Rheumatoid arthritis, ulcerative colitis, eczema and Crohn's
 CC disease. They are also useful as anti-proliferative agents, in
 CC the treatment of small cell lung carcinoma or disorders involving the
 CC proliferation of fibroblasts.
 CC
 XX Sequence 11 AA:
 SO
 AAM09004 Length: 45 April 1, 2002 16:31 Type: P Check: 2602 ..
 1 SQARNDBCQE ZGHSQILKMF PSTWVYSQOT HERSRPKPOQ WFWLX
 !!AA_SEQUENCE 1.0
 ID AAR7310 standard; peptide: 11 AA.
 XX
 AC AAR7310;
 XX
 DT 08-MAR-1996 (first entry)
 DT
 XX
 DE Substance P.
 XX
 OS
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT 11
 FT Modified-site /note="amidated"

XX US5434158-A.
 PN
 XX 18-JUL-1995.
 PD
 XX
 PF 26-APR-1994; 94US-0233487.
 XX
 PR 26-APR-1994; 94US-0233487.
 PR
 XX (MERI) MERCK & CO INC.
 PA
 XX Shah SK;
 PI
 XX WPI: 1995-268290/35.
 DR
 XX New 1'-subst. spiro-indoline-3,4'-piperidine derivs. - useful as
 PT selective neurokinin-3 antagonists, e.g. for treating CNS disorders,
 PT migraine or esp. asthma.
 XX
 PS Disclosure; Column 1; 16pp: English.
 XX
 CC This sequence represents Substance P. This sequence, and those shown in
 CC AAR7311 and AAR7312 are tachykinins. These three sequences are
 CC pharmacologically active neuropeptides, and are neurokinin receptor
 CC agonists. Neurokinin receptors are widely distributed throughout the
 CC mammalian nervous system, circulatory system and peripheral tissues.
 CC Neurokinin receptors are involved in sensory perception. These
 CC sequences were used in the design and testing of neurokinin antagonists.
 CC These antagonists could be used in the treatment of conditions
 CC characterised by overstimulation of tachykinin receptors. The
 CC antagonists can also be used, for the treatment of neurodegenerative
 CC disorders (e.g. Alzheimer's disease), demyelinating diseases (e.g.
 CC multiple sclerosis), respiratory diseases, optalmic diseases, addiction
 CC disorders, adverse immune reactions, gastrointestinal disorders, bladder
 CC function disorders, fibrosing and collagen diseases. The antagonists can
 CC also be used as diagnostic agents.
 CC
 XX Sequence 11 AA:
 SO
 AAR7310 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
 1 SQARNDBCQE ZGHSQILKMF PSTWVYSQOT HERSRPKPOQ FFGIM
 !!AA_SEQUENCE 1.0
 ID AAR74982 standard; peptide: 11 AA.
 XX
 AC AAR74982;
 XX
 DT 19-JAN-1996 (first entry)
 DT
 XX
 DE [D-Arg1, D-Phe5, D-Trp7,9, Leu11]-Substance P.
 XX
 XX Vasoactive intestinal peptide; VIP; conjunctiva; goblet cell;
 KW mucous secretion; keratoconjunctivitis; Sjogren's syndrome;
 KW Vitamin A deficiency; anaesthetic cornea; Stevens-Johnson syndrome; eye;
 KW inactive trachoma; thermal burn; chemical burn; superior limb keratitis;
 KW drug induced pseudopempigoid; atopic disease.
 XX
 OS
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT 1
 FT Misc-difference 1 /note="D-form residue"
 FT 5
 FT Misc-difference 5 /note="D-form residue"
 FT 7
 FT Misc-difference 7 /note="D-form residue"
 FT 9
 FT Misc-difference 9 /note="D-form residue"
 FT
 FT
 PN WO9513087-A1.
 XX
 PD 18-MAY-1995.

XX 10-NOV-1994; 94WO-US13084.
 PF 12-NOV-1993; 93US-0152175.
 PR (SCHE-) SCHEPENS EYE RES INST INC.
 XX Darft DA, Kessler TL;
 XX WPI: 1995-193902/25.
 DR
 XX Treatment of aberrant conjunctival goblet cell mucous secretion - by
 PT topical or subcutaneous admin of, eg. dopamine, serotonin, Substance
 PR P or vasoactive intestinal peptide
 XX
 PS Claim 6; : 67pp; English.
 XX
 CC This sequence represents an analogue of substance P and is used in
 CC the method of the invention for the treatment of patients suffering
 CC from aberrant conjunctival goblet cell mucous secretion. This is
 CC associated with a disorder of, or injury to, the eye. The treatment
 CC is especially useful for treating keratoconjunctivitis, Sjogren's
 CC syndrome, vitamin A deficiency, anaesthetic cornea, Stevens-Johnson
 CC syndrome, inactive trachoma, thermal and chemical burns, drug induced
 CC pseudophthalmoid, atopic diseases and superior limb keratitis. This
 CC VIP analogue acts to stimulate the neural system.
 XX
 SQ Sequence 11 AA;

AA074962 Length: 45 April 1, 2002 16:31 Type: P Check: 1342 ..

1 SQARNDBCOE ZGHSQILKMF PSTWYSQOT HERSRPPRY FFYL

!!AA_SEQUENCE 1.0

ID AAM32620 standard; Protein; 220 AA.

AC AAM32620;

DT 28-JAN-1998 (first entry)

DE Bacillus smithii nitrile hydratase subunit alpha.

XX Nitrile hydratase subunit alpha; nitrile hydratase subunit beta;
 KW acrylonitrile; acryloamide; biological catalysis; amide;
 KW thermally stable protein.
 XX

OS Bacillus smithii.

FH Key Location/Qualifiers

FT Misc-difference 1 /note= "May or may not be present in the protein"

FT Region 2..18 /label= N-terminal_sequence

PN JP09248188-A.

XX 22-SEP-1997.

PD 18-MAR-1996; 96JP-0060732.

PF 18-MAR-1996; 96JP-0060732.

PR 18-MAR-1996; 96JP-0060732.

XX (SUMO) SUMITOMO CHEM CO LTD.

DR WPI: 1997-520742/48.

XX N-PSDB; AAT92381.

XX Gene encoding nitrile hydratase - for producing amide from nitrile
 PT by biological catalysis

XX Claim 1; Page 9; 16pp; Japanese.
 PS
 CC The present sequence represents nitrile hydratase subunit alpha, a

CC novel protein isolated from Bacillus smithii. The protein has hydration
 CC activity for converting acrylonitrile into acryloamide. It is useful
 CC for producing amide from nitrile by biological catalysis.
 XX
 SQ Sequence 220 AA;

AAM32620 Length: 254 April 1, 2002 16:31 Type: P Check: 4569 ..

1 SQARNDBCOE ZGHSQILKMF PSTWYSQOT HERSMAIEOK LMDHHEVD

51 RRPNNHPPQ SFWEARAKAL ESLIEKRL SSDAIEVYK HYEELGPM

101 GAKYAKAWT DPEKQRLLE DPETVLELG YEGLOGENIR VVENTDTVHN

151 VVCTLCSCY PMPLLGLPPS WYKEPAVRSR VYKEPAKVLQ EFGDLDPDSV

201 EIRWDSSE VRFMYLPORP EGTEGMTEE LMQIVRDSM IGVAKVQRPK

251 VTQE

!!AA_SEQUENCE 1.0

ID AAM33181 standard; peptide; 11 AA.

AC AAM33181;

DT 29-JAN-1998 (first entry)

DE Mono-DTPA-Lys1 Substance P.

KW Substance P; radiolabel; diagnostic imaging; therapy;
 KW mono-DTPA-Lys1.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 1 /note= "DTPA-Lys"

FT Modified-site 11 /note= "amidated"

PN W09640292-A1.

XX 19-DEC-1996.

PD 07-JUN-1996; 96WO-US09706.

PF 07-JUN-1995; 95US-0480372.

PR (MLCW) MALLINCKRODT MEDICAL INC.

PA Srinivasan A;

DR WPI: 1997-087027/08.

XX Prepn. of pure radio-labelled peptide, e.g. for diagnostic imaging -
 PT by combining protected poly(amino:carboxylate) ligand with peptide
 PR and forming complex with radionuclide

XX Example 4; Page 12; 20pp; English.

CC Preparing a radiolabelled peptide composition, comprises combining
 CC a triamine or diamine chelating agent with a peptide, e.g. the
 CC present peptide, in a solid phase peptide synthesiser, and
 CC complexing a radionuclide with the chelate-peptide conjugate.
 CC Radiolabelled peptides or peptidomimetics can be used as diagnostic
 CC imaging agents, or in therapeutic applications, e.g. iodine(111)
 CC labeled pentetreotide can be used for somatostatin receptor
 CC imaging of neuroendocrine tumours. The radiolabelled products are
 CC obtained efficiently and inexpensively in high purity. The
 CC protected polyamino:carboxylate ligands can be added to the peptide
 CC by standard solution or solid phase peptide synthesis and
 CC deprotected with conventional reagents to give only the
 CC mono-addition product, free of di-addition product impurities. The

CC deprotected product can be labelled with medically useful
CC radionuclides, e.g. lanthanides or actinides, at any desired
CC location. Pre-derivatisation of individual amino acids is not
CC required.

XX Sequence 11 AA;

AAW3181 Length: 45 April 1, 2002 16:31 Type: P Check: 477 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPRQO FFGIM

!!AA_SEQUENCE 1.0
ID AAW3180 standard; peptide; 11 AA.

XX AAW3180;

DT 29-JAN-1998 (first entry)

XX Mono-DTPA-Arg1 Substance P.

DE Mono-DTPA-Arg1 Substance P.
XX Substance P: radiolabel; diagnostic imaging; therapy;
KW mono-DTPA-Arg1.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "DTPA-Arg"

FT Modified-site 11 /note= "amidated"

XX WO9640292-A1.

XX 19-DEC-1996.

XX 07-JUN-1996; 96WO-US09706.

XX 07-JUN-1995; 95US-0480372.

XX (MLCW) MALLINCKRODT MEDICAL INC.

XX Srinivasan A;

DR WPI; 1997-087027/08.

XX Prepn. of pure radio:labelled peptide, e.g. for diagnostic imaging
PT by combining protected poly(amino:carboxylate) ligand with peptide
PT and forming complex with radionuclide

PS Example 3; Page 12; 20pp; English.

CC Preparing a radiolabelled peptide composition, comprises combining
CC a triamine or diamine chelating agent with a peptide, e.g. the
CC present peptide, in a solid phase peptide synthesiser, and
CC complexing a radionuclide with the chelate-peptide conjugate.

CC Radiolabelled peptides or peptidomimetics can be used as diagnostic
CC imaging agents, or in therapeutic applications, e.g. Iodine(111)

CC Labelling pentatreotide can be used for somatostatin receptor
CC imaging of neuroendocrine tumours. The radiolabelled products are

CC obtained efficiently and inexpensively in high purity. The
CC protected polyamino:carboxylate ligands can be added to the peptide

CC by standard solution or solid phase peptide synthesis and
CC deprotected with conventional reagents to give only the

CC mono-addition product, free of di-addition product impurities. The
CC deprotected product can be labelled with medically useful

CC radionuclides, e.g. lanthanides or actinides, at any desired
CC location. Pre-derivatisation of individual amino acids is not
CC required.

XX Sequence 11 AA;

AAW3180 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPRQO FFGIM
!!AA_SEQUENCE 1.0
ID AAW26509 standard; Protein; 492 AA.

XX AAW26509;

DT 06-JAN-1998 (first entry)

XX Amyloid precursor protein substrate APP-REP 751.

XX Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; mutagen; secretase; Alzheimer's disease; human;
KW APP-REP 751; PCLL602.

XX APP-REP 751; PCLL602.

XX Chimeric Homo sapiens.

OS Chimeric synthetic.

XX Key Location/Qualifiers

FT Peptide 362..372 /label= SP
FT /note= "substance P reporter epitope"

FT Domain 389..430 /label= BAP
FT /note= "beta-amyloid protein"

FT Cleavage-site 404..405 /note= "secretase cleavage site"

FT Domain 417..440 /label= Transmembrane

FT Peptide 488..492 /label= ME
FT /note= "Met-enkephalin reporter epitope"

XX US5656477-A.

XX 12-AUG-1997.

XX 01-MAY-1992; 92US-0877675.

XX 20-SEP-1993; 93US-0123659.

XX 01-MAY-1992; 92US-0877675.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobson JS, Vittek MP;

DR WPI; 1997-414594/38.

DR P-PSDB; AAT87083.

XX Nucleic acid encoding amyloid precursor muten(s) - comprising
PT reporter gene and coding sequence, for identifying compounds which
PT modify the activity of proteolytic enzymes which cleave APP

PS Disclosure; Fig 7; 84pp; English.

CC This polypeptide, designated APP-REP 761, comprises an amyloid
CC precursor protein (APP) that has a 276-amino acid deletion of the
CC native APP and which carries Substance P and Met-enkephalin epitope

CC markers placed, respectively, on the N-terminal and C-terminal
CC sites of the beta-amyloid protein (BAP) domain. APP-REP 751 can

CC be used in a claimed method for screening for a compound which
CC reduces the formation of beta-amyloid protein, determined by

CC measuring the amount of marker in a medium containing transfected
CC cells. The method is used to detect compounds which inhibit the

CC activity of proteolytic enzymes which cleave APP to generate BAP
CC fragments. Such compounds can be used in the treatment of e.g.

CC Alzheimer's disease. The deletion of a 276 amino acid portion of
CC APP distinguishes the construct from endogenously expressed APP,

CC and beneficially increases the resolution of APP-REP fragments
CC resulting from the proteolytic cleavage by secretase or other

CC amyloidogenic, BAP-generating cleavage events.

XX Sequence 492 AA;

AAW26509 Length: 526 April 1, 2002 16:31 Type: P Check: 2172

```

1  SQARNDBCE ZGHSQILKMF PSTWYVSQOT HERSMLPGIA LLLAAMTAR
51  ALEVPDNGA GLAEPQIAM FCGRLNMNM VONGKWDSP SGTKTCIDTK
101 EGILGYCGEV YPELQITNVV EANOPTYQN WCKRGKRQCK THPHFVIPYR
151 CLVGEFVSIA LLVPDKCKFL HQERMDYCEI HLHMTVAKE TCSEKSTNLH
201 DYGMLLPGCI DKFRGVEFVC CPLAESDNV DSADAEEDS DVMWGADTD
251 YADGSEDKV EVAREEVAE VEEBEADDE DDEGDVEVE EAEPYEERAT
301 ERTTSIATTT TTTESVSEV VREVCSEQAE TGPCRAMISR WYFDYTEGKC
351 APFFYGCGG NRRNFDTEY CMAVCSAIP TTAASPDVAV DKYLERPRQ
401 QFFGLMGSJT NIKTEEISEV KMDAEFRHDS GYEVHOKLV FFAEDVGSNK
451 GAIGLWVG VVIATVIYIT LVMLKKQYT SIHNGVEVD AAVTPEERHL
501 SKMQNGYEN PTYKFEEDMO NYGGEF

!!AA_SEQUENCE 1.0
ID  AAW26510 standard; Protein; 487 AA.
XX
AC  AAW26510;
XX
DT  06-JAN-1998 (first entry)
XX
DE  Amyloid precursor protein substrate APP-REP 751.
XX
KM  Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KM  substrate; mutelin; secretase; Alzheimer's disease; human;
KM  APP-REP 751; PCLL621.
XX
OS  Chimeric Homo sapiens.
OS  Chimeric synthetic.
XX
FH  Key
FT  Location/Qualifiers
FT  /label= SP
FT  /note= "substance P reporter epitope"
FT  389..430
FT  /label= BAP
FT  /note= "beta-amyloid protein"
FT  404..405
FT  /note= "secretase cleavage site"
FT  417..440
FT  /label= Transmembrane
XX
PM  US5656477-A.
XX
PD  12-AUG-1997.
XX
PF  01-MAY-1992; 92US-0877675.
XX
PR  20-SEP-1993; 93US-0123659.
PR  01-MAY-1992; 92US-0877675.
XX
PA  (AMCY ) AMERICAN CYANAMID CO.
XX
PI  Jacobsen JS, Vittek MP;
XX
DR  WPI: 1997-414594/38.
DR  P-PSDB: AAT87083.
XX
PT  Nucleic acid encoding amyloid precursor mutelin(s) - comprising
PT  reporter gene and coding sequence; for identifying compounds which
PT  modify the activity of proteolytic enzymes which cleave APP
XX

```

PS Disclosure: Fig 8; 84pp; English.

```

XX  This polypeptide, designated APP-REP 761, comprises an amyloid
CC  precursor protein (APP) that has a 276-amino acid deletion of the
CC  native APP and which carries a substance P epitope markers placed
CC  N-terminal to the beta-amyloid protein (BAP) domain. APP-REP 751
CC  can be used in a claimed method for screening for a compound which
CC  reduces the formation of beta-amyloid protein, determined by
CC  measuring the amount of marker in a medium containing transfected
CC  cells. The method is used to detect compounds which inhibit the
CC  activity of proteolytic enzymes which cleave APP to generate BAP
CC  fragments. Such compounds can be used in the treatment of e.g.
CC  Alzheimer's disease. The deletion of a 276 amino acid portion of
CC  APP distinguishes the construct from endogenously expressed APP,
CC  and beneficially increases the resolution of APP-REP fragments
CC  resulting from the proteolytic cleavage by secretase or other
CC  amyloidogenic, BAP-generating cleavage events.
XX
SQ  Sequence 487 AA;

```

AAW26510 Length: 521 April 1, 2002 16:31 Type: P Check: 8039

```

1  SQARNDBCE ZGHSQILKMF PSTWYVSQOT HERSMLPGIA LLLAAMTAR
51  ALEVPDNGA GLAEPQIAM FCGRLNMNM VONGKWDSP SGTKTCIDTK
101 EGILGYCGEV YPELQITNVV EANOPTYQN WCKRGKRQCK THPHFVIPYR
151 CLVGEFVSIA LLVPDKCKFL HQERMDYCEI HLHMTVAKE TCSEKSTNLH
201 DYGMLLPGCI DKFRGVEFVC CPLAESDNV DSADAEEDS DVMWGADTD
251 YADGSEDKV EVAREEVAE VEEBEADDE DDEGDVEVE EAEPYEERAT
301 ERTTSIATTT TTTESVSEV VREVCSEQAE TGPCRAMISR WYFDYTEGKC
351 APFFYGCGG NRRNFDTEY CMAVCSAIP TTAASPDVAV DKYLERPRQ
401 QFFGLMGSJT NIKTEEISEV KMDAEFRHDS GYEVHOKLV FFAEDVGSNK
451 GAIGLWVG VVIATVIYIT LVMLKKQYT SIHNGVEVD AAVTPEERHL
501 SKMQNGYEN PTYKFEEDMO N

!!AA_SEQUENCE 1.0
ID  AAW26393 standard; Protein; 492 AA.
XX
AC  AAW26393;
XX
DT  15-DEC-1997 (first entry)
XX
DE  Amyloid precursor protein substrate APP-REP 751.
XX
KM  Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KM  substrate; mutelin; secretase; Alzheimer's disease; human;
KM  APP-REP 751; PCLL602.
XX
OS  Chimeric Homo sapiens;
OS  Chimeric synthetic.
XX
FH  Key
FT  Location/Qualifiers
FT  /label= SP
FT  /note= "substance P reporter epitope"
FT  389..430
FT  /label= BAP
FT  /note= "beta-amyloid protein"
FT  404..405
FT  /note= "secretase cleavage site"
FT  417..440
FT  /label= Transmembrane
FT  488..492
FT  /label= ME

```

FT /note= "Met-enkephalin reporter epitope"
XX
PN US5652092-A.
XX
PD 29-JUL-1997.
XX
PF 01-MAY-1992; 92US-0877675.
XX
PR 20-SEP-1993; 93US-0123659.
PR 01-MAY-1992; 92US-0877675.
PR 05-JUN-1995; 95US-0462859.
XX
PA (AMCY) AMERICAN CYANAMID CO.
XX
PI Jacobsen JS, Vitek MP;
XX WPI: 1997-392937/36.
DR N-PSDB; AAT84561.
XX
PT Screening for compounds which reduce beta-amyloid protein formation
PT - using cells which express a construct encoding a marker and an
PT amyloid precursor muten derived from APP isoforms
XX
XX Disclosure; Fig 7, 84pp; English.
XX
PS This polypeptide, designated APP-REP 761, comprises an amyloid
CC precursor protein (APP) that has a 276-amino acid deletion of the
CC native APP and which carries Substance P and Met-enkephalin epitope
CC markers placed, respectively, on the N-terminal and C-terminal
CC sites of the beta-amyloid protein (BAP) domain. APP-REP 751 can
CC be used in a claimed method for screening for a compound which
CC reduces the formation of beta-amyloid protein, determined by
CC measuring the amount of marker in a medium containing transfected
CC cells. The method is used to detect compounds which inhibit the
CC activity of proteolytic enzymes which cleave APP to generate BAP
CC fragments. Such compounds can be used in the treatment of e.g.
CC Alzheimer's disease. The deletion of a 276 amino acid portion of
CC APP distinguishes the construct from endogenously expressed APP,
CC and beneficially increases the resolution of APP-REP fragments
CC resulting from the proteolytic cleavage by secretase or other
CC amyloidogenic, BAP-generating cleavage events.
XX
SQ Sequence 492 AA:

AAM26393 Length: 526 April 1, 2002 16:31 Type: P Check: 2172 ..
1 SQARNDBCQE ZGHSQILKMF PSTWYVSQOT HERSMLPGLA LLLAAWTAR
51 ALEVPIDGNA GLAEPOIAM FCGRLNMNMN VQNGKNDSDP SGTKTCTDITK
101 EGILOYCOEV YPELOITNVV EANOPIYIION WCKRGKRCKC THPHVIPIPR
151 CLVGEFVSDA LLVPDKCKFL HOERMDVCET HLHWHVAKK TCSEKSTNLH
201 DYGMILPCGI DKFRGVEFVC CPLAESDNV DSADAEEDSD DVMWGADTID
251 YADGSEDKV EVAREEVAE VEEDADDE DDEDSGEVEE EAEPEYEAT
301 ERTTSATTT TTTTSEVEE VREYCSQDAE TCGPCRAMISR WYFDYTEGC
351 ABFFYGGCGG NRNPDTEEY CMAVCGSAIP TTAASTPRDAV DYLERPKPO
401 OFFGMLGSLT NIKTEISEV KMDAEFRHDS GYEVNHOKLV FPAEDVGSNK
451 GALIGLVGSG VVIATVIVIT LVMLKKKOYT SIHNGVEVD AAVTPBERHL
501 SKMOQNGYEN PTYKFEQMO NYGGFM
!!AA_SEQUENCE 1.0
ID AAM26394 standard; Protein: 487 AA.
XX
AC AAM26394;
XX

DI 15-DEC-1997 (first entry)
XX
DE Amyloid precursor protein substrate APP-REP 751.
XX
KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
KW substrate; muten; secretase; Alzheimer's disease; human;
KW APP-REP 751; PCLL621.
XX
OS Chimeric Homo sapiens;
OS Chimeric synthetic.
XX
XX Key location/Qualifiers
FH 362..372
FT Peptide /label= SP
FT /note= "substance P reporter epitope"
FT 389..430
FT Domain /label= BAP
FT /note= "beta-amyloid protein"
FT Cleavage-site 404..405
FT /note= "secretase cleavage site"
FT Domain 417..440
FT /label= Transmembrane
XX
XX US5652092-A.
XX
PN 29-JUL-1997.
PD 01-MAY-1992; 92US-0877675.
XX
PF 20-SEP-1993; 93US-0123659.
XX PR 01-MAY-1992; 92US-0877675.
PR 05-JUN-1995; 95US-0462859.
XX
XX (AMCY) AMERICAN CYANAMID CO.
XX
XX Jacobsen JS, Vitek MP;
XX WPI: 1997-392937/36.
DR N-PSDB; AAT84562.
XX
PT Screening for compounds which reduce beta-amyloid protein formation
PT - using cells which express a construct encoding a marker and an
PT amyloid precursor muten derived from APP isoforms
XX
XX Disclosure; Fig 8; 84pp; English.
XX
PS This polypeptide, designated APP-REP 761, comprises an amyloid
CC precursor protein (APP) that has a 276-amino acid deletion of the
CC native APP and which carries a Substance P epitope markers placed
CC N-terminal to the beta-amyloid protein (BAP) domain. APP-REP 751
CC can be used in a claimed method for screening for a compound which
CC reduces the formation of beta-amyloid protein, determined by
CC measuring the amount of marker in a medium containing transfected
CC cells. The method is used to detect compounds which inhibit the
CC activity of proteolytic enzymes which cleave APP to generate BAP
CC fragments. Such compounds can be used in the treatment of e.g.
CC Alzheimer's disease. The deletion of a 276 amino acid portion of
CC APP distinguishes the construct from endogenously expressed APP,
CC and beneficially increases the resolution of APP-REP fragments
CC resulting from the proteolytic cleavage by secretase or other
CC amyloidogenic, BAP-generating cleavage events.
XX
SQ Sequence 487 AA:

AAM26394 Length: 521 April 1, 2002 16:31 Type: P Check: 8039 ..
1 SQARNDBCQE ZGHSQILKMF PSTWYVSQOT HERSMLPGLA LLLAAWTAR
51 ALEVPIDGNA GLAEPOIAM FCGRLNMNMN VQNGKNDSDP SGTKTCTDITK
101 EGILOYCOEV YPELOITNVV EANOPIYIION WCKRGKRCKC THPHVIPIPR
151 CLVGEFVSDA LLVPDKCKFL HOERMDVCET HLHWHVAKK TCSEKSTNLH

```

201 DYGMLLPCGI DKFRGVEFYC CPLAESDNV DSADAEEDDS DVMWGGADTD
251 YAQGSSEDKVY EVAEEBEVAE VEEBEADDE DDEGDDEVEE EAEPEFEAT
301 ERTTSIAFTT TTTTESVEEV VREVCSEAE TGPCRAMISR WYFDVTEGKC
351 APEFYGGJGG NRRNPDTEEV CMAVCGSAIP TTAASTPDAY DKYLERPKPQ
401 QPFGLMGSLT NIKTEISEV KMDAEFRHDS GYEVHQKLV FFAEDVGSNK
451 GAIGLMVGG VVIATYIVIT LVMLKKOYT SIHHGVEVD AAVTPEERHL
501 SKMQNGTEN PTKKFEQMO Q

!!AA_SEQUENCE 1.0
ID AAM16339 standard; protein; 401 AA.
XX
AC AAM16339;
XX
DT 05-SEP-1997 (first entry)
XX
DE DAB389-SP-Gly fusion toxin.
XX
KM DAB389-SP-Gly; amidated polypeptide binding ligand; drug delivery;
XX diptheria toxin; substance P; cancer; therapy.
XX
OS Synthetic.
XX
PN WO9713410-A1.
XX
PD 17-APR-1997.
XX
PF 11-OCT-1996; 96WO-US16237.
XX
PR 13-OCT-1995; 95US-0005431.
XX
PA (BOST-) BOSTON MEDICAL CENT CORP.
XX
PI Fisher CE, Leeman SE, Murphy JR, Vanderspek JC;
XX WPI, 1997-235583/21.
XX DR N-PSDB; AAM163359.
XX
XX
XX Hybrid molecule for targeting compound, especially a toxin, into
XX cells - includes polypeptide able to transport the compound across
XX cytoplasmic membranes and amidated ligand, useful for treatment of
XX cancer
XX
XX Example 1; Page 22-23; 51pp; English.
XX
XX DAB389-SP-Gly (AAM16339) is a hybrid toxin comprising DAB389 (i.e.
XX amino acids 1-386 plus His-484 and Ala-485 of mature diptheria
XX toxin) fused to C-terminal glycine-extended substance P. It was
XX expressed in E. coli HMS174(DE3) transformants using a vector
XX that carried DAB389-SP-Gly DNA (see also AAM163359). The fusion
XX protein was then amidated using peptidylglycino-alpha-amidating
XX monooxygenase. The amidated fusion protein used to target DAB389
XX toxin to specific cells contg. substance P receptors, esp. cancer
XX cells. For human IM9 (chronic myelogenous leukaemia) cells contg.
XX approx. 4000 substance P receptors per cell, the IC50 for amidated
XX DAB389-SP-Gly was 18 pM.
XX
SQ Sequence 401 AA;

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AAM16339 Length: 435 April 1, 2002 16:31 Type: P Check: 9887 ..

```

1 SQARNDBCE ZGHSQILKMF PSTWVVSQOT HERSMGADV VDSKSFVME
51 NFSSTHGTRP GYVDSIQKGI QPKSGTQGN YDDDMWGFYS TUNKXDAACY
101 SVNNEPFLSG KAGGVVKTYY PGLTKVLALK VDNAETIKKE LGISTLEPLM

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151 EQVGTETEFIK RFGDASRVY LSLPFAEGSS SVEYINNMQ AKALSYELEI
201 NFETRCKRGQ DAMYEMAQA CAGNRVRSY GSSLSCINLD MWYIRKXTIT
251 KISLKEHCP IKNMSESPN KTVSEKAKQ YLEEFHOTAL EHPELSELKT
301 VTGTPVFAQ ANYAAMVNV AQVIDSETAD NLEKTPAALS ILPGISVNG
351 IADGAVHHNT EEIVAQIAL SLMVAQAIP LVGELVDIGF AAVNFVESII
401 NLFQVYHNSY NRPATSPGKH THARKPQOF FGLMG

!!AA_SEQUENCE 1.0
ID AAM04616 standard; peptide; 11 AA.
XX
AC AAM04616;
XX
DT 13-AUG-1997 (first entry)
XX
DE Substance P peptide for mass spectrometry analysis.
XX
KM Mass spectrometry; polymer analysis; biopolymer analysis.
XX
OS Synthetic.
XX
PN WC09636986-A1.
XX
PD 21-NOV-1996.
XX
PF 17-MAY-1996; 96WO-US071146.
XX
PR 19-MAY-1995; 95US-0447175.
XX PR 19-MAY-1995; 95US-0446055.
XX
PA (PERS-) PERSEPTIVE BIOSYSTEMS INC.
XX
PI Patterson DH, Tarr GE;
XX
XX WPI, 1997-012308/01.
XX
XX
XX Sequencing polymers, e.g. DNA, RNA, peptide nucleic acids, proteins,
XX etc. - by obtaining mass to charge ratios of polymer fragments,
XX pref. using mass spectrometer, and performing statistical analysis
XX
XX Example 2; Page 32; 86pp; English.
XX
XX A method of obtaining sequence information about a polymer (e.g. DNA,
XX RNA, peptide nucleic acids, proteins, peptides and carbohydrates)
XX comprising monomers of known mass has been claimed. The present
XX sequence represents a substance P peptide, and was used as
XX an example as a digestion before analysis by mass spectrometry,
XX using this novel on-plate strategy. Total sequence information
XX from a nine well digestion can be represented in a single digestion or
XX it is often derived from two or more wells. The methods, apparatus and
XX kit (claimed) can be used for the analysis of polymers, particularly
XX biopolymers, e.g. DNA, RNA, peptide nucleic acids, proteins, peptides
XX and carbohydrates. It provides a rapid, automated and cost effective
XX sequencing of polymers, with a statistical certainty.
XX
SQ Sequence 11 AA;

```

AAM04616 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCE ZGHSQILKMF PSTWVVSQOT HERSRPRKPOQ FGLM

```

!!AA_SEQUENCE 1.0
ID AAM79775 standard; peptide; 11 AA.
XX
AC AAM79775;
XX
DT 07-JAN-1999 (first entry)
XX
DE Substance P.

```


XX Tachykinin; neurokinin; NK1; receptor; antagonist; cystic fibrosis;
 KW Substance P.
 XX Mammalia.
 OS
 XX US5830854-A.
 PN
 XX 03-NOV-1998.
 PD
 XX 14-DEC-1993; 93US-0166437.
 PE
 XX 14-DEC-1992; 92GB-0026056.
 PR 14-DEC-1992; 92GB-0026047.
 PR
 XX (MERI) MERCK SHARP & DOHME LTD.
 PA
 XX Hargreaves RJ;
 P1
 DR WPI; 1998-609287/51.
 XX
 XX Treatment of cystic fibrosis - comprises administration of
 PT tachykinin receptor antagonist which is a neurokinin-1 receptor
 PT antagonist
 PT
 PS Disclosure; Column 1; 12pp; English.
 XX
 CC The invention relates to the new use of tachykinin receptor antagonists
 CC (particularly NK1 receptor antagonists) for the treatment of cystic
 CC fibrosis. The present sequence is that of Substance P, one of three
 CC known mammalian tachykinins.
 XX
 SQ Sequence 11 AA;

AAW79775 Length: 45 April 1, 2002 16:31 Type: P Check: 242 ..

1 SQARNDBOE ZGHSQILKMF PSTWVYSQOT HERSRKPQE FFGLM

!!AA_SEQUENCE 1.0
 ID AAW50978 standard; peptide; 11 AA.
 XX

AC AAW50978;

DT 31-JUL-1998 (first entry)

XX Substance P analogue [D-Arg1,D-Pro2,D-Phe7,D-His9].

XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
 KW Substance P; cancer; inhibition; growth hormone releasing factor;
 KW spantide.
 XX
 XX Synthetic.

OS

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

FT

PN EP835662-A2.

PD 15-APR-1998.

XX 11-DEC-1996; 96EP-0309012.

XX 08-OCT-1996; 96US-0727679.

PR 16-AUG-1996; 96IN-0001822.

XX (NAIM-) NAT INST IMMUNOLOGY.
 PA
 XX Jaggi M, Mukherjee R;
 PI
 XX WPI; 1998-208959/19.
 DR
 XX Composition containing analogues of vasoactive intestinal peptide,
 PT somatostatin - bombesin and substance P, for treatment of tumours
 PT and for inhibiting over-expression of these peptide(s)
 XX
 XX Disclosure; Page 13; 49pp; English.
 PS
 XX
 CC The invention relates to a new composition which comprises: (i) the
 CC somatostatin analogue SOM2 AGCKNFDMKTPNSDC (3-14 disulphide bridge),
 CC and (ii) at least 4 of the peptides: antagonist of vasoactive
 CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
 CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
 CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
 CC more general compositions containing peptide analogues of somatostatin,
 CC VIP, bombesin and substance P. The compositions are used in human or
 CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
 CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
 CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
 CC breast, kidney or particularly rectum and colon, and (b) to prevent,
 CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
 CC cells express receptors for VIP, somatostatin, bombesin and/or substance
 CC P. The present sequence represents a substance P analogue.
 XX
 SQ Sequence 11 AA;

AAW50978 Length: 45 April 1, 2002 16:31 Type: P Check: 765 ..

1 SQARNDBOE ZGHSQILKMF PSTWVYSQOT HERSRKPQO FFHLM

!!AA_SEQUENCE 1.0
 ID AAW50966 standard; peptide; 11 AA.
 XX

AC AAW50966;

DT 31-JUL-1998 (first entry)

XX Substance P analogue, spantide I.

XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
 KW Substance P; cancer; inhibition; growth hormone releasing factor;
 KW spantide.
 XX
 XX Synthetic.

OS

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

FT

PN EP835662-A2.

PD 15-APR-1998.

XX 11-DEC-1996; 96EP-0309012.

XX 08-OCT-1996; 96US-0727679.

PR 16-AUG-1996; 96IN-0001822.

XX (NAIM-) NAT INST IMMUNOLOGY.

PA Jaggi M, Mukherjee R;

XX

DR WPI; 1998-208959/19.
XX
XX Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)
XX
XX Disclosure; Page 13; 49pp; English.
XX
XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCKNFdWKPTSDC (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue, spantide I.
CC
SQ Sequence 11 AA;

AAW50966 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..

1 SQARNDCQE ZGHSQILKMF PSTWVVSQOT HERSRPRPQO WFWLL

!!AA_SEQUENCE 1.0
ID AAW50968 standard; peptide; 11 AA.
AC AAW50968;
XX
XX 31-JUL-1998 (first entry)
DT
XX
XX Substance P analogue, [D-Pro2,D-Phe7,D-Trp9].
DE
XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor;
KM spantide.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH MISC-difference 2 /note= "D-form residue"
FT MISC-difference 7 /note= "D-form residue"
FT MISC-difference 9 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
FT
XX
XX EP835662-A2.
PN
XX
XX 15-APR-1998.
PD
XX
XX 11-DEC-1996; 96EP-0309012.
PF
XX
XX 08-OCT-1996; 96US-0727679.
PR
XX 16-AUG-1996; 96IN-0001822.
XX
XX (NATM-) NAT INST IMMUNOLOGY.
PA
XX Jaggi M, Mukherjee R;
PI
XX
XX WPI; 1998-208959/19.
DR
XX
XX Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)
PT

XX
XX Disclosure; Page 13; 49pp; English.
PS
XX
XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCKNFdWKPTSDC (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.
CC
SQ Sequence 11 AA;

AAW50968 Length: 45 April 1, 2002 16:31 Type: P Check: 1410 ..

1 SQARNDCQE ZGHSQILKMF PSTWVVSQOT HERSRPRPQO FFWLM

!!AA_SEQUENCE 1.0
ID AAW50969 standard; peptide; 11 AA.
AC AAW50969;
XX
XX 31-JUL-1998 (first entry)
DT
XX
XX Substance P analogue, [D-Pro2,D-Trp7,9].
DE
XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor;
KM spantide.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH MISC-difference 2 /note= "D-form residue"
FT MISC-difference 7 /note= "D-form residue"
FT MISC-difference 9 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
FT
XX
XX EP835662-A2.
PN
XX
XX 15-APR-1998.
PD
XX
XX 11-DEC-1996; 96EP-0309012.
PF
XX
XX 08-OCT-1996; 96US-0727679.
PR
XX 16-AUG-1996; 96IN-0001822.
XX
XX (NATM-) NAT INST IMMUNOLOGY.
PA
XX Jaggi M, Mukherjee R;
PI
XX
XX WPI; 1998-208959/19.
DR
XX
XX Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)
PT
PS Disclosure; Page 13; 49pp; English.
XX
XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCKNFdWKPTSDC (3-14 disulphide bridge),
CC

CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.

XX Sequence 11 AA:

AAW50969 Length: 45 April 1, 2002 16:31 Type: P Check: 2107 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRKPQO WFWLM

!!AA_SEQUENCE 1.0
ID AAW50972 standard; peptide: 11 AA.

XX AC AAW50972:

DT 31-JUL-1998 (first entry)

XX DE Substance P analogue, [D-Arg1,D-Phe5,D-Trp7,9,Leu11].

XX KW Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
XX Substante P; cancer; inhibition; growth hormone releasing factor;
XX spanlide.

XX OS Synthetic.

XX FT Key Location/Qualifiers

FT FT Misc-difference 1 /note= "D-form residue"

FT FT Misc-difference 5 /note= "D-form residue"

FT FT Misc-difference 7 /note= "D-form residue"

FT FT Misc-difference 9 /note= "D-form residue"

FT FT Modified-site 11 /note= "D-form residue"

XX EP835662-A2.

XX PD 15-APR-1998.

XX PF 11-DEC-1996; 96EP-0309012.

XX PR 08-OCT-1996; 96US-0727679.

XX PR 16-AUG-1996; 96IN-0001822.

XX PA (NAIM-) NAT INST IMMUNOLOGY.

XX PI Jaggi M, Mukherjee R;

XX DR WPI: 1998-208959/19.

XX PT Composition containing analogues of vasoactive intestinal peptide,
XX somatostatin - bombesin and substance P, for treatment of tumours
XX and for inhibiting over-expression of these peptide(s)

XX PS Disclosure: Page 13; 49pp; English.

XX CC The invention relates to a new composition which comprises: (i) the
XX somatostatin analogue SOM2 AGCKNFRDWRTPSDC (3-14 disulphide bridge),
XX and (ii) at least 4 of the peptides: antagonist of vasoactive
XX intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
XX receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin

CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.

XX Sequence 11 AA:

AAW50972 Length: 45 April 1, 2002 16:31 Type: P Check: 1633 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRKPQO WFWLL

!!AA_SEQUENCE 1.0
ID AAW50958 standard; peptide: 11 AA.

XX AC AAW50958:

DT 31-JUL-1998 (first entry)

XX DE Substance P analogue, [D-Arg1,D-Pro2,D-Trp7,9,Leu11]-Substance P.

XX KW Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
XX Substante P; cancer; inhibition; growth hormone releasing factor.

XX OS Synthetic.

XX FT Key Location/Qualifiers

FT FT Misc-difference 1 /note= "D-form residue"

FT FT Misc-difference 2 /note= "D-form residue"

FT FT Misc-difference 7 /note= "D-form residue"

FT FT Misc-difference 9 /note= "D-form residue"

FT FT Modified-site 11 /note= "D-form residue"

XX EP835662-A2.

XX PD 15-APR-1998.

XX PF 11-DEC-1996; 96EP-0309012.

XX PR 08-OCT-1996; 96US-0727679.

XX PR 16-AUG-1996; 96IN-0001822.

XX PA (NAIM-) NAT INST IMMUNOLOGY.

XX PI Jaggi M, Mukherjee R;

XX DR WPI: 1998-208959/19.

XX PT Composition containing analogues of vasoactive intestinal peptide,
XX somatostatin - bombesin and substance P, for treatment of tumours
XX and for inhibiting over-expression of these peptide(s)

XX PS Disclosure: Page 12; 49pp; English.

XX CC The invention relates to a new composition which comprises: (i) the
XX somatostatin analogue SOM2 AGCKNFRDWRTPSDC (3-14 disulphide bridge),
XX and (ii) at least 4 of the peptides: antagonist of vasoactive
XX intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
XX receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
XX antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
XX more general compositions containing peptide analogues of somatostatin,
XX VIP, bombesin and substance P. The compositions are used in human or
XX veterinary medicine: (a) to kill (or inhibit multiplication of) tumour

CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.
XX
XX

SO Sequence 11 AA;

AAW50958 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..

1 SQARNDBCQE ZGHSQILKMF PSTWYVSQOT HERSRRKPPQ WFWL

!!AA_SEQUENCE 1.0

ID AAW50942 standard; peptide; 11 AA.

AC AAW50942;

XX 31-JUL-1998 (first entry)

DE Substance P antagonist (SP1).

KW Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;
KM Substance P; cancer; inhibition.

XX Synthetic.

FT Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 5 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-size 13 /note= "C-terminal amide"

PN EP835662-A2.

PD 15-APR-1998.

PF 11-DEC-1996; 96EP-0309012.

PR 08-OCT-1996; 96US-0727679.

PR 16-AUG-1996; 96IN-0001822.

PA (NAIM-) NAT INST IMMUNOLOGY.

PI Jaggi M, Mukherjee R;

DR WPI: 1998-208959/19.

XX Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin - bombesin and substance P, for treatment of tumours
XX and for inhibiting over-expression of these peptide(s)

PS Claim 1: Page 4; 49pp; English.

XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 AGCNRFDWKPTSDC (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer

CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents substance P antagonist (SP1).

XX Sequence 11 AA;

AAW50942 Length: 45 April 1, 2002 16:31 Type: P Check: 1633 ..

1 SQARNDBCQE ZGHSQILKMF PSTWYVSQOT HERSRRKPPQ WFWL

!!AA_SEQUENCE 1.0

ID AAW44744 standard; Protein; 492 AA.

AC AAW44744;

XX 01-JUN-1998 (first entry)

DE APP-REP 751 protein from PCLL602.

KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
KM epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
KW Alzheimer's disease; cleavage.

XX Homo sapiens.

OS Synthetic.

PN US5693478-A.

PD 02-DEC-1997.

PF 05-JUN-1995; 95US-0464247.

PR 20-SEP-1993; 93US-0123659.

PR 01-MAY-1992; 92US-0877675.

PR 05-JUN-1995; 95US-0464247.

PA (AMCY) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vittek MP;

DR WPI: 1998-031744/03.

DR N-PSDB; AAW05849.

XX Amyloid precursor mutelin reporter molecule assay containing antibody

PT recognised marker - used to study pathways associated with

PT Alzheimer's disease

XX Disclosure: Fig 7; 84pp; English.

PS This is the amino acid sequence of a novel amyloid precursor protein

CC (APP) designated APP-REP 751, contained in construct PCLL602. The

CC sequence comprises a mutant version of the APP 751 isoform of human APP

CC which contains a deletion of 276 amino acids from the central region.

CC The deleted region is replaced by a substrate P reporter epitope sequence

CC (RPRQDFGDM) and a Met-enkephalin reporter epitope (YGGK) is fused at

CC the C-terminus. The shorter protein is generated for ease of detection

CC based on size difference with the wild type APP protein and also by

CC detection of the reporter epitopes. The mutant protein can be used in

CC a method to study secretase and beta-amyloid protein (BAP)-generating

CC pathways associated with Alzheimer's disease by studying proteolytic

CC cleavage of the reporter polypeptides.

XX Sequence 492 AA;

AAW44744 Length: 526 April 1, 2002 16:31 Type: P Check: 2172 ..

1 SQARNDBCQE ZGHSQILKMF PSTWYVSQOT HERSMLRGLA LLLAAMTAR

51 ALEVPDNGNA GLAEPQIAM FCGRLNMNM VQNGKWDSDP SGTKTCTIDTK

101 EGLGYQCEV YPELOITNVV EANOPTION WCKRGKQCK TPNHVIPIYR

151 CLVGEFVSDA LLYPDCKFL HQERMVCEY HLHWHTVAKE TCSEKSTNLH

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201 DYGMLLPGCI DKFRGVEFVC CPLAEESDNV DSADAEEDDS DVMWGADTDT
251 YADGSEDKV EVAREEVAAE VEEEDADDE DDEGDEVEE EAEPRYEAT
301 ERTSIATTT TTTSVEEV VREVCSEAE TGPCRAMISR WYFDTEGKC
351 APFYGGCGG NNNPDTEEY CMAVCSAIP TTAASTPDV DKYLERPQ
401 QFFGLMGLT NIKTEISEV KMDAEFRHDS GYEVHHOKLV FFAEDVGSNK
451 GAIGLWGG VVIATVIYIT LVMLKKQYT SIHGVVEVD AAVTPEERHL
501 SKMQNGYEN PTYKFEOMQ NYGFM

!!AA_SEQUENCE 1.0
ID AAM44745 standard; Protein: 487 AA.
AC AAM44745;
DT 01-JUN-1998 (first entry)
DE APP-REP 751 protein from pCLL621.
XX
XX Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
KW Alzheimer's disease; cleavage.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX US5693478-A.
XX
XX 02-DEC-1997.
XX
XX 05-JUN-1995; 95US-0464247.
XX
XX 20-SEP-1993; 93US-0123659.
XX 01-MAY-1992; 92US-0877675.
XX 05-JUN-1995; 95US-0464247.
XX
XX (AMCY ) AMERICAN CYANAMID CO.
XX
XX Jacobsen JS, Vittek MP;
XX
XX WPI: 1998-031744/03.
XX N-PSDB: AAV05850.
XX
XX Amyloid precursor mutain reporter molecule containing antibody
XX recognised marker - used to study pathways associated with
XX Alzheimer's disease
XX
XX Disclosure: Fig 8; 84pp; English.
XX
XX This is the amino acid sequence of a novel amyloid precursor protein
XX (APP) designated APP-REP 751, contained in construct pCLL621. The
XX sequence comprises a mutant version of the APP 751 isoform of human APP
XX which contains a deletion of 276 amino acids from the central region.
XX The deleted region is replaced by a substrate P reporter epitope
XX sequence (RRPRQDFGLM). In contrast to the APP-REP 751 encoded by the
XX construct pCLL602 (AAM44744), this sequence does not contain a
XX Met-enkephalin reporter epitope (YGGFM) fused at the C-terminus of the
XX coding sequence. The shorter protein is generated for ease of detection
XX based on size difference with the wild type APP protein and also by
XX detection of the reporter epitopes. The mutant protein can be used in a
XX method to study secretase and beta-amyloid protein (BAP)-generating
XX pathways associated with Alzheimer's disease by studying proteolytic
XX cleavage of the reporter polypeptides.
XX
XX Sequence 487 AA;
XX
AAM44745 Length: 521 April 1, 2002 16:31 Type: P Check: 8039
1 SOARNDBOE ZGHSOILKMF PSTWVVSQOT HERSMILPGIA LILLAMTAR

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51 ALEVPDNGA GLLAPOIAM FCGRLNMHN YONGKWDSDP SGFTCIDTK
101 BGLIOQCEV YPELOITNV EANOPTION WCKRGKQCK THPHVITYR
151 CLVGEFVSDA LVPDKCKFL HOERMDVCEY HLMHTVAKE TCSEKSTNLH
201 DYGMLLPGCI DKFRGVEFVC CPLAEESDNV DSADAEEDDS DVMWGADTDT
251 YADGSEDKV EVAREEVAAE VEEEDADDE DDEGDEVEE EAEPRYEAT
301 ERTSIATTT TTTSVEEV VREVCSEAE TGPCRAMISR WYFDTEGKC
351 APFYGGCGG NNNPDTEEY CMAVCSAIP TTAASTPDV DKYLERPQ
401 QFFGLMGLT NIKTEISEV KMDAEFRHDS GYEVHHOKLV FFAEDVGSNK
451 GAIGLWGG VVIATVIYIT LVMLKKQYT SIHGVVEVD AAVTPEERHL
501 SKMQNGYEN PTYKFEOMQ N

!!AA_SEQUENCE 1.0
ID AAM42978 standard; Protein: 492 AA.
AC AAM42978;
DT 01-MAY-1998 (first entry)
DE Amyloid precursor protein mutant APP-APP 751.
XX
XX Beta-amyloid peptide; BAP; extracellular BAP plaque;
XX cerebrovascular deposit; Alzheimers disease; Downs syndrome;
XX amyloid precursor protein; APP; secretase; BAP aggregation;
XX abnormal proteolytic cleavage.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Protein 1..487
XX FT /note= "App-APP 751"
XX FT Peptide 488..492
XX FT /note= "Met-enkephalin reporter epitope"
XX
XX US5703209-A.
XX
XX 30-DEC-1997.
XX
XX 05-JUN-1995; 95US-0464248.
XX
XX 20-SEP-1993; 93US-0123659.
XX 01-MAY-1992; 92US-0877675.
XX
XX (AMCY ) AMERICAN CYANAMID CO.
XX
XX Jacobsen JS, Vittek MP;
XX
XX WPI: 1998-076482/07.
XX N-PSDB: AAV04865.
XX
XX Amyloid precursor protein fusion polypeptides - comprising APP
XX fragment and marker, useful for research and drug screening
XX
XX Disclosure: Fig 7A-Q; 84pp; English.
XX
XX The present sequence represents an amyloid precursor protein (APP),
XX which has a deletion of 276 amino acids to within 15 amino acids of the
XX beta-amyloid peptide (BAP) domain. The protein also contains the
XX Met-enkephalin reporter epitope at the carboxy terminus. Abnormal
XX accumulation of extracellular BAP in plaques and cerebrovascular deposits
XX is characteristic in brains of individuals suffering from Alzheimers
XX disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
XX protein which is derived from a larger amyloid precursor protein (APP).

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CC APP is expressed as an integral membrane protein, and is cleaved by
 CC secretase, between BAP 16lys and 17leu. Cleavage at this site precludes
 CC amyloidogenesis and results in the release of the amino-terminal APP
 CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and
 CC APP-770. These isoforms are derived by alternative splicing. APP-RP 751
 CC is constructed by ligating restriction fragments representing N- and
 CC C-terminal APP-751 cDNA and substrate P reporter epitope sequences.
 CC APP can be used as a substrate for studying abnormal proteolytic cleavage
 CC which results in the release of BAP, and also to screen for drugs that
 CC will inhibit such cleavage.

XX Sequence 492 AA:

AA042978 Length: 526 April 1, 2002 16:31 Type: P Check: 2172 ..

1 SQARNRBCOE ZGHSQILKMF PSTWYSQOT HERSMLPGLA LLLLAAMTAR
 51 ALEVPIDGNA GLAEPQIAM FCGRLNMHN VONGKWDSP SGTKTCIDTK
 101 EGLQYCOEV YPELQITNVV EANOPTIION WCKRGKQCK THPHVPIYR
 151 CLVGEFVSDA LLVPDKCKFL HQERMDYCET HLHMTYAKE TCSEKSTNLH
 201 DYGMILPCGI DKFRGVFVC CPLAESDNV DSADAEEDS DVMWCGADTD
 251 YADGSEDKVY EVAEEEEVAAE VEEEDADDE DDEDGDEVEE EAEEPYEAT
 301 ERTTSIATTT TTTTESVEEV VREYCSQAE TGPCRAMISR WYFDTEGKC
 351 APFFYGGCGG NNNNFDTEBY CMAVCGSAIP TTAASPPDAV DYLBRRPKQ
 401 QFFGLMGSLT NIKTEISEV KMDAEFRHDS GYEVHOKLY FFAEDVGSNK
 451 GATIGLMVGG VVIATVIVIT LVMLKKROYT SIHNGVEVD AAVTBERHL
 501 SKMQNGYEN PTYKFFEQMQ NYGCFM

IIAA_SEQUENCE 1.0

ID AA042979 standard; Protein; 487 AA.

XX AA042979;

XX 01-MAY-1998 (first entry)

XX Amyloid precursor protein mutant APP-APP 751.

XX Beta-amyloid peptide; BAP; extracellular BAP plaque;

KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;

KW amyloid precursor protein; APP; secretase; BAP aggregation;

KW abnormal proteolytic cleavage.

XX OS Synthetic.

OS Homo sapiens.

XX US5703209-A.

XX 30-DEC-1997.

XX 05-JUN-1995; 95US-0464248.

XX 20-SEP-1993; 93US-0123659.

XX 01-MAY-1992; 92US-0877675.

XX (AMCY) AMERICAN CYANAMID CO.

XX Jacobsen JS, Vitek MP;

XX WPI; 1998-076482/07.

XX N-PSDB; AAV04866.

XX Amyloid precursor protein fusion polypeptides - comprising APP
 PT fragment and marker, useful for research and drug screening
 XX

PS Disclosure; Fig 8A-Q; 84pp; English.

XX The present sequence represents an amyloid precursor protein (APP),
 CC which has a deletion of 276 amino acids to within 15 amino acids of the
 CC beta-amyloid peptide (BAP) domain. The protein also contains the abnormal
 CC accumulation of extracellular BAP in plaques and cerebrovascular deposits
 CC is characteristic of individuals suffering from Alzheimers
 CC disease and Downs syndrome. BAP is a poorly soluble, self-aggregating
 CC protein which is derived from a larger amyloid precursor protein (APP).
 CC APP is expressed as an integral membrane protein, and is cleaved by
 CC secretase, between BAP 16lys and 17leu. Cleavage at this site precludes
 CC amyloidogenesis and results in the release of the amino-terminal APP
 CC fragment. Three major isoforms of APP exist: APP-695, APP-751 and
 CC APP-770. These isoforms are derived by alternative splicing. APP-RP 751
 CC is constructed by ligating restriction fragments representing N- and
 CC C-terminal APP-751 cDNA and substrate P reporter epitope sequences.
 CC APP can be used as a substrate for studying abnormal proteolytic cleavage
 CC which results in the release of BAP, and also to screen for drugs that
 CC will inhibit such cleavage.

XX Sequence 487 AA:

AA042979 Length: 521 April 1, 2002 16:31 Type: P Check: 8039 ..

1 SQARNRBCOE ZGHSQILKMF PSTWYSQOT HERSMLPGLA LLLLAAMTAR
 51 ALEVPIDGNA GLAEPQIAM FCGRLNMHN VONGKWDSP SGTKTCIDTK
 101 EGLQYCOEV YPELQITNVV EANOPTIION WCKRGKQCK THPHVPIYR
 151 CLVGEFVSDA LLVPDKCKFL HQERMDYCET HLHMTYAKE TCSEKSTNLH
 201 DYGMILPCGI DKFRGVFVC CPLAESDNV DSADAEEDS DVMWCGADTD
 251 YADGSEDKVY EVAEEEEVAAE VEEEDADDE DDEDGDEVEE EAEEPYEAT
 301 ERTTSIATTT TTTTESVEEV VREYCSQAE TGPCRAMISR WYFDTEGKC
 351 APFFYGGCGG NNNNFDTEBY CMAVCGSAIP TTAASPPDAV DYLBRRPKQ
 401 QFFGLMGSLT NIKTEISEV KMDAEFRHDS GYEVHOKLY FFAEDVGSNK
 451 GATIGLMVGG VVIATVIVIT LVMLKKROYT SIHNGVEVD AAVTBERHL
 501 SKMQNGYEN PTYKFFEQMQ N

IIAA_SEQUENCE 1.0

ID AA042979 standard; Protein; 11 AA.

XX AA042973;

XX 01-MAY-1998 (first entry)

XX Substrate P reporter epitope.

XX Beta-amyloid peptide; BAP; extracellular BAP plaque;

KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;

KW amyloid precursor protein; APP; secretase; BAP aggregation;

KW abnormal proteolytic cleavage; substrate P reporter epitope.

XX OS Synthetic.

XX US5703209-A.

XX 30-DEC-1997.

XX 05-JUN-1995; 95US-0464248.

XX 20-SEP-1993; 93US-0123659.

XX 01-MAY-1992; 92US-0877675.

XX (AMCY) AMERICAN CYANAMID CO.

PI Jacobsen JS, Vittek MP;
XX WPI; 1998-076482/07.
XX
XX Amyloid precursor protein fusion polypeptides - comprising APP
PT fragment and marker, useful for research and drug screening
PS
XX Disclosure; Column 3; 84pp; English.
XX
CC Peptid sequence AAM42978 represents an amyloid precursor protein (APP),
CC which has a deletion of 276 amino acids to within 15 amino acids of the
CC beta-amyloid peptide (BAP) domain. The protein also contains the
CC Met-enkephalin reporter epitope at the carboxy terminus. Abnormal
CC accumulation of extracellular BAP in plaques and cerebrovascular
CC deposits is characteristic in brains of individuals suffering from
CC Alzheimer's disease and Downs syndrome. BAP is a poorly soluble,
CC self-aggregating protein which is derived from a larger amyloid precursor
CC protein (APP). APP is expressed as an integral membrane protein, and is
CC cleaved by secretase, between BAP 16lys and 17leu. Cleavage at this site
CC precludes amyloidogenesis and results in the release of the
CC amino-terminal APP fragment. Three major isoforms of APP exist: APP-695,
CC APP-751 and APP-770. These isoforms are derived by alternative splicing.
CC APP-RFP 751 is constructed by ligating restriction fragments representing
CC N- and C-terminal APP-751 cDNA and substrate P reporter epitope
CC sequences (present sequence) APP can be used as a substrate for studying
CC abnormal proteolytic cleavage which results in the release of BAP, and
CC also to screen for drugs that will inhibit such cleavage.
XX
SQ Sequence 11 AA:
AAM42973 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGLM
!!AA_SEQUENCE 1.0
ID AAY30985 standard; peptide; 11 AA.
XX
AC AAY30985;
XX
DT 21-OCF-1999 (first entry)
XX
DE Non-crosslinked protein particle peptide 34.
XX
KM Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
XX albumin; haemoglobin; nanometer; micrometer; clearance.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 11
XX /note="C-terminal amide"
XX
PN US5945033-A.
XX
PD 31-AUG-1999.
XX
PE 12-NOV-1996; 96US-0747137.
XX
PR 14-MAR-1994; 94US-0212546.
PR 15-JAN-1991; 91US-0641720.
PR 13-OCT-1992; 92US-0959560.
PR 01-JUN-1993; 93US-0069831.
PR 12-NOV-1996; 96US-0747137.
XX
PA (HBM-) HEMOSPHERE INC.
XX
PI Yen RCK;
XX
DR WPI; 1999-508153/42.
XX
XX Non-crosslinked protein particles for therapeutic and diagnostic use
XX
XX Example 22; Column 63-64; 65pp; English.
PS

XX
CC This invention describes a novel aqueous suspension of monodisperse
CC particles on non-crosslinked, non-denatured albumin (50-5000 nm) which
CC is stable against dissolving upon dilution with an alcohol-free aqueous
CC medium. The method involves (a) forming an aqueous solution containing
CC albumin and hemoglobin and (b) treating the aqueous solution with an
CC alcohol to cause the solution to become turbid. The particles are useful
CC as agents for in vivo administration, either of their own administration
CC or as a vehicle for other therapeutic or diagnostic agents. The method
CC permits the formation of albumin and hemoglobin particles in the
CC nanometer and micrometer size range, in a form closer to their natural
CC form than the forms of the prior art. The particles therefore constitute
CC a more closely controlled agent for in vivo administration, with greater
CC ease of clearance from the body after their period of usefulness.
XX
SQ Sequence 11 AA:
AAY30985 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGLM
!!AA_SEQUENCE 1.0
ID AAY34864 standard; Protein; 218 AA.
XX
AC AAY34864;
XX
DT 13-SEP-1999 (first entry)
XX
DE Chlamydia pneumoniae transmembrane protein sequence.
XX
KM Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KM sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KM vaccine; neutralising epitope.
XX
OS Chlamydia pneumoniae.
XX
PN WO9927105-A2.
XX
ED 03-JUN-1999.
XX
PE 20-NOV-1998; 98WO-IB01890.
XX
PR 04-NOV-1998; 98US-0107078.
PR 21-NOV-1997; 97FR-0014673.
XX
PA (GEST) GENSET.
XX
PI Griffiths R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae
XX
PS Page 809-810; Disclosure; 1912pp; English.
XX
CC AAY34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAX91990) of Chlamydia pneumoniae.
CC C. pneumoniae causes respiratory disease such as pneumonia and
CC bronchitis and is thought to be a contributing factor in heart
CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in
CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae.
XX
SQ Sequence 218 AA:
AAY34864 Length: 252 April 1, 2002 16:31 Type: P Check: 8364 ..
1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO GYPSPTAKK

51 LAQLEPGAIT LVKHNDRF PKETLAERIV DHSVAREIVD HCGTLIGTSA
101 NLSEPPSALT AQEIFADPAD HDLCIFEDGPC SHGLESTYVA SDPLYTYREG
151 LISRSVIEINI AGTEAKIFHR TSHAFSKHK IYTVKNQEOI VSFSLGSLDF
201 KGVCSEHPPR KNEYTRLREA LKRRTPSIYF IYDINTSDYP ELFPFLSPYV
251 IE

!!AA_SEQUENCE 1.0
ID AAY13564 standard; Protein: 1381 AA.

AC AAY13564;
XX
XX 30-JUL-1999 (first entry)
DT
XX Drosophila Robo 2 polypeptide.
DE
XX Comm polypeptide; Robo polypeptide; commissureless; roundabout;
KW modulation; nerve cell function.
XX
XX Drosophila sp.
XX WO9925833-A1.
XX 27-MAY-1999.
XX 13-NOV-1998; 98WO-US24327.
XX 14-NOV-1997; 97US-0065543.
PR
XX (REGC) UNIV CALIFORNIA.
PA
XX Goodman C, Kidd T, Mitchell KJ, Russell C, Tear G;
DR WPI; 1999-338008/28.
DR N-PSDB; AAX55768.
XX
XX Modulation of Robo-Comm polypeptide interactions
PT
XX Disclosure; Page 34-38; 56pp; English.
PS
XX

CC The invention relates to a method for modulating the amount of Comm
CC (commissureless) polypeptide in contact with a cell expressing active
CC Robo (roundabout) on its surface. The method comprises modulating the
CC effective amount of Comm polypeptide in contact with the cell, where the
CC amount of expressed active Robo is specifically modulated inversely with
CC the modulation of the effective amount of Comm in contact with the cell.
CC The method is used to modulate the amount of active Robo expressed on a
CC cell. The method can be used to screen for agents that modulate Robo:Comm
CC interactions. This is particularly useful for modulating nerve cell
CC function.

XX Sequence 1381 AA;

AAY13564 Length: 1415 April 1, 2002 16:31 Type: P Check: 940 ..

1 SQARNDBQGE ZGHSQILKMF PSTWVYSQOT HERSGENPRI IEHMDITVP
51 KNDPTEFKQO AEGNPTPTIQ WFKDGRLEKT DTGSHRIMLP AGGLEFLKVI
101 HSRRESDAQT YMCEAKNEFG VARSNATLQ VAVLRDEFRL EPANTRVAOG
151 EVALMEGJAP RGSPEQISW RKNQOTLNV GKKRIRIYDG GNLAIOEHRQ
201 SDDGRYQV VV KNYVGTRESA TAPLKVHVR FLIRPPQNGT AVVGSSVVFQ
251 CRIGGDPAPD VLMRRTASG NMPLRKFSWL HSASGRVHL EDRSLKLDYV
301 TLEDGGETTC EADNAVGGIT ATGILTVHAP PKFVIRPKNO LVEIGDEVLF

351 ECQANGHPRP TLVWSVEGNS SLLLPGRDG RMEVTLTPEG RSVLIAIFA
401 REDSGKVYTC NALNAVGSVS SRTVVSVDQ FELPPPIBO GPVNOQLPVK
451 SIIVLPCRTL GTPVPQYSWY LDIPIPIDVOE HERRNISDAG ALITSDLORH
501 EDEGLYTCVA SNRNGKSSWS GYLRLDPTN PIKFFRADE LSTYGPBGK
551 PQWKEGENS VTLSTRSNK VGGSSLYGVY IMFGEKNETD GWVAVGTRVQ
601 NTFQTOTGLL PGVNYFFLIR AENSHGISLP SPMSSEPIYWG TRYNSGLDL
651 SEARASLSLG DVELSNASV VDSTSMKLTW QIINCKRYEG FYVYAROLPN
701 PIVNNPAPVT SNTNPLLGST STSASASASA SALISTKPMI AAAGKROGET
751 NQSGGAPTP LNTKYRMITI LINGGASSCT ITGLVQYITLY EFFYIPFYKS
801 VEGKPSNSRI ARTLEDVPE APYGMETALL NSSAVFLKWK APELKRHGV
851 LLNHYIVRG IDTAHNSRI LTNVTIDAAS PTLVLANLTE GMYTVGVAA
901 GNNAGVGYPC VPATLRDPI TKRLDEPIQ RQVNDVLTQ PMFTILIGAI
951 LAVLMLSEGA MVEYKRRHM MKQSAINTMR GHTSDVLYKM PSLARNNG
1001 YWLDSTGGM VMRSPGDS LEMQKDIAD YAPVCGAPGS PAGGTSISGG
1051 SGGAGSGASG GDDIHGHS ERNQRYVE YSNIPTDYAE VSSGKAPSE
1101 YGRHGNASPA PYATSSILSP HQOQOQOQPR YQORVPYGV LQRPMPHYQ
1151 QOOHQOQOAO QTHQOHALQ OHQQLPPSNI YQOMSTSEI YPTNTPSRS
1201 YSEQYIYYPK DKQRIHITE NKLNSCHYTE AAPGAKQSSP ISSQFASVRR
1251 QQLPNCSTG RESARFVYN TDGKNQOQL LDLDSSMCY NGLDSCGG
1301 SPSPMAMLMS HEDHALYHT ADGDLDMER LYVKVDEQOP PQOQOQLIPL
1351 VPQHPAEGHL QSMRNOSTRS SRKNGQECIK EPELIIYABG SVASERSILS
1401 NSGCTSSOP AGHNV

!!AA_SEQUENCE 1.0
ID AAY08402 standard; Protein: 1380 AA.

AC AAY08402;

DT 24-JUL-1999 (first entry)

DE Drosophila sp. ROBO2 extracellular domain protein.

KW ROBO1, ROBO2; roundabout; nerve guidance; human; murine; cell function;
KW cell morphology; screening assay.

XX Drosophila sp.

XX WO9920764-A1.

XX 29-APR-1999.

XX 20-OCT-1998; 98WO-US22164.

XX 14-NOV-1997; 97US-0971172.

XX 20-OCT-1997; 97US-0062921.

XX (REGC) UNIV CALIFORNIA.

XX Goodman CS, Kidd T, Mitchell KJ, Tear G;

XX WPI; 1999-312615/26.
XX N-PSDB; AAX57251.

Robo polypeptides, a new immunoglobulin superfamily member
Claim 1: Page 52-56; 80pp; English.

This invention describes novel Robo (roundabout) polypeptides, involved in nerve guidance which have been isolated from *Drosophila* sp., *C. elegans*, human and murine samples. The products of the invention can be used to raise anti-Robo antibodies, which can be used to modulate cell function or morphology. The Robo polynucleotides and fragments are useful as probes and primers and for production of the Robo polypeptides. The probes and primers are also useful in screening assays.

Sequence 1380 AA;

AAV08402 Length: 1414 April 1, 2002 16:31 Type: P Check: 7245 ..

1 SQARNDBCE ZGHSQILKMF PSTWVVSQOT HERSGENPRI IEHPMDTVP
51 KNDPFTFNCQ AEGNPTPTIQ WFKDGRRLKT DTGSHRIMLP AGGLFELKVI
101 HSRRESDAQT YWCEAKNEEG VARSRNATLQ VAVLRDEFRL EPANTRVAG
151 EVALMECGAP RGSPEPOISW RKNQOTLNLV GNNRIRIVDG GNLAIOEARQ
201 SDDGRYOCVV KNVGCTRESA TAFLKVHVRP FLIRGPONQT AVGSSVVEQ
251 CRIGGDPLDP VLMRRTASGG NMPLRKFSWL HSASGRVHYL EDRSLKLDDV
301 TLEDMEGYTC EADNAVGCIT ATGILTVHAP PKFVIRPKNO IWEIGDEVLF
351 ECOANGHPRP TLYWSVEGNS SILLPGYRDG RMEVTLTPEG RSVLSIARPA
401 REDSGKVYTC NALNAVGSVS SRTVVSVDTO FELPEPTIEG GGVNQTLPVK
451 STVVLPCRTL GTPVPOVSWY LDGIPIDVQE HERRNLSDAG ALTIIDLORH
501 EDEGLITCYA SNRNKSSSMS GYLRLDPTPN PNKFFRAPE LSTYGPPEK
551 PQWKEGENS VTLSTRSNK VGSGLVGYV IEMFGNEND GWAVAGTRVQ
601 MTTFTOTGLL PGVNYFELLIR AENSHGLSLP SPNSEPTVWG TRYENSGDL
651 SEARASLBSG DVELSNASV VDSSTMKLTW QIINGRYVEG FYVYARQLPN
701 PIYNNAPAPT SNTNPLGST STSASASASA SALISRKPN IAAAGRDGET
751 NMSGGAPTP LNTKYRMLTI LNSGGASSCT ITGLVOYTYL EEFIPEPKS
801 VEGKPSNSRI ARTLEDVPS E APYGMEALLL NSSAVFLKWK APELDRHGV
851 LNTYHYIVG IDTAHNFTRI LTNVTIDAAS PTLVLANLTE GMYTYGVAA
901 GNNAGVGYPC VPATLRDLP I TKRLDPPINQ RDHAVNDVLQ PMFTILLGAI
951 LAVLMLSPGA WVFYKRKHHM MKGALNTMR GNHTSDVLKM PLSARNGNG
1001 YMLDSSTGGM VWRSPSGDS LEMOKDHIAD YAPVCCAPGS PAGGGTSSCG
1051 SGGAGSGASG GDDIHGHGS ERNOORYVE YSNIPTDYAE VSSFGKAPSE
1101 YGRHGNASPA PYATSSILSP HQOQOQOOPR YQORPVGYG LQRPMPHYQ
1151 QOQHQQQQAQ QTHQHQALQ QHQQLPSPNI YQQMSTTSEI YPTNCPSPS
1201 VYSEQYYRK DKORHIHEN KLSNCHTEA APGAKOSSPT SSQFASVRQ
1251 QLPNCSIGR ESARPKVLNT DQGRNQOML DLDGSSMCYN GLADSGCGS
1301 PSPMAMLMGH EDEHALYHTA DGDLDMERL YKVVEQOPP QQQOQLIPV
1351 PQHPABGHQ SWRNOSTRSS RKNQOECKE PSELIYAPGS VASERSLSN

1401 SSGSTSSQPA GHNV

11AA_SEQUENCE 1.0
ID AAV03156 standard; peptide; 11 AA.

AAV03156;

10-JUN-1999 (first entry)

Substance P.

Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;

substance P.

Synthetic.

US5891842-A.

06-APR-1999.

12-APR-1996; 96US-0631434.

09-APR-1993; 93US-0044954.

12-APR-1996; 96US-0631434.

(TUFT) TUFTS COLLEGE.

Kream RM;

WPI; 1999-253906/21.

Synergistic method for enhancing opioid analgesia and anaesthesia

within a human

Disclosure; Column 14; 20pp; English.

This sequence represents substance P used in the method of the invention. The method is for enhancing opioid analgesia within a human subject for a duration of 15 minutes comprises concurrent administration of substance P, or one of its precursors. The method is used to elicit opioid analgesia and anaesthesia, either prior to or after the occurrence of a nociceptive event. The components have a synergistic effect. The method allows use of low doses of opioid that produce little or no physiological effect reducing conventional risks of toxicity and addiction, and allows the use of low doses of substance P and its related analogs that limit their in vivo physiological consequences. The analgesia is naloxone reversible allowing diminishment or complete elimination of opioid analgesia if desired and on demand. The treatment provides a durable analgesic effect, but only minimally disturbs and interrupts the normal metabolic processes of the body.

Sequence 11 AA;

AAV03156 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIM

11AA_SEQUENCE 1.0
ID AAV03157 standard; peptide; 12 AA.

AAV03157;

10-JUN-1999 (first entry)

Substance P-Glycine.

Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;

substance P.

Synthetic.

US5891842-A.

PD 06-APR-1999.
XX
XX 12-APR-1996; 96US-0631434.
XX
PR 09-APR-1993; 93US-0044954.
PR 12-APR-1996; 96US-0631434.
XX
PA (TUFT) TUFTS COLLEGE.
XX
XX
PI Kream RM:
XX
XX WPI, 1999-253906/21.
DR
XX
XX Synergistic method for enhancing opioid analgesia and anaesthesia
PT within a human
XX
XX
PS Disclosure; Column 14; 20pp; English.
XX
XX This sequence represents substance P used in the method of the
CC invention. The method is for enhancing opioid analgesia within a human
CC subject for a duration of 15 minutes comprises concurrent administration
CC of substance P, or one of its precursors. The method is used to elicit
CC opioid analgesia and anaesthesia, either prior to or after the occurrence
CC of a nociceptive event. The components have a synergistic effect. The
CC method allows use of low doses of opioid that produce little or no
CC physiological effect reducing conventional risks of toxicity and
CC addiction, and allows the use of low doses of substance P and its related
CC analogs that limit their in vivo physiological consequences. The
CC analgesia is naloxone reversible allowing diminishment or complete
CC elimination of opioid analgesia if desired and on demand. The treatment
CC provides a durable analgesic effect, but only minimally disturbs and
CC interrupts the normal metabolic processes of the body.
XX
SQ Sequence 12 AA;
AAV03157 Length: 46 April 1, 2002 16:31 Type: P Check: 3988 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FGLMG
ID AAY03158 standard; peptide; 13 AA.
XX
AC AAY03158;
XX
XX 10-JUN-1999 (first entry)
DT
XX
XX Substance P-Glycine-Lysine.
DE
XX
XX Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
KW substance P.
XX
XX Synthetic.
OS
XX
XX US5891842-A.
PN
XX
XX 06-APR-1999.
PD
XX
XX 12-APR-1996; 96US-0631434.
PF
XX
XX 09-APR-1993; 93US-0044954.
PR
XX
XX 12-APR-1996; 96US-0631434.
PR
XX
XX (TUFT) TUFTS COLLEGE.
PA
XX
XX
PI Kream RM:
XX
XX WPI, 1999-253906/21.
DR
XX
XX Synergistic method for enhancing opioid analgesia and anaesthesia
PT within a human
XX
XX
PS Disclosure; Column 14; 20pp; English.

CC This sequence represents substance P used in the method of the
CC invention. The method is for enhancing opioid analgesia within a human
CC subject for a duration of 15 minutes comprises concurrent administration
CC of substance P, or one of its precursors. The method is used to elicit
CC opioid analgesia and anaesthesia, either prior to or after the occurrence
CC of a nociceptive event. The components have a synergistic effect. The
CC method allows use of low doses of opioid that produce little or no
CC physiological effect reducing conventional risks of toxicity and
CC addiction, and allows the use of low doses of substance P and its related
CC analogs that limit their in vivo physiological consequences. The
CC analgesia is naloxone reversible allowing diminishment or complete
CC elimination of opioid analgesia if desired and on demand. The treatment
CC provides a durable analgesic effect, but only minimally disturbs and
CC interrupts the normal metabolic processes of the body.
XX
SQ Sequence 13 AA;
AAV03158 Length: 47 April 1, 2002 16:31 Type: P Check: 7513 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FGLMGK
ID AAY03159 standard; peptide; 14 AA.
XX
AC AAY03159;
XX
XX 10-JUN-1999 (first entry)
DT
XX
XX Substance P-Glycine-Lysine-Arginine.
DE
XX
XX Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
KW substance P.
XX
XX Synthetic.
OS
XX
XX US5891842-A.
PN
XX
XX 06-APR-1999.
PD
XX
XX 12-APR-1996; 96US-0631434.
PF
XX
XX 09-APR-1993; 93US-0044954.
PR
XX
XX 12-APR-1996; 96US-0631434.
PR
XX
XX (TUFT) TUFTS COLLEGE.
PA
XX
XX
PI Kream RM:
XX
XX WPI, 1999-253906/21.
DR
XX
XX Synergistic method for enhancing opioid analgesia and anaesthesia
PT within a human
XX
XX
PS Disclosure; Column 14; 20pp; English.
XX
XX This sequence represents substance P used in the method of the
CC invention. The method is for enhancing opioid analgesia within a human
CC subject for a duration of 15 minutes comprises concurrent administration
CC of substance P, or one of its precursors. The method is used to elicit
CC opioid analgesia and anaesthesia, either prior to or after the occurrence
CC of a nociceptive event. The components have a synergistic effect. The
CC method allows use of low doses of opioid that produce little or no
CC physiological effect reducing conventional risks of toxicity and
CC addiction, and allows the use of low doses of substance P and its related
CC analogs that limit their in vivo physiological consequences. The
CC analgesia is naloxone reversible allowing diminishment or complete
CC elimination of opioid analgesia if desired and on demand. The treatment
CC provides a durable analgesic effect, but only minimally disturbs and
CC interrupts the normal metabolic processes of the body.
XX
SQ Sequence 14 AA;
AAV03159 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPRKPOQ FFGLMGR

11AA_SEQUENCE 1.0
ID AAY03162 standard; peptide: 9 AA.
XX
AC AAY03162;
XX
DT 10-JUN-1999 (first entry)
XX
DE Substance P fragment P/1-9#.
XX
KW Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
KW substance P.
XX
OS Synthetic.
XX
PN US5891842-A.
XX
PD 06-APR-1999.
XX
PE 12-APR-1996; 96US-0631434.
XX
PR 09-APR-1993; 93US-0044954.
PR 12-APR-1996; 96US-0631434.
XX
PA (TUFT) TUFTS COLLEGE.
XX
FI Kream RM:
XX
DR WPI; 1999-253906/21.
XX
PT Synergistic method for enhancing opioid analgesia and anaesthesia
PT within a human
XX
PS Disclosure; Column 14; 20pp; English.
XX
CC This sequence is a fragment of substance P used in the method of the
CC invention. The method is for enhancing opioid analgesia within a human
CC subject for a duration of 15 minutes comprises concurrent administration
CC of substance P, or one of its precursors. The method is used to elicit
CC opioid analgesia and anaesthesia, either prior to or after the occurrence
CC of a nociceptive event. The components have a synergistic effect. The
CC method allows use of low doses of opioid that produce little or no
CC physiological effect reducing conventional risks of toxicity and
CC addiction, and allows the use of low doses of substance P and its related
CC analogs that limit their in vivo physiological consequences. The
CC analgesia is naloxone reversible allowing diminishment or complete
CC elimination of opioid analgesia if desired and on demand. The treatment
CC provides a durable analgesic effect, but only minimally disturbs and
CC interrupts the normal metabolic processes of the body.
XX
SQ Sequence 9 AA:
AAY03162 Length: 43 April 1, 2002 16:31 Type: P Check: 3913 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPRKPOQ FFG

11AA_SEQUENCE 1.0
ID AAW99689 standard; peptide: 11 AA.
XX
AC AAW99689;
XX
DT 03-JUN-1999 (first entry)
XX
DE Substance P analogue #6.
XX
KW Substance P receptor antagonist; analgesic; inhibitor; NMDA blocker;
KW nontoxic N-methyl-D-aspartate receptor antagonist; muscular pain;
KW musculoskeletal pain; chronic pain; neuropathic pain; migraine.
XX
OS Synthetic.
XX

FH Key Location/Qualifiers
FT Modified-site 10. 11
FT FT /note= "Leu-psi(CH2-NH)-Leu"
FT Modified-site 11
FT FT /note= "amidated"
XX
PN W09907413-A1.
XX
PD 18-FEB-1999.
XX
PE 26-MAY-1998; 98WO-US10707.
XX
PR 11-AUG-1997; 97US-0055233.
XX
PA (ALGO-) ALGOS PHARM CORP.
XX
PI Caruso FS;
XX
DR WPI; 1999-167216/14.
XX
PT New analgesic composition comprises - a substance P receptor
PT antagonist with a substance P receptor antagonist potentiator, used
PT for the treatment of pain
XX
PS Claim 3; Page 29; 54pp; English.
XX
CC A method has been developed for treating pain with: (a) a substance P
CC receptor antagonist; and (b) a substance P receptor antagonist
CC potentiator, i.e. N-methyl-D-aspartate (NMDA) receptor antagonist or
CC substance that blocks at least 1 major intracellular consequence of
CC NMDA receptor activation. The method can be used for treating muscular,
CC musculoskeletal, chronic or neuropathic pain, or migraine. The present
CC sequence represents a substance P analogue for use in the method.
XX
SQ Sequence 11 AA:
AAW99689 Length: 45 April 1, 2002 16:31 Type: P Check: 677 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPRKPOQ FFG

11AA_SEQUENCE 1.0
ID AAW99690 standard; peptide: 11 AA.
XX
AC AAW99690;
XX
DT 03-JUN-1999 (first entry)
XX
DE Substance P analogue #7.
XX
KW Substance P receptor antagonist; analgesic; inhibitor; NMDA blocker;
KW nontoxic N-methyl-D-aspartate receptor antagonist; muscular pain;
KW musculoskeletal pain; chronic pain; neuropathic pain; migraine.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT FT /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT FT /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT FT /note= "D-form residue"
FT Modified-site 9. 10 /note= "Tyr-psi(CH2-NH)-Leu"
FT FT /note= "Tyr-psi(CH2-NH)-Leu"
FT Modified-site 11 /label= Nle
FT FT /note= "Norleucine, amidated"
XX
PN W09907413-A1.
XX
PD 18-FEB-1999.
XX
PE 26-MAY-1998; 98WO-US10707.

```

XX 11-AUG-1997; 97US-0055233.
PR (ALGO-) ALGOS PHARM CORP.
XX Caruso FS;
XX WPI; 1999-167216/14.
XX New analgesic composition comprises - a substance P receptor
PT antagonist with a substance P receptor antagonist potentiator, used
PT for the treatment of pain
XX Claim 3; Page 29; 54pp; English.
XX A method has been developed for treating pain with: (a) a substance P
CC receptor antagonist; and (b) a substance P receptor antagonist or
CC potentiator, i.e. N-methyl-D-aspartate (NMDA) receptor antagonist or
CC substance that blocks at least 1 major intracellular consequence of
CC NMDA receptor activation. The method can be used for treating muscular,
CC musculoskeletal, chronic or neuropathic pain, or migraine. The present
CC sequence represents a substance P analogue for use in the method.
XX Sequence 11 AA;
SQ
AAW99690 Length: 45 April 1, 2002 16:31 Type: P Check: 2602 ..
1 SQARNDBCOE ZGHSQILKMF PSTWYSQOR HERSRKPQO WFWLX
11AA_SEQUENCE 1.0
ID AAW99691 standard; peptide; 11 AA.
XX AAW99691;
XX 03-JUN-1999 (first entry)
XX Substance P analogue #8.
XX
XX Substance P receptor antagonist; analgesic; inhibitor; NMDA blocker;
XX nontoxic N-methyl-D-aspartate receptor antagonist; muscular pain;
XX musculoskeletal pain; chronic pain; neuropathic pain; migraine.
XX Synthetic.
XX Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-form residue"
XX FT Misc-difference 7 /note= "D-form residue"
XX FT Modified-sits 7.8 /note= "D-form residue"
XX FT Misc-difference 9 /note= "D-form residue"
XX FT Modified-site 11 /label= Nle
XX FT /note= "Norleucine, amidated"
XX WO9907413-A1.
XX 18-FEB-1999.
XX 26-MAY-1998; 98WO-US10707;
XX 11-AUG-1997; 97US-0055233.
XX (ALGO-) ALGOS PHARM CORP.
XX Caruso FS;
XX WPI; 1999-167216/14.
XX New analgesic composition comprises - a substance P receptor
PT antagonist with a substance P receptor antagonist potentiator, used

```

```

PT for the treatment of pain
XX Claim 3; Page 29; 54pp; English.
XX A method has been developed for treating pain with: (a) a substance P
CC receptor antagonist; and (b) a substance P receptor antagonist or
CC potentiator, i.e. N-methyl-D-aspartate (NMDA) receptor antagonist or
CC substance that blocks at least 1 major intracellular consequence of
CC NMDA receptor activation. The method can be used for treating muscular,
CC musculoskeletal, chronic or neuropathic pain, or migraine. The present
CC sequence represents a substance P analogue for use in the method.
XX Sequence 11 AA;
SQ
AAW99691 Length: 45 April 1, 2002 16:31 Type: P Check: 2602 ..
1 SQARNDBCOE ZGHSQILKMF PSTWYSQOR HERSRKPQO WFWLX
11AA_SEQUENCE 1.0
ID AAW74445 standard; Protein; 1184 AA.
XX AAW74445;
XX 12-MAY-1999 (first entry)
XX Human nucleotide pyrophosphohydrolase, NTPPH-1.
XX NTPPH-1; human: nucleotide pyrophosphohydrolase; arthropathy; therapy;
XX immunological disorders; cancer; haemodialysis; infection;
XX extracorporeal circulation.
XX Homo sapiens.
XX US5876963-A.
XX 02-MAR-1999.
XX 27-AUG-1997; 97US-0918914.
XX 27-AUG-1997; 97US-0918914.
XX HUTCHINSON N.
XX (HUTC/) HUTCHINSON N.
XX (LAWT/) LAWTON M.
XX (MAGN/) MAGNA H.
XX (MITC/) MITCHELL P.
XX (MURR/) MURRY L E.
XX (YOCU/) YOCUM S.
XX HUTCHINSON N, Lawton M, Magna H, Mitchell P, Murry LE;
XX Yocum S;
XX WPI; 1999-189634/16.
XX N-PSDB; AAX18449.
XX New human nucleotide pyrophosphohydrolase - useful for providing
PT methods for identifying and treating arthropathies, immunological
PT disorders, and cancer
XX Claim 1; Fig 1; 42pp; English.
XX This sequence represents the human nucleotide pyrophosphohydrolase,
CC designated NTPPH-1, of the invention. NTPPH-1 antagonists, antibodies,
CC agonists, proteins, complementary sequences or vectors can be used to
CC treat and identify arthropathies (e.g. calcium pyrophosphate dihydrate
CC deposition disease, degenerative joint disease, fibromyalgia,
CC haemochromatosis, osteoarthritis, progressive systemic sclerosis,
CC pseudogout, psoriasis, rheumatoid arthritis and lupus erythematosus);
CC immunological disorders (e.g. AIDS, allergies, anaemia, asthma,
CC ulcerative colitis, dermatomyositis, diabetes mellitus, emphysema,
CC glomerulonephritis, gout, multiple sclerosis, osteoporosis and
CC pancreatitis), trauma; complications of cancer, haemodialysis, and
CC extracorporeal circulation; viral, bacterial, fungal, parasitic,
CC protozoal, and helminthic infections; and cancer (e.g. adenocarcinoma,

```

CC lymphoma, melanoma, myeloma, sarcoma, leukaemia, or teratocarcinoma of
 CC the bone and bone marrow, brain, breast, cervix, gastrointestinal tract,
 CC kidney, liver, lung, ovary, testis and skin).
 XX
 SO Sequence 1184 AA:

AAW74445 Length: 1218 April 1, 2002 16:31 Type: P Check: 9834 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVYSOOT HERSWVGTRKA WVFSLVLEV
 51 TSVLGRQTM L TQSVRRYQPG KKNPSIFAKP ADLTLESPEW TTMFNIDTPG
 101 GKGDYERLDA IREYVGDRC ARPLRLAET TDMTPAGSTG QVYHSGPREG
 151 FMCINREQRP GQNCNNTVR FLCPPGSLRR DTERIWSFWS PWSKCSAAG
 201 QTGVQTRIRI CLAEWVSLCS EASEGQHOM GODCTACDILT CPMQOVNADC
 251 DACMCOPEML HGAVSLPFGA PASGAAYILL TKTPKLLTQT DSDGRFRIPG
 301 LCPDGKSLK ITRKVFAPIV LMPKTSLKA ATIKAEFRA ETPYMWNPPE
 351 TKRARGOSV SLCCKATGKP RPDKYFWYHN DTLDPSTLYK HESKLVLRKL
 401 QOHAGEYFC KAQSDAGAVK SKVAQLIVIA SDETPCNPVP ESYLIRLPHD
 451 CPOANTNFY YDVGRCPVKT CAGQDNGIR CRDAVQNCG ISKKEEREIO
 501 CSGYTLPTKV AKECSCQRC TERSIVRGV SAADNGEPMR FGHVYMGNSR
 551 VSMGKYKFTV TLHVPODTER LVLTFFVDRLO KEVNTTKVLP FNKKSAAVFH
 601 EIKMKCRKEP ILEAMETNI IPLGEVVGED PMAELEISR SFYQNGEPI
 651 IGKVKASVTF LDPRNISTAT AAOCTDLNFIN DEGDFFPLRT YGMSVDFRD
 701 EVTSEPLNAG KVKVHLDSTQ VKMPEHISTV KLSLNPDTG LMEBEGDFKF
 751 ENORNRKRED RTFLVGNLEI RERRLFNDLV PESRRCFVKV RAYISERLPL
 801 SEQIOGVVIS VINLEPRTGF LSNPRAMGRP DSVITGPNGA CVPAFCDDOS
 851 PDASAVYLA SLAGEELQAV ESSPKFNPNA IGVPOPYLTK LNYRTDHD
 901 PRVKKTAFOI SMAKPRNSA EESNGPIYAF ENLRACEEAP PSAHFRFYQ
 951 IEGDRYDINT VPENEDDPM S WTEDYLAAMP KMEFRACIY KVKIVGPLEV
 1001 NVSRNMGCT HRTVGLYLG IRDVRSTRDR DQPNVSACL EFKCSGMLYD
 1051 QDRVORTLVK VIIPGSCRA SVNPMLEHYL VNHLPYLVANN DTSEYTMAP
 1101 LDPLGHNTGI YTYVDQDPT AKELIAGRCF DGTSGSSSI MKNVGYALT
 1151 FNCVERQYQR QSAFOYLQST PAQSPAAGTV QGRVPSRRQO RASRGQROS
 1201 GVVASLREPR VAQOPLIN
 !!AA_SEQUENCE 1.0
 ID AAW92709 standard; peptide: 11 AA.
 XX
 AC AAW92709;
 XX
 DT 30-APR-1999 (first entry)
 DE Human tachykinin agonist beta-amyloid peptide fragment #55.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenital anglopathy.
 XX
 OS Homo sapiens.
 XX

PH Key Location/Qualifiers
 FT Modified-site 9
 FT /label= Megly
 FT /note= "N-methyl-glycine (sarcosine)"
 FT Modified-site 11
 FT /note= "Residue is Met(O2)"
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PE 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI: 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS Disclosure: Column 35-36; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital anglopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SO Sequence 11 AA:

AAW92709 Length: 45 April 1, 2002 16:31 Type: P Check: 1217 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVYSOOT HERSRPPQO FFGIX

!!AA_SEQUENCE 1.0
 ID AAW92711 standard; peptide: 8 AA.
 XX
 AC AAW92711;
 XX
 DT 30-APR-1999 (first entry)
 DE Human tachykinin agonist beta-amyloid peptide fragment #57.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenital anglopathy.
 XX
 OS Homo sapiens.
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PE 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI: 1999-189630/16.
 XX

PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 PS Disclosure: Column 35-36; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SQ Sequence 8 AA;
 AAW92711 Length: 42 April 1, 2002 16:31 Type: P Check: 860 ..
 1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FF
 !!AA_SEQUENCE 1.0
 ID AAW92715 standard; peptide; 11 AA.
 AC AAW92715;
 DT 30-APR-1999 (first entry)
 DE Human tachykinin agonist beta-amyloid peptide fragment #61.
 XX
 KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KM hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 10
 FT /label= Mewet
 FT /note= "N-methyl-leucine"
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 PI Yankner BA;
 DR WPI: 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 PS Disclosure: Column 37-38; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SQ Sequence 11 AA;

AAW92715 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
 1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFGFM
 !!AA_SEQUENCE 1.0
 ID AAW92716 standard; peptide; 11 AA.
 AC AAW92716;
 DT 30-APR-1999 (first entry)
 DE Human tachykinin agonist beta-amyloid peptide fragment #62.
 XX
 KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KM hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
 XX
 OS Homo sapiens.
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 PI Yankner BA;
 DR WPI: 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 PS Disclosure: Column 37-38; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SQ Sequence 11 AA;
 AAW92716 Length: 45 April 1, 2002 16:31 Type: P Check: 898 ..
 1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFGFM
 !!AA_SEQUENCE 1.0
 ID AAW92717 standard; peptide; 11 AA.
 AC AAW92717;
 DT 30-APR-1999 (first entry)
 DE Human tachykinin agonist beta-amyloid peptide fragment #63.
 XX
 KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KM hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 11
 FT /label= Mewet

```

FT      /note= "N-methyl-methionine"
XX
XX      US5876948-A.
XX
XX      02-MAR-1999.
XX
XX      27-JUL-1991; 91US-0737371.
XX
XX      29-JUL-1991; 91US-0737371.
XX      27-JUL-1990; 90US-0559173.
XX
XX      (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX      Yankner BA;
XX
XX      WPI; 1999-189630/16.
XX
XX      Screening for neurotoxin inhibitors - by testing compounds for their
XX      effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX      Disclosure; Column 37-38; 28pp; English.
XX
XX      This invention describes a method for screening compounds for inhibiting
XX      a neurotoxin. The method involves incubating tachykinin agonists with
XX      neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX      used for identifying compounds for treating diseases characterised by an
XX      undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX      Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX      with amyloidosis and non-inherited congenital angiodopathy with cerebral
XX      haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX      beta-amyloid peptide fragments.
XX
XX      Sequence 11 AA;
XX
XX      AAW92717 Length: 45 April 1, 2002 16:31 Type: P Check: 1217 ..
XX
XX      1 SQARNDBOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGIX
XX
!!AA_SEQUENCE 1.0
ID      AAW92718 standard; peptide: 11 AA.
XX
XX      AAW92718;
XX
XX      30-APR-1999 (first entry)
XX
XX      Human tachykinin agonist beta-amyloid peptide fragment #64.
XX
XX      Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX      Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX      hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX      Homo sapiens.
XX
XX      US5876948-A.
XX
XX      02-MAR-1999.
XX
XX      27-JUL-1991; 91US-0737371.
XX
XX      29-JUL-1991; 91US-0737371.
XX      27-JUL-1990; 90US-0559173.
XX
XX      (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX      Yankner BA;
XX
XX      WPI; 1999-189630/16.
XX
XX      Screening for neurotoxin inhibitors - by testing compounds for their
XX      effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX      Disclosure; Column 37-38; 28pp; English.
XX

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CC      This invention describes a method for screening compounds for inhibiting
CC      a neurotoxin. The method involves incubating tachykinin agonists with
CC      neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC      used for identifying compounds for treating diseases characterised by an
CC      undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC      Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC      with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC      haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC      beta-amyloid peptide fragments.
XX
XX      Sequence 11 AA;
XX
XX      AAW92718 Length: 45 April 1, 2002 16:31 Type: P Check: 857 ..
XX
XX      1 SQARNDBOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLP
XX
!!AA_SEQUENCE 1.0
ID      AAW92719 standard; peptide: 11 AA.
XX
XX      AAW92719;
XX
XX      30-APR-1999 (first entry)
XX
XX      Human tachykinin agonist beta-amyloid peptide fragment #65.
XX
XX      Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
XX      Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX      hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX      Homo sapiens.
XX
XX      Key Location/Qualifiers
XX      Modified-site 9 /label= Methyl
XX      FT /note= "N-methyl-glycine"
XX
XX      US5876948-A.
XX
XX      02-MAR-1999.
XX
XX      27-JUL-1991; 91US-0737371.
XX
XX      29-JUL-1991; 91US-0737371.
XX      27-JUL-1990; 90US-0559173.
XX
XX      (CHIL-) CHILDRENS MEDICAL CENT.
XX
XX      Yankner BA;
XX
XX      WPI; 1999-189630/16.
XX
XX      Screening for neurotoxin inhibitors - by testing compounds for their
XX      effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX      Disclosure; Column 39-40; 28pp; English.
XX
XX      This invention describes a method for screening compounds for inhibiting
XX      a neurotoxin. The method involves incubating tachykinin agonists with
XX      neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX      used for identifying compounds for treating diseases characterised by an
XX      undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX      Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX      with amyloidosis and non-inherited congenital angiodopathy with cerebral
XX      haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX      beta-amyloid peptide fragments.
XX
XX      Sequence 11 AA;
XX
XX      AAW92719 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
XX
XX      1 SQARNDBOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLM
XX
!!AA_SEQUENCE 1.0

```

```

ID AAW92720 standard; peptide; 11 AA.
XX
XX AAW92720;
AC
XX
XX 30-APR-1999 (first entry)
DT
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #66.
DE
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 10
FT /label= Meteu
FT /note= "N-methyl-leucine"
XX
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 27-JUL-1991; 91US-0737371.
PF
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX Yankner BA;
XX
XX WPI; 1999-189630/16.
DR
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 39-40; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX Sequence 11 AA;
SQ
AAW92720 Length: 45 April 1, 2002 16:31 Type: P Check: 722
1 SQARNDBCQE ZGHSQILKMF PSTWVSQOT HERSRPRPOQ FFGLM
11AA_SEQUENCE 1.0
ID AAW92721 standard; peptide; 11 AA.
XX
XX AAW92721;
AC
XX
XX 30-APR-1999 (first entry)
DT
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #67.
DE
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 11
FT /label= Meteu
FT

```

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FT
XX
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 27-JUL-1991; 91US-0737371.
PF
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX Yankner BA;
XX
XX WPI; 1999-189630/16.
DR
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX Disclosure; Column 39-40; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
XX Sequence 11 AA;
SQ
AAW92721 Length: 45 April 1, 2002 16:31 Type: P Check: 898
1 SQARNDBCQE ZGHSQILKMF PSTWVSQOT HERSRPRPOQ FFGPM
11AA_SEQUENCE 1.0
ID AAW92708 standard; peptide; 11 AA.
XX
XX AAW92708;
AC
XX
XX 30-APR-1999 (first entry)
DT
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #54.
DE
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 7
FT /note= "Modification results in p-chloro-Phe"
FT Modified-site 8
FT /note= "Modification results in p-chloro-Phe"
XX
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 27-JUL-1991; 91US-0737371.
PF
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX Yankner BA;
XX
XX WPI; 1999-189630/16.
DR

```


XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS Disclosure: Column 33-34; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SQ Sequence 11 AA;

AAW92708 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCOE ZGHSQILKMF PSTWYSOOT HERSRPPQO FPGLM

!!AA_SEQUENCE 1.0
 ID AAW92677 standard; peptide; 11 AA.
 XX
 AC AAW92677;
 XX
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #23.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
 XX
 OS Homo sapiens.
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS Disclosure: Column 19-20; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SQ Sequence 11 AA;

AAW92677 Length: 45 April 1, 2002 16:31 Type: P Check: 1109 ..

1 SQARNDBCOE ZGHSQILKMF PSTWYSOOT HERSRPPQO FPGLM

!!AA_SEQUENCE 1.0
 ID AAW92678 standard; peptide; 11 AA.
 XX
 AC AAW92678;
 XX
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #24.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 9 /note= "D-form residue"
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS Disclosure: Column 19-20; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SQ Sequence 11 AA;

AAW92678 Length: 45 April 1, 2002 16:31 Type: P Check: 1109 ..

1 SQARNDBCOE ZGHSQILKMF PSTWYSOOT HERSRPPQO FPGLM

!!AA_SEQUENCE 1.0
 ID AAW92679 standard; peptide; 11 AA.
 XX
 AC AAW92679;
 XX
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #25.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
 XX
 OS Homo sapiens.
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.

XX 27-JUL-1991; 91US-0737371.
PF 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 21-22; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;
AAM92679 Length: 45 April 1, 2002 16:31 Type: P Check: 254 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPRQO FFGIM
11AA_SEQUENCE 1.0
ID AAM92680 standard; peptide; 11 AA.
XX
AC AAM92680;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #26.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 8 /note= "Residue is N-methyl-phenylalanine"
FT
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 21-22; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting

CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;
AAM92680 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPRQO FFGIM
11AA_SEQUENCE 1.0
ID AAM92681 standard; peptide; 11 AA.
XX
AC AAM92681;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #27.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 8 /note= "Residue is N-methyl-glycine"
FT
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 21-22; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;
AAM92681 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPRQO FFGIM
11AA_SEQUENCE 1.0
ID AAM92682 standard; peptide; 11 AA.
XX

AC AAW92682;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #28.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PE 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 21-22; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
CC
XX Sequence 11 AA;
SQ
AAW92682 Length: 45 April 1, 2002 16:31 Type: P Check: 4 ..
1 SQARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRPPCQ FFCIM
!!AA_SEQUENCE 1.0
ID AAW92683 standard; peptide; 11 AA.
XX
AC AAW92683;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #29.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PE 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 23-24; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
CC
XX Sequence 11 AA;
SQ
AAW92683 Length: 45 April 1, 2002 16:31 Type: P Check: 1726 ..
1 SQARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRPPCQ FFCIM
!!AA_SEQUENCE 1.0
ID AAW92684 standard; peptide; 11 AA.
XX
AC AAW92684;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #30.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PE 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 23-24; 28pp; English.
XX

PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 23-24; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
CC
XX Sequence 11 AA;
SQ
AAW92683 Length: 45 April 1, 2002 16:31 Type: P Check: 1726 ..
1 SQARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRPPCQ FFCIM
!!AA_SEQUENCE 1.0
ID AAW92684 standard; peptide; 11 AA.
XX
AC AAW92684;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #30.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PE 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 23-24; 28pp; English.
XX

CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

AAM92664 Length: 45 April 1, 2002 16:31 Type: P Check: 1523 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVYSOOT HERSRPRXPQ FPGXM

11AA_SEQUENCE 1.0
ID AAM92685 standard; peptide; 11 AA.

AC AAM92685;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #31.

DE Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KM Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.

OS Homo sapiens.

PN US5876948-A.

PD 02-MAR-1999.

PE 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PA Yankner BA;

PI WPI; 1999-189630/16.

DR Screening for neurotoxin inhibitors - by testing compounds for their

PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX Disclosure; Column 23-24; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting

CC a neurotoxin. The method involves incubating tachykinin agonists with

CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be

CC used for identifying compounds for treating diseases characterised by an

CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,

CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage

CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral

CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human

CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

AAM92665 Length: 45 April 1, 2002 16:31 Type: P Check: 9726 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVYSOOT HERSRPRXPQ FPGLC

11AA_SEQUENCE 1.0

ID AAM92686 standard; peptide; 11 AA.

AC AAM92686;

DT 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #32.
DE
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
KM hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified-site 5
FT FT /note="Residue is homocysteine"
FT Modified-site 11
FT FT /note="Residue is homocysteine"

PN US5876948-A.

PD 02-MAR-1999.

PE 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PA Yankner BA;

PI WPI; 1999-189630/16.

DR Screening for neurotoxin inhibitors - by testing compounds for their

PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX Disclosure; Column 23-24; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting

CC a neurotoxin. The method involves incubating tachykinin agonists with

CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be

CC used for identifying compounds for treating diseases characterised by an

CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,

CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage

CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral

CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human

CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

AAM92686 Length: 45 April 1, 2002 16:31 Type: P Check: 1490 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVYSOOT HERSRPRXPQ FPGIX

11AA_SEQUENCE 1.0

ID AAM92665 standard; peptide; 9 AA.

AC AAM92665;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #11.

DE Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KM Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
XX
OS Homo sapiens.

PN US5876948-A.

PD 02-MAR-1999.

PE 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS Disclosure; Column 15-16; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 CC
 XX
 SQ Sequence 9 AA;
 AAW92665 Length: 43 April 1, 2002 16:31 Type: P Check: 3913 ..
 1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPPQO FFG
 !!AA_SEQUENCE 1.0
 ID AAW92666 standard; peptide; 11 AA.
 XX
 AC AAW92666;
 XX
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #12.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
 XX
 OS Homo sapiens.
 XX
 PN US5876948-A.
 PD 02-MAR-1999.
 XX
 PF 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS Disclosure; Column 15-16; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.

XX
 SQ Sequence 11 AA;
 AAW92666 Length: 45 April 1, 2002 16:31 Type: P Check: 1501 ..
 1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPPQO YFGLM
 !!AA_SEQUENCE 1.0
 ID AAW92667 standard; peptide; 11 AA.
 XX
 AC AAW92667;
 XX
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #13.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 11
 FT /note="Residue is ethionine"
 XX
 PN US5876948-A.
 PD 02-MAR-1999.
 XX
 PF 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS Disclosure; Column 15-16; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SQ Sequence 11 AA;
 AAW92667 Length: 45 April 1, 2002 16:31 Type: P Check: 1217 ..
 1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPPQO FFG
 !!AA_SEQUENCE 1.0
 ID AAW92668 standard; peptide; 11 AA.
 XX
 AC AAW92668;
 XX
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #14.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

KW hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 11 /label= Nle
 FT
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PE 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 PS
 XX Disclosure; Column 15-16; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 a neurotoxin. The method involves incubating tachykinin agonists with
 neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 used for identifying compounds for treating diseases characterised by an
 undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease.
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 with amyloidosis and non-inherited congenital angiodystrophy with cerebral
 haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 beta-amyloid peptide fragments.
 CC
 CC
 CC
 SQ Sequence 11 AA;
 AAW92668 Length: 45 April 1, 2002 16:31 Type: P Check: 1217 ..
 1 SOARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRPPQO FEGIX
 !!AA-SEQUENCE 1.0
 ID AAW92674 standard; peptide; 11 AA.
 XX
 AC AAW92674;
 XX
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #20.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
 XX
 OS Homo sapiens.
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PE 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 DR WPI; 1999-189630/16.

XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS
 XX Disclosure; Column 19-20; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 a neurotoxin. The method involves incubating tachykinin agonists with
 neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 used for identifying compounds for treating diseases characterised by an
 undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease.
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 with amyloidosis and non-inherited congenital angiodystrophy with cerebral
 haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 beta-amyloid peptide fragments.
 CC
 CC
 CC
 SQ Sequence 11 AA;
 AAW92674 Length: 45 April 1, 2002 16:31 Type: P Check: 464 ..
 1 SOARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRPPQO FEGIX
 !!AA-SEQUENCE 1.0
 ID AAW92675 standard; peptide; 11 AA.
 XX
 AC AAW92675;
 XX
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #21.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 9 /note="D-form residue"
 FT
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PE 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 PS
 XX Disclosure; Column 19-20; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 a neurotoxin. The method involves incubating tachykinin agonists with
 neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 used for identifying compounds for treating diseases characterised by an
 undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease.
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 with amyloidosis and non-inherited congenital angiodystrophy with cerebral
 haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 beta-amyloid peptide fragments.
 CC
 CC
 CC
 SQ Sequence 11 AA;

AAW92675 Length: 45 April 1, 2002 16:31 Type: P Check: 464 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFLM

!!AA_SEQUENCE 1.0

ID AAW92676 standard; peptide: 11 AA.

AC AAW92676;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #22.

KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Modified-site 9

FT /label= Megly /note= "N-methyl-glycine (Sarcosine)"

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PI Yankner BA;

DR WPI; 1999-189630/16.

PT Screening for neurotoxin inhibitors - by testing compounds for their

PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PS Disclosure; Column 19-20; 28pp; English.

CC This invention describes a method for screening compounds for inhibiting

CC a neurotoxin. The method involves incubating tachykinin agonists with

CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be

CC used for identifying compounds for treating diseases characterised by an

CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease.

CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage

CC with amyloidosis and non-inherited congenital angiodopathy with cerebral

CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human

CC beta-amyloid peptide fragments.

CC Sequence 11 AA;

AAW92676 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFLM

!!AA_SEQUENCE 1.0

ID AAW92731 standard; peptide: 11 AA.

AC AAW92731;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #77.

KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.

XX

OS Homo sapiens.

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PI Yankner BA;

DR WPI; 1999-189630/16.

PT Screening for neurotoxin inhibitors - by testing compounds for their

PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PS Disclosure; Column 43-44; 28pp; English.

CC This invention describes a method for screening compounds for inhibiting

CC a neurotoxin. The method involves incubating tachykinin agonists with

CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be

CC used for identifying compounds for treating diseases characterised by an

CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,

CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage

CC with amyloidosis and non-inherited congenital angiodopathy with cerebral

CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human

CC beta-amyloid peptide fragments.

CC Sequence 11 AA;

AAW92731 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFLM

!!AA_SEQUENCE 1.0

ID AAW92656 standard; peptide: 11 AA.

AC AAW92656;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #2.

KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

PA (CHIL-) CHILDRENS MEDICAL CENT.

PI Yankner BA;

XX

XX DR WPI: 1999-163630/16.
 XX XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX XX
 PS Disclosure: Column 11-12: 28pp: English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SQ Sequence 11 AA:
 AAW92656 Length: 45 April 1, 2002 16:31 Type: P Check: 2107 ..
 1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRRKPOQ WFWLM
 11AA_SEQUENCE 1.0
 ID AAW92657 standard; peptide: 11 AA.
 XX
 AC AAW92657;
 XX
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #3.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition: neurotoxin; treatment:
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 27-JUL-1991: 91US-0737371.
 XX
 PR 29-JUL-1991: 91US-0737371.
 PR 27-JUL-1990: 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI: 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS Disclosure: Column 11-12: 28pp: English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage

CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SQ Sequence 11 AA:
 AAW92657 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..
 1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRRKPOQ WFWLM
 11AA_SEQUENCE 1.0
 ID AAW94412 standard; peptide: 12 AA.
 XX
 AC AAW94412;
 XX
 DT 15-APR-1999 (first entry)
 XX
 DE Cancer protease-sensitive amino acid linker PAP-215 and PAP-216.
 XX
 KW Ricin-like toxin; cancer; viral infection; parasitic infection;
 KW linker; B chain; A chain; protease; fungal infection; malaria;
 KW leucocyte proliferation; cytomegalovirus; herpes; hepatitis;
 KW rhinovirus; laryngotracheitis; poliomyelitis; varicella zoster;
 KW cystic fibrosis; multiple sclerosis.
 XX
 OS Undefined.
 OS Synthetic.
 OS
 PN WO9849311-A2.
 XX
 PD 05-NOV-1998.
 XX
 PF 30-APR-1998: 98WO-CA00394.
 XX
 PR 29-OCT-1997: 97US-0063715.
 PR 30-APR-1997: 97US-0045148.
 XX
 PA (DNOC-) DE NOVO ENZYME CORP.
 XX
 PI Borgford T;
 XX
 DR WPI: 1999-009431/01.
 XX
 PT New nucleic acid encoding ricin-like toxin with an interchain linker
 PT cleaved by protease - is specific for diseased cells, useful for,
 PT e.g. killing selectively cancer or infected cells
 XX
 PS Claim 24; Fig 21: 352pp: English.
 XX
 CC The present invention describes new purified and isolated nucleic acids
 CC (I) encoding: (i) the A and B chains of a ricin-like toxin (II); and
 CC (ii) a heterologous linker, joining the two chains and including a
 CC cleavage recognition site for a disease-specific protease (III). Also
 CC described are: (1) plasmids or baculovirus transfer vectors that contain
 CC (I); and (2) recombinant protein (IV) consisting of the A and B chains
 CC of (II) joined by the specified linker. (IV), produced by expression of
 CC (I) in host cells, are used to inhibit or kill diseased cells that
 CC produce (III), particularly for treating cancers (e.g. leucocyte
 CC proliferation; cancer of ovary, pancreas, breast or prostate; glioma) or
 CC infections caused by fungi, parasites (e.g. malaria) or viruses (e.g.
 CC cytomegalovirus (CMV), herpes, hepatitis, rhinovirus, laryngotracheitis,
 CC poliomyelitis or varicella zoster), also cystic fibrosis and multiple
 CC sclerosis. Alternatively, (I) is used to express (IV) in vivo. (IV) is
 CC toxic specifically for (III)-expressing cells and does not depend for
 CC specificity on a cell-binding component. When used to treat virus-
 CC infected cells, transcytosis and cytotoxicity of (IV) are increased by
 CC retrograde translocation from endoplasmic reticulum to cytoplasm (which
 CC some viruses exploit to avoid immune detection), so selectively and
 CC safely are further improved. (IV) are not toxic until chain A is
 CC released and this occurs only in target cells. The present sequence
 CC represents a specifically claimed cancer protease-sensitive amino acid
 CC linker from the present invention.
 XX

PT prolyl tripeptidyl-peptidase, active analog, fragment or variant useful
 PT for identifying its inhibitor which is useful for protecting an animal
 PT from a periodontal disease such as gingivitis and periodontitis
 XX
 PS Example 4; Page 37; 58pp; English.
 CC
 CC The present sequence represents a substrate which was used to test
 CC the activity of prolyl tripeptidyl-peptidases PTP-A and DPP IV. The
 CC prolyl tripeptidyl-peptidase has an antidiolytic activity, and cleaves
 CC a peptide bond in a target polypeptide having at least 4 amino acids.
 CC This bond is between a proline and an amino acid attached to the
 CC alpha-carboxyl group end of the proline. The polypeptide is useful for
 CC identifying inhibitors. These inhibitors are then useful for reducing
 CC the growth of bacterium or for protecting an animal from a periodontal
 CC disease such as gingivitis and periodontitis caused by Porphyromonas
 CC gingivalis.
 CC
 SQ Sequence 11 AA;
 AAB18483 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
 1 SQARNDBDCE ZGHSQILKMF PSTWVVSQOT HERSRPRPQQ FFCGLM
 !!AA-SEQUENCE 1.0
 ID AAB23027 standard; peptide; 11 AA.
 AC AAB23027;
 XX
 DT 16-JAN-2001 (first entry)
 XX
 DE Human/rat tachykinin Substance P.
 XX
 XX Substance P; tachykinin; human; rat; magnesium binding defect;
 KM sodium sensitive essential hypertension; insulin resistance;
 KM type 2 diabetes; antibody; immunoassay; quantification.
 XX
 OS Homo sapiens.
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 11 /note= "C-terminal amide"
 FT
 XX
 PN WO200054053-A1.
 PD 14-SEP-2000.
 XX
 PF 09-MAR-2000; 2000WO-US03707.
 XX
 PR 10-MAR-1999. 99US-0265690.
 XX
 PA (WELL/) WELLS I C.
 XX
 PI Wells IC;
 XX
 DR WPI; 2000-587457/55.
 XX
 PT Detecting magnesium binding defects associated with abnormal
 PT physiological states such as sodium-sensitive essential hypertension
 PT and type 2 insulin-resistant diabetes mellitus, comprises measuring a
 PT specific pentapeptide in blood -
 XX
 PS Disclosure: Page 5; 21pp; English.
 CC The invention relates to a method for detecting magnesium binding
 CC defects. The method comprises quantitating a tachykinin C-terminal
 CC pentapeptide (e.g., AAB23025) and its degradation products (e.g.,
 CC AAB23026) in blood using an antibody specific for the generalised
 CC mammalian tachykinin C-terminal pentapeptide
 CC Phe-(Phe/Val)-Gly-Leu-Met-NH2 (AAB23028). The method is useful for
 CC detecting cellular magnesium binding defects which are associated with
 CC abnormal physiological states such as sodium-sensitive essential
 CC hypertension and type 2 diabetes mellitus. The present sequence

CC represents the tachykinin Substance P from human and rat. C-terminal
 CC fragments (AAB23025, AAB23026) of the present sequence may be assayed
 CC according to the method of the invention.
 XX
 SQ Sequence 11 AA;
 AAB23027 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
 1 SQARNDBDCE ZGHSQILKMF PSTWVVSQOT HERSRPRPQQ FFCGLM
 !!AA-SEQUENCE 1.0
 ID AAB08303 standard; peptide; 11 AA.
 AC AAB08303;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE Amino acid sequence of Substance P analogue SPL.
 XX
 XX Vasoactive intestinal peptide; VIP; analogue; somatostatin; SOM1; SOM2;
 KM VIP1; VIP2; VIP3; BOM1; bombesin; SPL; substance P; Mu2-7; tumour growth;
 KM tumour angiogenesis; metastasis; cancer; angiogenesis; adenocarcinoma;
 KM leukaemia; lymphoma.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue"
 FT Misc-difference 5 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT
 XX
 PN WO200047221-A1.
 PD 17-AUG-2000.
 XX
 PF 11-FEB-2000; 2000WO-US03559.
 XX
 PR 11-FEB-1999; 99US-0248381.
 XX
 PA (NAIM-) NAT INST IMMUNOLOGY.
 PA (DABU-) DABUR RES FOUND.
 PA (CORD/) CORD J I.
 XX
 PI Mukherjee R, Jaggi M, Prasad S, Burman AC, Rajendran P, Mathur A;
 PI Singh AT;
 XX
 DR WPI; 2000-549083/50.
 XX
 PT Novel therapeutically active composition comprising at least 5
 PT peptides, useful for treating angiogenesis especially as a result of
 PT adenocarcinomas -
 XX
 PS Disclosure: Page 8; 42pp; English.
 CC The present sequence represents an analogue of Substance P. The
 CC specification describes therapeutically active compositions comprising
 CC at least one analogue of somatostatin (chosen from SOM1 and SOM2), and
 CC at least four analogues chosen from vasoactive intestinal peptide (VIP) 1
 CC (a VIP antagonist), VIP2 (a VIP receptor binding inhibitor), VIP3 (a VIP
 CC receptor antagonist), BOM1 (a bombesin antagonist), and SPL (a substance
 CC P antagonist). The combination of these 7 analogues is known as Mu2-7.
 CC Mu2-7 is used as an anticancer drug to restrict tumour growth and spread
 CC by inhibiting tumour angiogenesis. Mu2-7, in addition, inhibits
 CC metastasis through its antiangiogenic activity in all cancers. The
 CC peptides are useful for the treatment and prevention of angiogenesis,
 CC especially as a result of adenocarcinomas of the colon, breast, lung,
 CC prostate, kidney, leukaemias or lymphomas.
 CC

SQ Sequence 11 AA;
AAB08303 Length: 45 April 1, 2002 16:31 Type: P Check: 1633 ..
1 SOARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRPPQ WFWLL
!!AA_SEQUENCE 1.0
ID AAB08313 standard; peptide; 11 AA.
XX AAB08313;
AC AAB08313;
DT 04-DEC-2000 (first entry)
XX
XX Amino acid sequence of an antiangiogenic peptide.
DE
XX Vasoactive intestinal peptide; VIP; analogue; somatostatin; SOM1; SOM2;
KM VIP1; VIP2; VIP3; BOM1; bombesin; SPI; substance P; Mu-7; tumour growth;
KM tumour angiogenesis; metastasis; cancer; angiogenesis; adenocarcinoma;
KW leukaemia; lymphoma.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "D-form residue"
FT Modified-site 5 /label= Aib
FT /note= "alpha-aminoisobutyric acid"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 10 /label= Aib
FT /note= "alpha-aminoisobutyric acid"
FT Modified-site 11 /note= "amidated residue"
FT
FT
FT
XX WO200047221-A1.
PN
XX 17-AUG-2000.
PD
XX 11-FEB-2000; 2000WO-US03559.
PF
XX 11-FEB-1999; 99US-0248381.
PR
XX (NAIM-) NAT INST IMMUNOLOGY.
PA (DABU-) DABUR RES FOUND.
PA (CORD/) CORD J I.
XX
PI Mukherjee R, Jaggi M, Prasad S, Burman AC, Rajendran P, Mathur A;
PI Singh AT;
PI
XX WPI: 2000-549083/50.
DR
XX Novel therapeutically active composition comprising at least 5
PT peptides, useful for treating angiogenesis especially as a result of
PT adenocarcinomas -
XX
XX Claim 11; Page 31; 42pp; English.
PS
XX AAB08304-15 represent peptides which have an antiangiogenic effect. The
CC specification describes therapeutically active compositions comprising
CC at least one analogue of somatostatin (chosen from SOM1 and SOM2), and
CC at least four analogues chosen from vasoactive intestinal peptide (VIP)
CC 1 (a VIP antagonist), VIP2 (a VIP receptor binding inhibitor), VIP3 (a
CC VIP receptor antagonist), BOM1 (a bombesin antagonist), and SPI (a
CC substance P antagonist). The combination of these 7 analogues is known as
CC Mu-7. Mu-7 is used as an anticancer drug to restrict tumour growth and
CC spread by inhibiting tumour angiogenesis. Mu-7, in addition, inhibits
CC metastasis through its antiangiogenic activity in all cancers. The
CC peptides are useful for the treatment and prevention of angiogenesis,
CC especially as a result of adenocarcinomas of the colon, breast, lung,

CC prostate, kidney, leukemias or lymphomas.
XX
SQ Sequence 11 AA;
AAB08313 Length: 45 April 1, 2002 16:31 Type: P Check: 2863 ..
1 SOARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSRPPQ WFWLL
!!AA_SEQUENCE 1.0
ID AAB06257 standard; peptide; 17 AA.
XX AAB06257;
AC AAB06257;
DT 16-OCT-2000 (first entry)
XX
XX Substance P analogue #1.
DE
XX Substance P; SP; neurokinin-1 receptor; NK-1R; nociception; SSP-SAP;
KW saproin; SAP; analgesic; anti-inflammatory; neuroprotective;
KW anti-asthmatic; anti-allergic; dermatological; anti-ulcer;
KW tranquiliser; immunosuppressive; anti-migraine; cytostatic;
KW substance P antagonist; cytotoxic; ribosome inactivator;
KW prostaglandin antagonist; cancer; respiratory disease; asthma;
KW allergic rhinitis; ophthalmic disease; conjunctivitis;
KW allergic dermatitis; psoriasis; ulcerative colitis; Crohn's disease;
KW gastrointestinal disorder; anxiety; psychosis; rheumatoid arthritis;
KW carcinoma; lupus erythematosus conjunctivitis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 17 /note= "linked to Sarlmec(02)-amide"
FT
FT
FT
XX US6063758-A.
PN
XX 16-MAY-2000.
PD
XX 09-JUL-1997; 97US-0890157.
PF
XX 09-JUL-1997; 97US-0890157.
PR
XX (ADTA-) ADVANCED TARGETING SYSTEMS INC.
PA
PI Lappi DA, Wiley RG;
PI
XX WPI: 2000-430049/37.
DR
XX
XX New conjugates comprising substance P or its analog, and a
PT ribosome-inactivating protein (for example saproin), for alleviating
PT pain and treating disorders associated with neurokinin-1 receptor -
XX
XX Claim 1; Column 2; 21pp; English.
PS
XX The present sequence is an analogue of substance P (SP), which binds
CC to the neurokinin-1 receptor (NK-1R), is best known for its role in
CC nociception. It is secreted by small unmyelinated C-fibres of the
CC peripheral nervous system that are thought to be primary nociceptive
CC neurons. The present sequence may be conjugated to Saproin (SAP), a
CC ribosome-inactivating protein, to produce SSP-SAP. The conjugate may be
CC used to control chronic pain by specifically targeting cells having NK1
CC receptors, and inhibiting proliferation of or causing death of these
CC cells. It may also be used to treat NK-1R-associated disorders
CC including respiratory conditions (e.g. asthma, allergic rhinitis),
CC ophthalmic conditions (e.g. conjunctivitis), cutaneous conditions (e.g.
CC allergic dermatitis, psoriasis), intestinal conditions (e.g. ulcerative
CC colitis, Crohn's disease), gastrointestinal disorders, central nervous
CC system disorders (e.g. anxiety, psychosis), inflammatory diseases (e.g.
CC rheumatoid arthritis), proliferative conditions (e.g. carcinoma),
CC disorders related to immune enhancement or suppression (e.g. lupus
CC erythematosus conjunctivitis), and especially migraine.
XX
XX Sequence 17 AA;

AAB06257 Length: 51 April 1, 2002 16:31 Type: P Check: 1860 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSCYGGG GGGRRPRPQGF

51 F

11AA_SEQUENCE 1.0
ID AAB06258 standard; peptide; 20 AA.XX
AC AAB06258;XX
DT 16-OCT-2000 (first entry)XX
DE Substance P analogue #2.XX
KW Substance P; SP; neurokinin-1 receptor; NK-1R; nociception; NTF-SAP;
KW Saporin; SAP; analgesic; anti-inflammatory; neuroprotective;
KW anti-asthmatic; anti-allergic; dermatological; anti-ulcer;
KW tranquilizer; immunosuppressive; anti-migraine; cyostatic;
KW substance P antagonist; cytotoxic; ribosome inactivator;
KW prostaglandin antagonist; cancer; respiratory disease; asthma;
KW allergic rhinitis; ophthalmic disease; conjunctivitis;
KW allergic dermatitis; psoriasis; ulcerative colitis; Crohn's disease;
KW gastrointestinal disorder; anxiety; psychosis; rheumatoid arthritis;
KW carcinoma; lupus erythematosus conjunctivitis.XX
OS Synthetic.FH Key Location/Qualifiers
FT Modified-site 20
FT /note="C-terminal amide"XX
PN US6063758-A.XX
PD 16-MAY-2000.XX
PF 09-JUL-1997; 97US-0890157.XX
PR 09-JUL-1997; 97US-0890157.XX
PA (ADTA-) ADVANCED TARGETING SYSTEMS INC.XX
PI Lappi DA, Wiley RG;XX
DR WPI; 2000-430049/37.XX
PT New conjugates comprising substance P or its analog, and a
PT ribosome-inactivating protein (for example saporin), for alleviating
PT pain and treating disorders associated with neurokinin-1 receptor -XX
PS Claim 1; Column 2; 21pp; English.XX
CC The present sequence is an analogue of substance P (SP). SP, which binds
CC to the neurokinin-1 receptor (NK-1R), is best known for its role in
CC nociception. It is secreted by small unmyelinated C-fibres of the
CC peripheral nervous system that are thought to be primary nociceptive
CC neurons. The present sequence may be conjugated to Saporin (SAP), a
CC ribosome-inactivating protein, to produce NTF-SAP. The conjugate may be
CC used to control chronic pain by specifically targeting cells having NK1
CC receptors, and inhibiting proliferation of or causing death of these
CC cells. It may also be used to treat NK-1R-associated disorders
CC including respiratory conditions (e.g. asthma, allergic rhinitis),
CC ophthalmic conditions (e.g. conjunctivitis), cutaneous conditions (e.g.
CC allergic dermatitis, psoriasis), intestinal conditions (e.g. ulcerative
CC colitis, Crohn's disease), gastrointestinal disorders, central nervous
CC system disorders (e.g. anxiety, psychosis), inflammatory diseases (e.g.
CC rheumatoid arthritis), proliferative conditions (e.g. carcinoma),
CC disorders related to immune enhancement or suppression (e.g. lupus
CC erythematosus conjunctivitis), and especially migraine.XX
SQ Sequence 20 AA;

AAB06258 Length: 54 April 1, 2002 16:31 Type: P Check: 3738 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSCYGGG GGGRRPRPQGF

51 FGILM

11AA_SEQUENCE 1.0
ID AAB06260 standard; peptide; 11 AA.XX
AC AAB06260;XX
DT 16-OCT-2000 (first entry)XX
DE Substance P.XX
KW Substance P; SP; neurokinin-1 receptor; NK-1R; nociception; saporin; SAP;
KW analgesic; anti-inflammatory; neuroprotective; anti-asthmatic;
KW anti-allergic; dermatological; anti-ulcer; tranquilizer;
KW immunosuppressive; anti-migraine; cyostatic; substance P antagonist;
KW cytotoxic; ribosome inactivator; prostaglandin antagonist; cancer;
KW respiratory disease; asthma; allergic rhinitis; ophthalmic disease;
KW conjunctivitis; allergic dermatitis; psoriasis; ulcerative colitis;
KW Crohn's disease; gastrointestinal disorder; anxiety; psychosis;
KW rheumatoid arthritis; carcinoma; lupus erythematosus conjunctivitis.XX
OS unidentified.FH Key Location/Qualifiers
FT Modified-site 11
FT /note="C-terminal amide"XX
PN US6063758-A.XX
PD 16-MAY-2000.XX
PF 09-JUL-1997; 97US-0890157.XX
PR 09-JUL-1997; 97US-0890157.XX
PA (ADTA-) ADVANCED TARGETING SYSTEMS INC.XX
PI Lappi DA, Wiley RG;XX
DR WPI; 2000-430049/37.XX
PT New conjugates comprising substance P or its analog, and a
PT ribosome-inactivating protein (for example saporin), for alleviating
PT pain and treating disorders associated with neurokinin-1 receptor -XX
PS Disclosure; Column 14; 21pp; English.XX
CC The present sequence is substance P (SP), which binds to the neurokinin-1
CC receptor (NK-1R). SP is secreted by small unmyelinated C-fibres of the
CC peripheral nervous system that are thought to be primary nociceptive
CC neurons. The present sequence may be conjugated to Saporin (SAP), a
CC ribosome-inactivating protein, to produce SP-SAP. The conjugate may be
CC used to control chronic pain by specifically targeting cells having NK1
CC receptors, and inhibiting proliferation of or causing death of these
CC cells. It may also be used to treat NK-1R-associated disorders
CC including respiratory conditions (e.g. asthma, allergic rhinitis),
CC ophthalmic conditions (e.g. conjunctivitis), cutaneous conditions (e.g.
CC allergic dermatitis, psoriasis), intestinal conditions (e.g. ulcerative
CC colitis, Crohn's disease), gastrointestinal disorders, central nervous
CC system disorders (e.g. anxiety, psychosis), inflammatory diseases (e.g.
CC rheumatoid arthritis), proliferative conditions (e.g. carcinoma),
CC disorders related to immune enhancement or suppression (e.g. lupus
CC erythematosus conjunctivitis), and especially migraine.XX
SQ Sequence 11 AA;

AAB06260 Length: 45 April 1, 2002 16:31 Type: P Check: 1196 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRRPWW FGILM

!!AA_SEQUENCE 1.0
ID AAG05042 standard; Protein: 314 AA.
XX
AC AAG05042;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1298.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
PD
XX 06-SEP-2000.
PD
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 9905-0121825.
PR 05-MAR-1999; 9905-0123180.
PR 09-MAR-1999; 9905-0123548.
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PR 25-MAR-1999; 9905-0126264.
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PR 01-APR-1999; 9905-0127462.
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PR 01-FEB-2000; 2000US-0179388.
PR 01-FEB-2000; 2000US-0179395.
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PR 04-FEB-2000; 2000US-0180206.

PR 04-FEB-2000; 2000US-0180207.
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PR 15-FEB-2000; 2000US-0182516.
PR 17-FEB-2000; 2000US-0183165.
PR 17-FEB-2000; 2000US-0183166.
XX
XX (CERE-) CERES INC.
XX
XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
XX MPI; 2000-507395/46.
DR N-PSDB; AAC32966.
XX
XX
XX New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
XX
XX Claim 19; SEQ ID 1298; 344bp + CD-ROM; English.
XX
XX The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3' UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
XX
XX Sequence 314 AA;
SO
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1 SOARDBCOE ZGHSQILKMF PSTWYVSQOT HERSMREAO LGGHILRSIGM
51 TVARTHMHDW IILVLVILE CVLLIHFPY RFVGKDMTMD LSYPLKNTV
101 PIWSVPYVAM LLPVIFIFI YFRRDVYDL HHAVALGLAS VLVAVALTDA
151 IKNAVGRPR DFEWRCRPDG KALYDSLGDV ICHGDKSVIR EGHKSFPBGH
201 TSMSESGIGF LSLYLSGKIQ AFDGKGVAK LCIIVILPLF AALVGSIFVD
251 DVMHMQDVF AGGLGLAIS TICYLQFPP PYHTEGMPY AYFOVLEAAR
301 VOGANGAVQ QPPQVANGGE EEDGGEGLH LVDNPLMRE EDVETGRG
!!AA_SEQUENCE 1.0
ID AG05043 standard; Protein: 299 AA.
XX
XX AG05043;
AC
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XX 17-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1299.
XX
XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX

OS Arabidopsis thaliana.
XX
XX EPI033405-A2.
PN
XX
XX
PD 06-SEP-2000.
PF
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XX 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
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PR 29-MAR-1999; 99US-0126785.
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PR 01-JUN-1999; 99US-0137222.
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PR 07-JUN-1999; 99US-0137724.
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XX

PA (CERE-) CERES INC.
XX Alexandrov N., Brover V., Chen X., Subramanian G., Troukhan ME;
PI Zheng L., Dumas J;
XX WPI: 2000-507395/46.
DR N-PSDB; AAC32966.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
PS Claim 19; SEQ ID 1299; 344bp + CD-ROW; English.
XX
CC The present sequence is a putative protein frgment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3' UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
XX
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AAG05043 Length: 333 Apr11 1, 2002 16:31 Type: P Check: 69
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101 IFIFIFRRRR DVEDLHNAVL GLLYSVLYTA VLTDAIKNAV GRPRDFEWR
151 CEPDGKALYD SLGDVICHGD KSVIRGHSKS PFSGHTSMSE SGLPFLSYL
201 SKGIOAFDQK GHVAKLCIVI LPLLPALYG ISRVDDYWHH WQDFAGGL
251 GLAISTICYL QFPPPYHTE GWSGYAVFOY LEARVCGAA NGAVQOPPO
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ID AAG05044 standard; Protein: 292 AA.
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AC AAG05044;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 1300.
XX
KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PM EP103405-A2.
PD 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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 XX
 PA (CERE-) CERES INC.
 XX
 PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
 PI Zheng L, Dumas J;
 XX
 XX WPI; 2000-507395/46.
 DR N-PSDB; AAC32966.
 XX
 PT New sequence determined DNA fragments (SDFs) from different plant
 PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
 PT protein coding sequences, untranslated regions, or as 3' termination
 PT sequences -
 XX
 PS Claim 19; SEQ ID 1300; 344pp + CD-ROM; English.

XX The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
XX

SO Sequence 292 AA:

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IIAA-SEQUENCE 1.0
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XX AAG06751:

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 3640.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

PN EP1033405-A7.

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PA (CERE-) CERES INC.
XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
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XX WPI: 2000-507395/46.
DR N-PSDB; AAC33599.
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XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
XX
PS Claim 19; SEQ ID 3640; 344pp + CD-ROM; English.
XX
XX The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
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CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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 PA (CERE-) CERES INC.
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 PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
 PI Zheng L, Dumas J;
 DR WPI; 2000-507395/46.
 DR N-PSDB; AAC33599.
 XX
 PT New sequence determined DNA fragments (SDFs) from different plant
 PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
 PT protein coding sequences, untranslated regions, or as 3' termination
 PT sequences -
 PT
 XX
 PS Claim 19; SEQ ID 3641; 344pp + CD-ROM; English.
 XX
 CC The present sequence is a putative protein fragment from
 CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
 CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
 CC library which could then be sequenced, allowing the putative protein
 CC sequence(s) to be obtained. This sequence may be useful for protein
 CC identification and for aiding in the elucidation of signal transduction
 CC and metabolic pathways. Its coding sequence has a use in the control of
 CC gene expression as a promoter, coding sequence, 3'UTR or termination
 CC sequence, for controlling the behaviour of a gene within the chromosome,
 CC as a tool for use in genetic mapping, including a use in hybridisation
 CC assays, for recognition or isolation of similar DNA fragments, or for
 CC the identification of a particular organism.
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KM Protein identification; signal transduction pathway; metabolic pathway;
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PA (CERE-) CERES INC.
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PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
DR WPI: 2000-507395/46.
DR N-PSDB: AAC33599.
XX
XX New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
PS Claim 19; SEQ ID 3642; 344bp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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AC AAG10034;
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DT 17-OCT-2000 (first entry)
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KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

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XX (CERE-) CERES INC.
 PA Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
 XX Zheng L, Dumas J;
 PI WPI: 2000-507395/46.
 DR N-PSDB; AAC34872.
 XX
 PT New sequence determined DNA fragments (SDFs) from different plant
 PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
 PT protein coding sequences, untranslated regions, or as 3' termination
 PT sequences -
 XX
 PS Claim 19; SEQ ID 8196; 344bp + CD-ROW; English.
 CC The present sequence is a putative protein fragment from
 CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
 CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
 CC library which could then be sequenced, allowing the putative protein
 CC sequence(s) to be obtained. This sequence may be useful for protein
 CC identification and for aiding in the elucidation of signal transduction
 CC and metabolic pathways. Its coding sequence has a use in the control of
 CC gene expression as a promoter, coding sequence, 3'UTR or termination
 CC sequence, for controlling the behaviour of a gene within the chromosome,
 CC as a tool for use in genetic mapping, including a use in hybridisation
 CC assays, for recognition or isolation of similar DNA fragments, or for
 CC the identification of a particular organism.
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AC AAG10035;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 8197.

KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

OS Arabidopsis thaliana.

XX EPI033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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PA (CERE-) CERES INC.
XX
XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
XX WPI; 2000-507395/46.
DR N-PSDB; AAC34872.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
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PT sequences -
XX
PS Claim 19; SEQ ID 8197; 344pp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
XX
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KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
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PA	(CERE-) CERES INC.	
XX		
PI	Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;	
PI	Zheng L, Dumas J;	
XX		
DR	WPI: 2000-507395/46.	
XX	N-PSDB: AAC34872.	
XX		
PT	New sequence determined DNA fragments (SDFs) from different plant	
PT	species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,	
PT	protein coding sequences, untranslated regions, or as 3' termination	
PT	sequences -	
XX		
PS	Claim 19; SEQ ID 8198; 344bp + CD-ROM; English.	
XX		
CC	The present sequence is a putative protein fragment from	
CC	Arabidopsis thaliana. Its coding sequence was isolated by carrying out	
CC	RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA	
CC	library which could then be sequenced, allowing the putative protein	
CC	sequence(s) to be obtained. This sequence may be useful for protein	
CC	identification and for aiding in the elucidation of signal transduction	
CC	and metabolic pathways. Its coding sequence has a use in the control of	
CC	gene expression as a promoter, coding sequence, 3'UTR or termination	
CC	sequence, for controlling the behaviour of a gene within the chromosome	
CC	as a tool for use in genetic mapping, including a use in hybridisation	

CC	assays, for recognition or isolation of similar DNA fragments, or for
CC	the identification of a particular organism.
XX	
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151	WSFAGLTFLS LVUSGRIKAF NNEGHAKLIC LVIFPLAAC LVCISRYDY
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DT	17-OCT-2000 (first entry)
DE	
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 12362.
KX	Protein identification: signal transduction pathway; metabolic pathway;
MW	hybridisation assay; genetic mapping; gene expression control; promoter;
KM	termination sequence.
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OS	Arabidopsis thaliana.
XX	
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PD	06-SEP-2000.
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PF	25-FEB-2000; 2000EP-0301439.
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 PR PA
 (CERE-) CERES INC.
 XX
 PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
 PI Zheng L, Dumas J;
 XX
 PI WPI: 2000-507395/46.
 DR N-PSDB: AAC36049.
 XX
 PT New sequence determined DNA fragments (SDFs) from different plant
 PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
 PT protein coding sequences, untranslated regions, or as 3' termination
 PT sequences -
 PS
 PS Claim 19; SEQ ID 12362; 344pp + CD-ROM; English.
 XX
 CC The present sequence is a putative protein fragment from
 CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
 CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
 CC library which could then be sequenced, allowing the putative protein
 CC sequence(s) to be obtained. This sequence may be useful for protein
 CC identification and for aiding in the elucidation of signal transduction
 CC and metabolic pathways. Its coding sequence has a use in the control of
 CC gene expression as a promoter, coding sequence, 3' UTR or termination
 CC sequence, for controlling the behaviour of a gene within the chromosome,
 CC as a tool for use in genetic mapping, including a use in hybridisation
 CC assays, for recognition or isolation of similar DNA fragments, or for
 CC the identification of a particular organism.
 XX
 XX Sequence 302 AA;
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KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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XX Arabidopsis thaliana.
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PA (CERE-) CERES INC.
XX
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
DR N-PSDB; AAC36049.
DR WPI; 2000-507395/46.
XX
XX New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
XX Claim 19; SEQ ID 12364; 344pp + CD-ROM; English.
PS
XX
XX The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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KW termination sequence.
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PA (CERE-) CERES INC.
XX
XX
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
XX WPI: 2000-507395/46.
DR N-PSDB: AAC36228.
XX
XX
PT New sequence determined DNA fragments (SDFs) from different plant
species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,

PT protein coding sequences, untranslated regions, or as 3' termination
sequences -
XX
PS Claim 19; SEQ ID 13018; 344pp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
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CC the identification of a particular organism.
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XX (CERE-) CERES INC.

PI Alexandrov N, Brower V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;

DR WPI; 2000-507395/46.
DR N-PSDB; AAC36351.

XX New sequence determined DNA fragments (SDPs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -

PS Claim 19; SEQ ID 13483; 344pp + CD-ROM; English.

XX The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.

XX Sequence 314 AA;

AA013842 Length: 348 April 1, 2002 16:31 Type: P Check: 1234

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XX 17-OCT-2000 (first entry)
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DE Protein identification; signal transduction pathway; metabolic pathway;
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XX Arabidopsis thaliana.
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XX Alexandrov N, Brower V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
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XX WPI: 2000-507395/46.
XX N-PSDB; AAC36351.
XX
XX New sequence determined DNA fragments (SDFs) from different plant
XX species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
XX protein coding sequences, untranslated regions, or as 3' termination
XX sequences -
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XX Claim 19; SEQ ID 13484; 344pp + CD-ROM; English.
XX
XX The present sequence is a putative protein fragment from
XX Arabidopsis thaliana. Its coding sequence was isolated by carrying out
XX RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
XX library which could then be sequenced, allowing the putative protein
XX sequence(s) to be obtained. This sequence may be useful for protein
XX identification and for aiding in the elucidation of signal transduction
XX and metabolic pathways. Its coding sequence has a use in the control of
XX gene expression as a promoter, coding sequence, 3'UTR or termination
XX sequence, for controlling the behaviour of a gene within the chromosome,
XX as a tool for use in genetic mapping, including a use in hybridisation
XX assays, for recognition or isolation of similar DNA fragments, or for
XX the identification of a particular organism.
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XX
XX 151 CFPDGRKALYD SLGDVICHGD KSVIREGHSK PSFGHTSMSE SGLGFLSLYL.
XX
XX 201 SGKIQAFDGK GHVAKLCTIVI LPLLFAALVG ISRVDDYWHH WQDYFAGGL
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XX
XX AC AAG13844;
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XX DT 17-OCT-2000 (first entry)
XX
XX DE Arabidopsis thaliana protein fragment SNO ID NO: 13485.
XX
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX OS Arabidopsis thaliana.
XX
XX XX EP1033405-A2.
XX
XX XX 06-SEP-2000.
XX
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(CERE-) CERES INC.

XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX

DR WPI: 2000-507395/46.
DR N-PSDB: AAC36351.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences ..
XX
PS Claim 19; SEQ ID 13485; 344bp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
XX
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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW terminator sequence.
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(CERE-) CERES INC.
Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
Zheng L, Dumas J;
WPI: 2000-507395/46.
N-PSDB: AAC36760.
New sequence determined DNA fragments (cDNAs) from different plant
species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
protein coding sequences, untranslated regions, or as 3' termination
sequences -
Claim 19; SEQ ID 14987; 344pp + CD-ROM; English.
The present sequence is a putative protein fragment from
Arabidopsis thaliana. Its coding sequence was isolated by carrying out
RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
library which could then be sequenced, allowing the putative protein
sequence(s) to be obtained. This sequence may be useful for protein
identification and for aiding in the elucidation of signal transduction
and metabolic pathways. Its coding sequence has a use in the control of
gene expression as a promoter. coding sequence, 3'UTR or termination
sequence, for controlling the behaviour of a gene within the chromosome,
as a tool for use in genetic mapping, including a use in hybridisation
assays, for recognition or isolation of similar DNA fragments, or for
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XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX WPI: 2000-507395/46.
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PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
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PS Claim 19; SEQ ID 14988; 344pp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3' UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
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PT sequences -
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XX
CC The present sequence is a putative protein frgment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
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CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
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CC gene expression as a promoter, coding sequence, 3' UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
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(CERE-) CERES INC.
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PI Alexandrov H, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
DR MPI: 2000-507395/46.
N-PSDB: AAC37833.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
PS Claim 19; SEQ ID 18830; 344bp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
XX
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DT 17-OCT-2000 (first entry)
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KM termination sequence.
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PA (CERE-) CERES INC.
PI Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumes J;
DR WPI; 2000-507395/46.
DR N-PSDB; AAC37833.
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PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
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PS Claim 19; SEQ ID 18831; 344pp + CD-ROM; English.
CC The present sequence is a putative protein fragment from

CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
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CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3' UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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KW termination sequence.
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 PA (CERE-) CERES INC.
 XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
 PI Zheng L, Dumas J;
 PI WPI: 2000-507395/46.
 XX N-PSDB: AAC39473.
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 PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
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 PS Claim 19: SEQ ID 24762; 344pp + CD-ROM; English.
 XX
 CC The present sequence is a putative protein fragment from
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 CC gene expression as a promoter, coding sequence, 3' UTR or termination
 CC sequence, for controlling the behaviour of a gene within the chromosome,
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PR 17-FEB-2000; 2000US-0183166.

PA (CERE-) CERES INC.

PI Alexandrov N, Brower V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;

XX WPI; 2000-507395/46.

DR N-PSDB; AAC39473.

PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -

PS Claim 19; SEQ ID 24763; 344pp + CD-ROM; English.

CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.

XX Sequence 314 AA;

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1 SOARDBCOE ZGHSQILKMF PSTWVYSQOT HERSMREAO GGHTRLSHGM

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101 PIWSVPYAM LLPVIFIFI YFRRRDVYDL HHAVLGLYS VLVTAVLDA

151 IKNAVGRRP DFWRCFPD KALYDSIGV ICHGKSVIR EGHKSPFSGH

201 TSWSPSIGLF LSLYLSKIO APDGKGVAK LCIIVILLLE AALVGISRVD

251 DYWHMDVAF AGGLGLAIS TICYLOFFPP PYHTEGMPY AYFOYLEAAR
301 VQGANGAVO QPPQVNNGE EEDGFMGLH LVONPTMRRE EYVEYGRG

!!AA_SEQUENCE 1.0
ID AAG22001 standard; Protein; 299 AA.

XX AAG22001;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 24764.

DE Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

XX Arabidopsis thaliana.

OS EP1033405-A2.

PN 06-SEP-2000.

PD 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 990US-0121825.

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XX (CERE-) CERES INC.
XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
XX Zheng L, Dumas J;
PI WPI; 2000-507395/46.
DR N-PSDB; AAC39473.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
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XX Claim 19; SEQ ID 24764; 344pp + CD-ROM; English.
XX
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CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
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XX
PA (CERE-) CERES INC.
PI Alexandrov N, Broyer V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX
DR WPI: 2000-507395/46.
DR N-PSDB; AAC42647.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
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PS Claim 19; SEQ ID 36337; 344bp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for adding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
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 PA (CERE-) CERES INC.
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 PI Zheng L, Lomas J;
 XX MPI; 2000-507395/46.
 DR N-PSDB; AAC42647.
 PT New sequence determined DNA fragments (SDFs) from different plant
 PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
 PT protein coding sequences, untranslated regions, or as 3' termination

PT sequences -
 XX Claim 19; SEQ ID 36338; 344pp + CD-ROM; English.
 XX The present sequence is a putative protein fragment from
 CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
 CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
 CC library which could then be sequenced, allowing the putative protein
 CC sequence(s) to be obtained. This sequence may be useful for protein
 CC identification and for aiding in the elucidation of signal transduction
 CC and metabolic pathways. Its coding sequence has a use in the control of
 CC gene expression as a promoter, coding sequence, 3'UTR or termination
 CC sequence, for controlling the behaviour of a gene within the chromosome,
 CC as a tool for use in genetic mapping, including a use in hybridisation
 CC assays, for recognition or isolation of similar DNA fragments, or for
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CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.

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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

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XX (CERE-) CERES INC.
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XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
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XX WPI: 2000-507395/46.
DR N-PSDB: AAC42695.
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XX New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
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XX Claim 19; SEQ ID 36513; 344bp + CD-ROM; English.
XX
XX The present sequence is a putative protein fragment from
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CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
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PR	(CERE-) CERES INC.	
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XX	Zheng L, Dumas J;	
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PT	protein coding sequences, untranslated regions, or as 3' termination	
PT	sequences -	
XX	Claim 19; SEQ ID 47857; 344pp + CD-ROM; English.	

xx The present sequence is a putative protein fragment from
cc *Arbidopsis thaliana*. Its coding sequence was isolated by carrying out
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cc sequence, for controlling the behaviour of a gene within the chromosome.
cc CC as a tool for use in genetic mapping, including a use in hybridisation
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DT 18-OCT-2000 (first entry)

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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana

PN EP1033405-A2.

PD 06-SEP-2000.

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PR 07-FEB-2000; 2000US-0180695.
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PR 17-FEB-2000; 2000US-0183165.
PR 17-FEB-2000; 2000US-0183166.
PA (CERE-) CERES INC.
XX Alexandrov N, Brower V, Chen X, Subramanian G, Troukhan ME:
PI Zheng L, Dumas J;
XX WPI: 2000-507395/46.
DR N-PSDB: AAC45813.
XX
PT New sequence determined DNA fragments (SDPs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
PS Claim 19: SEQ ID 47859; 344pp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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DT 18-OCT-2000 (first entry)
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KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
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PR 04-FEB-2000; 2000US-0180206.
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PA (CERE-) CERES INC.
XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX MPI; 2000-507395/46.
DR N-PSDB; AAC47339.
XX
XX New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
PS Claim 19; SEQ ID 53455; 344bp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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XX
PA (CERE-) CERES INC.
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PI Zheng L, Dumas J;
XX
DR WPI: 2000-507395/46.
DR N-PSDB: AAC47339.
XX
PS Claim 19; SEQ ID 53456; 344pp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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PR 15-FEB-2000; 2000US-0182516.
PR 17-FEB-2000; 2000US-0183165.
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PA (CERE-) CERES INC.
XX Alexandrov N, Brover V, Chen X, Subramanian G, Troukhan ME;
PI Zheng L, Dumas J;
XX WPI: 2000-507395/46.
DR N-PSDB: AAC47339.
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
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PT sequences -
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PS Claim 19; SEQ ID 53457; 344pp + CD-ROM; English.
XX
CC The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3' UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome,
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.
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151 WSPFALITFLS LYLGGKIKAF NNECHVAKLC LVTFPLAAC LVGISRVVDY
201 WHHWQDVENG ALIGTLVAAF CYROFYPNPY HEEGWPYAV FKAOERGV
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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PR 17-FEB-2000; 2000US-0183166.

XX
XX
XX (CERE-) CERES INC.
PA Alexandrov N., Brower V., Chen X., Subramanian G., Troukhan ME:
PI Zheng L., Dumas J;
XX
XX WPI: 2000-507395/46.
DR N-PSDB; AAC50204.
XX
XX
PT New sequence determined DNA fragments (SDFs) from different plant
PT species, e.g. corn, rice or Arabidopsis thaliana, useful as promoters,
PT protein coding sequences, untranslated regions, or as 3' termination
PT sequences -
XX
XX
PS Claim 19; SEQ ID 63963; 344pp + CD-ROM; English.
XX
XX The present sequence is a putative protein fragment from
CC Arabidopsis thaliana. Its coding sequence was isolated by carrying out
CC RT-PCR on all of the mRNA obtained from the plant, and creating a cDNA
CC library which could then be sequenced, allowing the putative protein
CC sequence(s) to be obtained. This sequence may be useful for protein
CC identification and for aiding in the elucidation of signal transduction
CC and metabolic pathways. Its coding sequence has a use in the control of
CC gene expression as a promoter, coding sequence, 3'UTR or termination
CC sequence, for controlling the behaviour of a gene within the chromosome
CC as a tool for use in genetic mapping, including a use in hybridisation
CC assays, for recognition or isolation of similar DNA fragments, or for
CC the identification of a particular organism.

XX	Sequence	59 AA:	
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IIAA	SEQUENCE 1.0		
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XX	12-SEP-2000 (first entry)		
DE	Human Zsig43 polypeptide.		
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XX	Zsig43: receptor: chromosome 17q21.1: recombinant production;		
KW	gene therapy.		
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OS	Homo sapiens.		
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FT	Zsig43 gene expression	/label= signal_peptide	
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PA	(ZYMO) ZYMOGENETICS INC.		
XX			
PI	Sheppard PO, Lok S;		
XX			
DR	WPI: 2000-400069/34.		
DR	N-PSDB: AAA29367, AAA29368.		
XX			
PS	Claim 1: Page 81-83: 88pp: English.		
XX			
XX	This is a putative receptor, Zsig43. The gene is strongly expressed		
CC	in heart, liver, skeletal muscle, adrenal gland, kidney and pancreatic		
CC	tissues. The Zsig43 gene resides on human chromosome 17 at 17q21.1. The		
CC	Zsig43 coding sequences may be used to detect Zsig43 gene expression in		
CC	samples and to analyze Zsig43 gene structure according to standard		
CC	methodologies (e.g. polymerase chain reaction (PCR) amplification). They		
CC	may also be used for the recombinant production of Zsig43 polypeptides		
CC	either in vitro (e.g. in a fermentation culture) or in vivo (e.g. as part		
CC	of a gene therapy protocol for rectifying inappropriate Zsig43 expression		
CC	in a patient). The proteins may be used to identify and produce agonists		
CC	and antagonists (especially antibodies which may then be used to modulate		
CC	Zsig43 expression and activity. Antibodies specific for Zsig43 may also		
CC	be used to detect the presence of Zsig43 gene expression products		
CC	according to standard methods (e.g. enzyme linked immunosorbant assays		
CC	(ELISAs) (claimed).		
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AAV6513 Length: 860 April 1, 2002 16:31 Type: P Check: 8290

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151 YASVSLYLLP ERPAFLILYE DLVHILLGSP GARSOPLOVF QRRARLPEVS

201 STYSOLMASL TPASTOQEMR APPAFLGTEA SSSGNGSMLE LMPLTAVSVH

251 LITGNGTEVP LSGPIHLSLP VPSETRALTY GTSIPAMWRD PKSGIWMANG

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351 FLITLIALA LVLVLLCLL IYYCRRRCLK PROQRKLQL SGPSDGNKRD

401 QATSMSQLHL ICGPLLEPAP SGDPPEAPPG PLHSAFSSSR DLASRDOFF

451 RTKPSASRP AAPSGARGG ESAGLGKARS AEGPGGLEPG LEBHRGPGS

501 AAFLHEPPS PPPEDHYLG HKGAABGKTP DEFLSQSYDQ LARPSLGOA

551 GQLIFCGSID HIKDNYRVNV MPTLVIPAHY VRLGGEAGAA GVGDEPARPE

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651 TIPVLFNEST MAOLNGELQA LTEKKILLELG VKPHPRAMFV SLDGSRNSQV

701 RHSTYIDLQAG GGARSTDSL DSGVDVHEAR PARRRAREE RERAPAPAP

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ID AAV58787 standard; Protein: 290 AA.

AC AAV58787;

XX

DT 08-MAY-2000 (first entry)

XX

DE Arabidopsis phosphatidic acid phosphatase ATPAP1.

XX

XX ATPAP1: phosphatidic acid phosphatase; PAP: diacylglycerol;

KM lipid; oilseed; vegetable oil; transgenic plant.

XX

OS Arabidopsis thaliana.

XX

XX WO200005385-A1.

PN

XX

PD 03-FEB-2000.

XX

PF 22-JUL-1999; 99WO-US16892.

XX

PR 24-JUL-1998; 98US-0122315.

XX

PA (CALJ) CALGENE LLC.

XX

PI Lassner MW, Ruezinsky D;

XX

XX WPI: 2000-182706/16.

DR N-PSDB: AA258188.

XX

PT New polynucleotide encoding phosphatase protein useful for modifying

XX the lipid composition in plant cells -

PS

XX Example 1; Fig 2; 49pp; English.

CC The present sequence is that of Arabidopsis thaliana phosphatidic

CC acid phosphatase ATPAP1, as deduced from a cDNA clone (see AA258188)

CC isolated from an Arabidopsis EST database on the basis of homology

CC to conserved regions (see AAV58720-21) of mouse, rat, human and

CC yeast PAs. The invention provides novel plant PAP nucleic acids

CC and PAP polypeptides active in the formation of diacylglycerol from

CC phosphatidic acid. Also provided are methods of using PAP nucleic

CC acids, in sense or antisense orientation, to modify or alter lipid

CC compositions or lipid levels in transgenic plants.

XX

SQ Sequence 290 AA:

AAV58787 Length: 324 April 1, 2002 16:31 Type: P Check: 2030

1 SOARDBOEC ZGHSQILKMF PSTWVYSQOT HERSMPEHL GAHTIRSGV

51 TVARFHMMDV LILLILVIE IVLVNIEPPH REVGEDMLTD LRYPLQDNFI

101 PFWAVPLIIV VLPEAVICVY YFIRNDVYDL HHAILGLRS VLITGVITDA

151 IKDAVGRPRP DFWRCFPDG IGIFHNNTKN VLCTGAKDV KEGHSPFSG

201 HTSWSEFAGG FLSLYLSGI RVEDGRGHA KLCIVILPLL VAALGVSRV

251 DDYWHHMDV FGAIIGLTV ATFCYLOFPF PRYDPDGWP HAYFQMLADS

301 RNDVDSAGM NHLSVOTEL ESVA

!!AA_SEQUENCE 1.0

ID AAV58788 standard; Protein: 348 AA.

AC AAV58788;

XX

DT 08-MAY-2000 (first entry)

XX

DE Arabidopsis phosphatidic acid phosphatase ATPAP2.

XX

XX ATPAP2: phosphatidic acid phosphatase; PAP: diacylglycerol;

KM lipid; oilseed; vegetable oil; transgenic plant.

XX

OS Arabidopsis thaliana.

XX

XX WO200005385-A1.

PN

XX

PD 03-FEB-2000.

XX

PF 22-JUL-1999; 99WO-US16892.

XX

PR 24-JUL-1998; 98US-0122315.

XX

PA (CALJ) CALGENE LLC.

XX

PI Lassner MW, Ruezinsky D;

XX

XX WPI: 2000-182706/16.

DR N-PSDB: AA258189.

XX

PT New polynucleotide encoding phosphatase protein useful for modifying

XX the lipid composition in plant cells -

PS

XX Example 1; Fig 3; 49pp; English.

XX

XX The present sequence is that of Arabidopsis thaliana phosphatidic

CC acid phosphatase ATPAP2, as deduced from DNA (see AA258189) isolated

CC from an Arabidopsis EST database on the basis of homology to

CC Arabidopsis ATPAP1 (see AAV58787). The invention provides novel

CC plant PAP nucleic acids and PAP polypeptides active in the

CC formation of diacylglycerol from phosphatidic acid. Also provided

CC are methods of using PAP nucleic acids, in sense or antisense

CC orientation, to modify or alter lipid compositions or lipid levels

CC in transgenic plants.

XX

SQ Sequence 348 AA:

AAV58788 Length: 382 April 1, 2002 16:31 Type: P Check: 1560 ..

1 SOARNDBCE ZGHSQILKMF PSTWVSQOT HERSHASATF LFNLSLSLR

51 DLHFLTFITIS FESSLEFWRN SQDOEAORGR MOEIDLVSHT IKSCHGRVAS

101 KKHNDWILIV ILIAIEIGLN LISPFYRYVG KDMNTDLKYP FKDNTPPIWS

151 VPIYAVLDP IYVCFEYLKR TCYVDLHHSI LGLLFAVLIT GYITDSIKVA

201 TGRPRNPFYW RCFPDGKELY DALGCVVCHG KAAEVKEGKH SPPSGHTSWS

251 FAGLFFLSLY LSGKIKAFNN EGHVAKLCLV IFFLLAACIV GISRVDDYWH

301 HMQDVFAGAL IGTIVAFCY RQFYNPYHE EGMGPAYFR AAOEGVPT

351 SSQNGDALRA MSLQMDSTSL ENMESGTSTA PR

!!AA_SEQUENCE 1.0

ID AAV58789 standard; Protein: 314 AA.

AC AAV58789;

DT 08-MAY-2000 (first entry)

DE Arabidopsis phosphatidic acid phosphatase ATPAP3.

XX

XX

DE Arabidopsis phosphatidic acid phosphatase; PAP; diacylglycerol;

XX

XX

KW lipid; oilseed; vegetable oil; transgenic plant.

XX

OS Arabidopsis thaliana.

XX

XX

PN WO200005385-A1.

PD 03-FEB-2000.

PF 22-JUL-1999; 99WO-US16892.

XX

XX

PR 24-JUL-1998; 98US-0122315.

XX

XX

PA (CALJ) CALGENE LLC.

PI Lassner MW, Ruezinsky D;

XX

XX

DR WPI: 2000-182706/16.

XX

DR N-PSDB: AAZ58190.

XX

PT New polynucleotide encoding phosphatase protein useful for modifying

XX

XX

PS the lipid composition in plant cells -

XX

PS Example 1: Fig 4; 49pp; English.

XX

CC The present sequence is that of Arabidopsis thaliana phosphatidic

CC acid phosphatase ATPAP3, as deduced from DNA (see AAZ58190) isolated

CC from an Arabidopsis EST database on the basis of homology to

CC Arabidopsis ATPAP1 (see AAV58787). The invention provides novel

CC plant PAP nucleic acids and PAP polypeptides active in the

CC formation of diacylglycerol from phosphatidic acid. Also provided

CC are methods of using PAP nucleic acids, in sense or antisense

CC orientation, to modify or alter lipid compositions or lipid levels

CC in transgenic plants.

XX

XX

SO Sequence 314 AA;

AAV58789 Length: 348 April 1, 2002 16:31 Type: P Check: 1234 ..

1 SOARNDBCE ZGHSQILKMF PSTWVSQOT HERSMREAO LGGHTRSHGM

51 TWAATHMHOM IIVLVVILE CVLLIHFPY RFYGRKMDMD LSYPLKSTIV

101 PIMSVPIYAM LLPVITFTI YFRRDVYDL HNAVLGLYS VLVTAVLTD

151 IKNAVGRPR DEFWRCPFDG KALYDSLGV ICHGDKSVIR EGHKSPSGH

201 TSWSFSGLGF LSYLSGRIQ AFDGKHVAK LCIVILPLF AALVGSIRVD

251 DYWHMQDYF AGGLGLAIS TICLYOFFPP PYHTEGMPY AYQVLEAAR

301 VOGAANGAVQ QPPPOVNNGE EEDGFGMLH LVDPPTMRRE EDVETGRC

!!AA_SEQUENCE 1.0

ID AAV58790 standard; Protein: 310 AA.

AC AAV58790;

DT 08-MAY-2000 (first entry)

DE Corn phosphatidic acid phosphatase.

XX

XX

KW phosphatidic acid phosphatase; PAP; diacylglycerol;

XX

XX

KW lipid; oilseed; vegetable oil; transgenic plant; maize; corn.

XX

OS Zea mays.

XX

XX

PN WO200005385-A1.

PD 03-FEB-2000.

PF 22-JUL-1999; 99WO-US16892.

XX

XX

PR 24-JUL-1998; 98US-0122315.

XX

XX

PA (CALJ) CALGENE LLC.

PI Lassner MW, Ruezinsky D;

XX

XX

DR WPI: 2000-182706/16.

XX

DR N-PSDB: AAZ58191.

XX

PT New polynucleotide encoding phosphatase protein useful for modifying

XX

XX

PS the lipid composition in plant cells -

XX

PS Example 1: Fig 5; 49pp; English.

XX

CC The present sequence is that of corn phosphatidic acid phosphatase

CC (PAP), as deduced from DNA (see AAZ58191) isolated from a corn EST

CC database on the basis of homology to an Arabidopsis PAP (see

CC AAV58787). The invention provides novel plant PAP nucleic acids and

CC PAP polypeptides active in the formation of diacylglycerol from

CC phosphatidic acid. Also provided are methods of using PAP nucleic

CC acids, in sense or antisense orientation, to modify or alter lipid

CC compositions or lipid levels in transgenic plants.

XX

XX

SO Sequence 310 AA;

AAV58790 Length: 344 April 1, 2002 16:31 Type: P Check: 5033 ..

1 SOARNDBCE ZGHSQILKMF PSTWVSQOT HERSMADQLG SYTIRSHMI

51 LARLHWYDI ILLLAVIDG LNIIEPFHR FVCKDMMTDL RYPMKGNIVP

101 FMAVPLIGII LPMALFVGIV FKKNFYDLH HGILGILYSV LITAVITDAI

151 KDGVGFRPDP FFWRCFPMGN DYYDNITGV ICGVKSVIK EGHKSPSGH

201 SSMVFAGLOF LAWYLACKLT AFDRKGIAK LCIVFLPLT AALVAVSVD

251 DYWHMQDYF AGGLGLTVA SFCYLOFFPY PRDGDALMPH AVAVRLAEEG

301 NSRNASYSV RPTETETVDI PGHGAIITLR ETLNDVESGS ARRL

!!AA_SEQUENCE 1.0

ID AAV58791 standard; Protein: 343 AA.

AC AAV58791;

```

XX 08-MAY-2000 (first entry)
XX
XX Soybean phosphatidic acid phosphatase soyPAP1.
DE Phosphatidic acid phosphatase; PAP; soyPAP1; diacylglycerol;
XX lipid; oilseed; vegetable oil; transgenic plant; soybean.
XX
XX Glycine max.
OS
XX WO200005385-A1.
XX
XX 03-FEB-2000.
XX
XX 22-JUL-1999; 99WO-US16892.
XX
XX 24-JUL-1998; 98US-0122315.
XX
XX (CALJ ) CALGENE LLC.
XX
XX PI Lasser MW, Ruezinsky D;
XX WPI: 2000-182706/16.
XX DR N-PSDB; AA258193.
XX
XX PT New polynucleotide encoding phosphatase protein useful for modifying
XX the lipid composition in plant cells -
XX
XX PS Example 1; Fig 8; 49pp; English.
XX
XX CC The present sequence is that of soybean phosphatidic acid
XX phosphatase soyPAP1, as deduced from DNA (see AA258193) isolated from
XX a soybean EST database on the basis of homology to an Arabidopsis
XX PAP (see AA258787). The invention provides novel plant PAP nucleic
XX acids and PAP polypeptides active in the formation of diacylglycerol
XX from phosphatidic acid. Also provided are methods of using PAP
XX nucleic acids, in sense or antisense orientation, to modify or alter
XX lipid compositions or lipid levels in transgenic plants.
XX
XX SO Sequence 343 AA;

AAV58791 Length: 377 April 1, 2002 16:31 Type: P Check: 9121 ..
1 SOARNDBQOE ZGHSQILKMF PSTWVYSQOT HERSMASWMD LRPFRRQSV
51 RTRRQEFETR EVOLGSHTVS SHGYAVARTN KHDWLILLLL VLYISLXTI
101 HRFHREVGKD MMTDLKYPLK SNTVPAMAIR IYAILLPTVI FLGYIIRRD
151 VYDLHNAVIG LIFSVLITAV FTEAIKNAVQ RPRDFEWRRC FPDGKDYDK
201 WGDVICHQDQ KVIKEGYKSF PSCHTSGSFS GLGFLSLVLS GKIAFDRKG
251 HVAKLCIVFL PLLVASLVGI SRVDYWHNM QDVFAAGLIG LTVATFCYLQ
301 FEPYPYHSEG WGPYAYFRML EESRGMTQYP SVQNSGQAOQ AEQAESQEE
351 QGLHGCWGLT LSRDHAAALN DCESGRG

!!AA_SEQUENCE 1.0
ID AAV58792 standard; Protein: 322 AA.
XX
XX AAV58792;
XX
XX 08-MAY-2000 (first entry)
XX
XX Soybean phosphatidic acid phosphatase soyPAP2.
XX
XX Phosphatidic acid phosphatase; PAP; soyPAP2; diacylglycerol;
XX lipid; oilseed; vegetable oil; transgenic plant; soybean.
XX
XX Glycine max.
XX
XX

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PN WO200005385-A1.
XX
XX 03-FEB-2000.
XX
XX 22-JUL-1999; 99WO-US16892.
XX
XX 24-JUL-1998; 98US-0122315.
XX
XX (CALJ ) CALGENE LLC.
XX
XX PI Lasser MW, Ruezinsky D;
XX WPI: 2000-182706/16.
XX DR N-PSDB; AA258194.
XX
XX PT New polynucleotide encoding phosphatase protein useful for modifying
XX the lipid composition in plant cells -
XX
XX PS Example 1; Fig 7; 49pp; English.
XX
XX CC The present sequence is that of soybean phosphatidic acid
XX phosphatase soyPAP2, as deduced from DNA (see AA258194) isolated from
XX a soybean EST database on the basis of homology to an Arabidopsis
XX PAP (see AA258787). The invention provides novel plant PAP nucleic
XX acids and PAP polypeptides active in the formation of diacylglycerol
XX from phosphatidic acid. Also provided are methods of using PAP
XX nucleic acids, in sense or antisense orientation, to modify or alter
XX lipid compositions or lipid levels in transgenic plants.
XX
XX SO Sequence 322 AA;

AAV58792 Length: 356 April 1, 2002 16:31 Type: P Check: 5772 ..
1 SOARNDBQOE ZGHSQILKMF PSTWVYSQOT HERSAPEIOL GMNTRISHT
51 RVARTNMHDW LILLLVIID AVLNLQPN RFVGGMMTD LRYPLKANTI
101 RFMAVPIAI LPLAVFLVY YFIRKDVYDL NHAIGLLFS VLITAVMTDA
151 IKDANGRRPR DFEWRCFRPDG KGVFDPVTSN VLCTGDKGI KEHGKSPFSG
201 HTSWSFAGLV YLAWYISGKL RAFDRGHVA KICLVFLPIL VAAMIAVSrv
251 DDYWHNMQDV FAGALIGMII ASFCYLQFPR PEYVDGWMCP HAYQMLAES
301 RNGAQRSTVN NEIHVQSAE LQAVSLYIPR QNDADTRGNS WDSSPMLGAS
351 QNVRTN

!!AA_SEQUENCE 1.0
ID AAV54319 standard; Protein: 2074 AA.
XX
XX AAV54319;
XX
XX 06-APR-2000 (first entry)
XX
XX Amino acid sequence of a murine PCTG4 protein.
XX
XX Human; PCTG4 region; X chromosome; q13 region; polymorphism;
XX mental retardation; autism; depression; bipolar affective disorder;
XX hypothyroidism; OPA gene; neuropsychiatric disorder.
XX
XX Mus sp.
XX
XX WO9955915-A2.
XX
XX 04-NOV-1999.
XX
XX 29-APR-1999; 99WO-US09365.
XX
XX 29-APR-1998; 98US-0083465.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX

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PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Philibert RA, Gims EI.
 XX WPI: 2000-126357/11.
 DR
 XX
 PT Identification of polymorphisms in the PCTG4 region of Xq13 for
 PT diagnosing mental retardation or autism -
 XX
 PS Example 7; Page 81-84; 100pp; English.
 XX
 CC The present sequence represents a murine PCTG4 protein. Polymorphisms
 CC in the human PCTG4 region of chromosome Xq13 are associated with
 CC mental retardation, autism, depression, bipolar affective disorder or
 CC hypothyroidism. One 12 bp insertion polymorphism occurs within the
 CC coding region of the human OPA gene, and introduces a 4 amino acid
 CC insertion in a putative OPA domain. This domain has been shown to be
 CC involved in tissue specific expression. Another polymorphism consists
 CC of a pentanucleotide repeat approximately 7 kb upstream of the 12 bp
 CC polymorphism. Another polymorphism consists of a dinucleotide repeat
 CC approximately 4.5 kb downstream of the 12 bp polymorphism. The
 CC specification describes a method for screening for polymorphisms in a
 CC PCTG4 nucleic acid sequence obtained from a subject. The PCTG4 related
 CC sequences within the q13 region of the X chromosome have polymorphisms
 CC associated with neuropsychiatric disorders. The methods can be used to
 CC screen for the presence of a heritably linked form of mental retardation,
 CC autism, depression, bipolar affective disorder or hypothyroidism.
 CC
 XX
 XX Sequence 2074 AA:
 SQ

AAV54319 Length: 2108 April 1, 2002 16:31 Type: P Check: 165 ..

1 SQARNDBCE ZGHSQILKMF PSTWVYSQOT HERSMNOKDN FWLTARSQS
 51 AINTWFTLTA GTKPLTHLAK KVFIFSKKEE VEGYLAKTIV PVMAANLIK
 101 MTCAYYAAMS ETKVKKKNTA DPEFTWTOII TKYLWEOLOK MAEYYRQPA
 151 GSGCGGSGTIG PLPHDVEMAI RQWDYNEKLA LFMQDGMLD RHEFLTWLE
 201 CPEKTRPED ELKLKLLPL LRTSGEVS AVLSRLAYF CTRRLALDLD
 251 GVSSHSHSVI AAGSTSLPT TPAOPPTSS TPSTPESDL MCPORPLVF
 301 GLSCILQITL LCCPSALVMH YSLTDSRIKT GSPLDHLPIA PSNLPMEGN
 351 SAFIQOVAK LREIEQIKE RGAVEVRMS FDKCEATAG FTIGRVLHTL
 401 EYLDHSFEER SDFSNSLDSL CNRIFGLGPS KDGHEISSDD DAVVSLCEW
 451 AVSCRSGRH RAMVVAKLE KROAEIEAER CGESEADEK GSVASGLSA
 501 PSAPTFQVYL LQFLDTQAPM LTPRSESER VEFNVLVLF CELIRHVES
 551 HNMVTCILIS RGLDAFGAPG PRPSPFDDP TDDPERKEAE GSSSSKLEDP
 601 GLSEMDIDP SSTVLFEDME KPDFSLFSPT MPCCKGSPS PEKPDVEKEV
 651 KPPAKEKIEG TLGILYDQPR HVOYATHFPI POEESCSHEC NQRLVLEFGV
 701 GKORDARHA IKKITKDIK VLNRKGTAEI DQLAIVPLN PGDLTFEGE
 751 DGQRRRRNRP EAPPTAEDIF AKFOHLSHYD QHOVTAQVSR NVLQITSEFA
 801 LGMSTHLLV QHVOFIDLM EYSLISGLI DPAIQLNML SVVAELLIK
 851 SSDLVGSYTT SLCLIAVAVL RHYHACILIN ODQMAQVEEG LCGVYKQGMN
 901 RSDGSSAERC ILAVLYDLYT SCSHLSKSKG ELFPDSCSV KNITVCNVEP
 951 SESNMRAPE FMDITLENPA AHFTYTTGLG KSLSEPNANR YSFVCNALMH
 1001 VCVGHHDPR VNDIAILCAE LTGYCKSLA EWLGVILKALC CSSNNGTCGF

1051 NDLCNVDS DLSFHDSLAT FVALIAROC LLEDLIRCA AIRSLNAC
 1101 SEDSEBGAR LTCRILLHLF KTRPOLNPGOS DGNKTVGIR SSCRHLLAA
 1151 SONRIVDGAV FAVLKAFFVL GDAELKSGF TVPGTEELP EEEGGGSSG
 1201 RROGGRNISV ETASLDVYAK YVLRISIQOE WYGERCLASL CEDSNDIQDP
 1251 VLSSAQORL MQLICYPHRL LDNEDGENQ RORIKRIIKN LDQWTMOSS
 1301 LELDLMIKOT PNTENSLLE NIARATIEVF QQSAETGSSS GSTASNMPSS
 1351 .SKTRPVLSL ERSGWLVAP LIAKLPTSVQ GHVLAAGEE LEKQIHGSS
 1401 SRKEKDROKO KSMLSLSQPF FLISVLTCLK GODEBREGLI ASLHSQVHOI
 1451 VINMRENOYL DCKPKQLMH EALKRLNV GMPFTVGRS TQOTTEMAQL
 1501 LLEITISGTV DMQSNNELFT TVLDMLSVLI NGTLAADSS ISQGSMEENK
 1551 RAYMLVAKL QKDLGERQSD SLEKVHQLP LPKONRDVIT CEPQGSILDT
 1601 KGNKTAGFDS IFKKEGLQVS TKOKISPMWL FEGIKPSTAP LSMAMEGTVR
 1651 VDRRAARGE E QORLLYHTH LRRPRAYVL EPLPLPEDE EPPAULLEP
 1701 EKKAPEPKT DKROAAPST EERKKKSTKG KKRSPATKN EDYMGGRS
 1751 GPYGVTPPD LLIHANPGSI SHLSYROSSM GLYTQNPPLP AGGPRVDYR
 1801 FVRLPMQKLP TRPTYPGLP TTMSTVMGLE PSSYKTSYVR QOQPTVPOQ
 1851 RLROLOQSO GMLGSSVHQ MTPSSSYGLQ TSQLSPSLD GYTSYVHVG
 1901 LQHTGPADP TRHLQORPSG YVHQAPTYG HGLISTORPS HQTLQOTPM
 1951 GTMTPLSAG VOAGVRSTSI LPEQOQOQOQ OQOQOQOQOQ OQOQOQOQOQ
 2001 QOQOQOQHIR QOQOQOQMLR QOQOQOQOQO QOQOQOQOQO QOQOQOQPHQ
 2051 QOQQAAPPQ QPOSQPOFOR QGLQOTQOQO QTAALVRLQI QQLNSTQPP
 2101 STNIFGRY
 11AA_SEQUENCE 1.0
 ID AAY54320 standard; Protein: 2023 AA.
 XX AC
 XX AAY54320;
 XX
 DT 06-APR-2000 (first entry)
 XX
 DE Amino acid sequence of a human PCTG4 protein.
 XX
 KW Human; PCTG4 region; X chromosome; q13 region; polymorphism;
 KW mental retardation; autism; depression; bipolar affective disorder;
 KW hypothyroidism; OPA gene; neuropsychiatric disorder.
 XX
 OS Homo sapiens.
 XX
 PN W09955915-A2.
 PD 04-NOV-1999.
 XX
 PF 29-APR-1999; 99WO-US09365.
 XX
 PR 29-APR-1998; 98US-0083465.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Philibert RA, Gims EI;
 XX

DR WPI; 2000-126357/11.
 XX Identification of polymorphisms in the PCTG4 region of Xq13 for
 PT diagnosing mental retardation or autism -
 XX Example 7; Page 81-84; 100pp; English.
 PS
 XX The present sequence represents a human PCTG4 protein. Polymorphisms
 CC in the human PCTG4 region of chromosome Xq13 are associated with
 CC mental retardation, autism, depression, bipolar affective disorder or
 CC hypothyroidism. One 12 bp insertion polymorphism occurs within the
 CC coding region of the human OPA gene, and introduces a 4 amino acid
 CC insertion in a putative OPA domain. This domain has been shown to be
 CC involved in tissue specific expression. Another polymorphism consists
 CC of a pentanucleotide repeat approximately 7 kb upstream of the 12 bp
 CC polymorphism. Another polymorphism consists of a dinucleotide repeat
 CC approximately 4.5 kb downstream of the 12 bp polymorphism. The
 CC specification describes a method for screening for polymorphisms in a
 CC PCTG4 nucleic acid sequence obtained from a subject. The PCTG4 related
 CC sequences within the q13 region of the X chromosome have polymorphisms
 CC associated with neuropsychiatric disorders. The methods can be used to
 CC screen for the presence of a heritably linked form of mental retardation,
 CC autism, depression, bipolar affective disorder or hypothyroidism.
 CC
 SQ Sequence 2023 AA;
 AAY54320 Length: 2057 April 1, 2002 16:31 Type: P Check: 8484 ..

1151 VETASLDVYA KYVLRISICQ EWWGERCLKS LCEDSNDLQD PVLSSAQQR
 1201 LMOLICTPHR LLDNENGEP QORIRKRILO NLDQOTAROS SLELOLMIKO
 1251 TPNNEMNSL ENIAKATIEV FOOSAETGSS SGSTASNMPS SSKTKPYLSS
 1301 LERSGWLVA PLIAKLPTVS QGHVLKAGE ELEKGQHLGS SSRKERDROK
 1351 OKSMSSLISQO PFLSLVLTCL KGQEQREGL LTSLSYOHQ IYNNMRDDOY
 1401 LDDCKPROML HEALKLRLNL VGMEDTVQR STQQTTEWAM LLEIIISGT
 1451 VDMQSNMELF TYVLDMLSVL INGTLAOMS SISGSMEN KRAYMLAKK
 1501 LOKLGEROS DSLEKVRQL PLPKOTRDYI TCEPQSLID TKCNKTAGFD
 1551 SIFKEGLOV STOKISPMQ LFEGLKPSAP LSWGMFGTVR VDRRVARGEE
 1601 QORLLYTHH LRPRRAYYL EPLPLPEDE EPAPTLLEP EKKAPPEPKT
 1651 DKPGAAPST EERKKSTKG KRSQPAIKT EDYKMGERS GPYGVIVPPD
 1701 LLAHPNPGSI THLVROGSI GLYTQNOPLP AGGPRVDPYR PVRLPMOKLP
 1751 TRPTYPGVLP TTMTGVMGLE PSSYKTSYR QQOPAVPOQ RLRQOLQOSQ
 1801 GMLGQSSVHQ MTPSSSYGLQ TSQGYTPYVS HVGLOQHTGP AGTWPPSYIS
 1851 SOPYOSTHPS TNPTLVDPTR HLOQRPBGVY HQQAPTYGNG LSTORFSHQ
 1901 TLQOTPMIST MTPMSAGVQ AGVRSIALP EQQOQQOQQOQ QQQOQQOQQOQ
 1951 QQQOQQOQYHI RQQOQQOQILR QQQOQQOQQOQ QQQOQQOQQOQ QQQOQQOQOQ
 2001 QQQQAAPOP QPQSQPOFOR QGLQOTQOQO QTAALVROLQ QQLSNTOPOP
 2051 STNIFGR
 11AA_SEQUENCE 1.0
 ID AAY6657 standard; protein; 1184 AA.
 XX
 AC AAY6657;
 XX
 DT 05-APR-2000 (first entry)
 XX
 DE Membrane-bound protein PRO1188.
 XX
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
 KW pharmaceutical; receptor immunoadhesin; gene mapping.
 OS Homo sapiens.
 XX
 PN WO963088-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 02-JUN-1999; 99WO-0512252.
 XX
 PR 02-JUN-1998; 98US-0087607.
 PR 02-JUN-1998; 98US-0087609.
 PR 02-JUN-1998; 98US-0087759.
 PR 03-JUN-1998; 98US-0087827.
 PR 04-JUN-1998; 98US-0088021.
 PR 04-JUN-1998; 98US-0088025.
 PR 04-JUN-1998; 98US-0088028.
 PR 04-JUN-1998; 98US-0088029.
 PR 04-JUN-1998; 98US-0088030.
 PR 04-JUN-1998; 98US-0088033.
 PR 04-JUN-1998; 98US-0088326.
 PR 05-JUN-1998; 98US-0088167.
 PR 05-JUN-1998; 98US-0088202.
 PR 05-JUN-1998; 98US-0088212.

CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
CC will also be useful for the preparation of PRO polypeptides, especially
CC by recombinant techniques.
XX
SO Sequence 1184 AA:

AAV66657 Length: 1218 April 1, 2002 16:31 Type: P Check: 668

1 SQARNDBCQE ZGHSQILKMF PSTWYVSQOT HERSAVGTGA WFSFLYLEV
51 TSVLGRQTM L TOSVRRVQPG KKNPSLIFAKP ADLIESPEBW TTWFNIDIPG
101 GKGDYERLDA IRFYGDRCV APRLEAFT TDWTPAGSTG QVYHGSFREG
151 FWCINREQRP GQNCNVTYR FLCPPGSLRR DTERIWSFWS PWSKSAACG
201 QTGVQTFTRI CLAEWVSLCS EASEGQHCHM GQDCTACLT CPMQVAVADC
251 DACMCQDFML HGAVSLPGGA PASGAATYLL TKTPKLLTQT DSDGRFRIRPG
301 LCPDGKSLK ITRKFPAPIV LTPMKTSLKA ATIKAEFYRA ETPYMWNPPE
351 TKARAQOSV SLOCKATGKP RPDKTFWYHN DTLDPSLIYK HESLVLRKL
401 QOHQAGEYFC KAOSDAGAVR SKVAQLIVTA SDETPPCNBPV ESYLIRLPHD
451 CFQATNSFY YDVGRCPVKT CAGQDNGIR CRDAVQNCBG ISKJEREIQ
501 CSGTTLPTKV AKESCQRCCT ETRSIYKGV SAADNGEPMR FGAVYMGNSR
551 VSMYTGKGT TLHVPODTER LVLTFFVDRLQ KEVNTTKVLP FNKGSAYFH
601 EIKMLRREK ILEAMETNI IFLGEVGED PMALEIPSR SFYRQNEPY
651 IGKTKASVTE LDPNRISTAT AAOITLNFIN DEGTFPLRT YGMSVDFRD
701 EYTSSEPINAG KVKVHLDSO VKMPEHISTV KWSLNPDTG LWEEGDFKFK
751 ENQRNRKED RTFLVGNLEI RERLEFNLV PESRRCFYKV RAYSERFLP
801 SEQIQGVVIS VINLEPRTGF LSNPRAMGRF DSVITGPNGA CVPAFCDDOS
851 PDAYSAYVLA SLAGEELQAV ESSPKFNPNVA IGVPQPYLTK LNYRRTDHD
901 PRVAKTAFQI SMAKPRNSA EESNGPIYAF ENLRACEAP PSAHFFRYQ
951 IEGRYDYNT VPFNEDDPMS WTEYLAWMP KPMERFACYI KVKIYPLEV
1001 NVRSRNGGT HRTVGLYK IRDVRSTRDR DQPNVSAQL EFKCSGMLYD
1051 QDRYDRTLK VIFQSCSRA SVNPMLEHL VNHLPYLVANN DTSYTYMLAP
1101 LDPIGHNYGI YTYTDODPRT AKETALGRCF DGTSDGSSRI MKNVGYALT
1151 FNCVEROVR QSAFOYLQST PAOSPAAGTV QGRVPSRRQO RASRGOROG
1201 GVVASLRFPR VAOQPLIN

11AA_SEQUENCE 1.0
ID AAV76061 standard; Protein; 128 AA.
XX
AC AAV76061;
XX
DE 27-MAR-2000 (first entry)
XX
DE Rat skin cell transmembrane protein, SEQ ID NO:316.
XX
KW Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
KW secreted; transmembrane; inflammation; cancer; neurological disease;
KW angiogenesis; tumour vascularisation; growth disorder;
KW developmental disorder; skin wound; hair follicle disorder;
KW anti-inflammatory; cytostatic; neuroprotective; vulnery.

XX
OS Rattus sp.
XX
PN WO955865-A1.
XX
PD 04-NOV-1999.
XX
PE 29-APR-1999; 99WO-NZ00051.
XX
PR 29-APR-1998; 98US-0069726.
PR 09-NOV-1998; 98US-0188930.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
PI Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;
DR WPI; 2000-072177/06.
XX
PT Novel polynucleotides useful for the treatment of various conditions
PT including wounds and cancer -
XX
PS Claim 4; Page 186-187; 235pp; English.
XX
CC The invention relates to novel nucleic acid sequences derived from rat
CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
CC cells. Polypeptides of the invention may be used to treat inflammation,
CC cancer and neurological diseases. The proteins may be used to stimulate
CC the growth and motility of keratinocytes, to inhibit the growth of
CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
CC modulate skin inflammation, to modulate epithelial cell growth and to
CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
CC to treat growth and developmental defects, skin wounds and hair follicle
CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded
CC by cDNA sequences derived from several mouse, rat or human skin cell
CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and
CC AAY76119 are proteins with an N-terminal signal sequence, indicating
CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,
CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
CC putative transmembrane domains.
XX
SQ Sequence 128 AA:

AAV76061 Length: 162 April 1, 2002 16:31 Type: P Check: 24

1 SQARNDBCQE ZGHSQILKMF PSTWYVSQOT HERSAERGT SGEGNALG
51 AELGVRLLE VAFLETELTP PQQRRIQPEE LMYRNPYVE AEYPTGPMF
101 VIAFLTPSL IFFAKFLRKA DATDSKQACL AASLALANG VFTNIKLIY
151 GRPRDDFFYR CF

11AA_SEQUENCE 1.0
ID AAY32382 standard; Peptide; 11 AA.
XX
AC AAY32382;
XX
DE 28-FEB-2000 (first entry)
XX
DE Cell differentiation, proliferation and maintenance factor peptide.
XX
KW Cell differentiation; cell proliferation; cell maintenance;
KW ectoderm-like cell; embryonic stem cell; pluripotent cell;
KW gene therapy; cell therapy; tissue transplant; organ transplant;
KW xerodermpigment; allotransplant; concomitant transplantation;
KW transgenic animal; substance P.
OS Synthetic.
XX
PN WO9953021-A1.
XX
PD 21-OCT-1999.

XX 09-APR-1999; 99WO-AU00265.
XX 09-APR-1998; 98AU-0002912.
PR 23-SEP-1998; 98AU-0006097.
XX (BRES-) BRESAGEN LTD.
XX
PI Bettes MD, Rathjen PD, Rathjen J;
XX WPI, 2000-061970/05.
DR
XX
XX New isolated biologically active factor capable of influencing
PT differentiation, proliferation or maintenance of pluripotent cells
PS
PS Claim 3; Page 123; 189pp; English.
XX
XX This sequence represents a peptide (substance P free acid) that can
CC form the low mol.wt. component of a novel biologically active factor
CC that is capable of influencing the differentiation, proliferation
CC and/or maintenance of pluripotent cells. The factor consists of a
CC low mol.wt. component selected from Pro, Pro-Ala, Ala-Pro-Gly,
CC Pro-Or-Pro, Gly-Gly, Gly-Pro-Ala, Gly-Pro-Or-Pro, a peptide given in
CC AA32378-42, or a protease digested (including collagenase digested)
CC collagen fragment, and a high mol.wt. component such as fibronectin.
CC The biologically active factor is obtained from conditioned media of
CC hepatic or hepatoma cells or cell lines or extraembryonic endodermal
CC cells or cell lines. The factor is capable of causing the
CC transition of pluripotent cells (e.g. embryonic stem cells in
CC adherent culture and in suspension culture) to pluripotent cells
CC having different properties, more specifically primitive
CC ectoderm-like (EPL) cells. The factor is also capable of
CC maintaining and supporting proliferation of these cells in vitro.
CC It also allows the isolation and maintenance of EPL cells derived
CC from in vitro and in vivo primitive ectoderm. These cells can be
CC used in allo-, concomitant- or xeno-transplantation, cell therapy,
CC tissue and organ augmentation or replacement, and gene therapy.
CC They can also be used for producing chimeric or transgenic animals.
XX
SQ Sequence 11 AA;
AA32382 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SQARNDBOE ZGHSQILKMF PSTWVYSQOT HERSRKPQO FFGLM
!!AA_SEQUENCE 1.0
ID AAY53610 standard; Protein; 214 AA.
XX
AC AAY53610;
XX
DT 11-FEB-2000 (first entry)
XX
DE The nitrile hydratase alpha subunit of *Bacillus* sp. BR449.
XX
XX *Bacillus* sp. BR449; nitrile hydratase; alpha subunit; beta subunit;
KW nitrile; amide; acrylonitrile; acrylamide; amidease.
XX
OS *Bacillus* sp.
XX
PN W09955719-A1.
PD 04-NOV-1999.
XX
PD 30-MAR-1999; 99WO-US06888.
XX
XX 29-APR-1998; 98US-0083485.
PR 10-FEB-1999; 99US-0248528.
XX
PA (UNMS) UNIV MICHIGAN STATE.
XX
PI Ortel PJ, Padmakumar R, Kim SH;
XX WPI, 2000-013413/01.

DR N-PSDB; AA36225, AA30407.
XX
XX Isolated nucleic acids encoding nitrile hydratase and amidase from
PT thermophilic *Bacillus*, useful for conversion of acrylonitrile to
PT acrylamide -
XX
XX Claim 31; Fig 11; 71pp; English.
XX
XX The present sequence represents the alpha subunit of a nitrile hydratase
CC of *Bacillus* sp. BR449 (ATCC 202119). The BR449 nitrile hydratase is
CC optimally active at greater than 55 degrees Celsius, and stable at
CC greater than 60 degrees Celsius. The enzyme contains cobalt, and converts
CC nitriles to amides without significant production of its corresponding
CC acid. As the BR449 nitrile hydratase, unlike known nitrile hydratases,
CC does not require a low temperature, cooling is not necessary and both
CC reaction rate and product solubility are improved. The enzyme also has
CC high resistance to substrate inhibition, allowing a high concentration
CC of acrylonitrile in the reaction mixture. The nitrile hydratase and cells
CC that express it, are used to convert acrylonitrile to acrylamide, a
CC starting material for polymers, and may also be used to hydrate many
CC other nitriles. The enzymatic production of acrylamide from acrylonitrile
CC generates fewer waste products and requires less energy than the
CC conventional copper-catalysed process. An associated amidase is used to
CC convert amides to the corresponding acid. The nitrile hydratase
CC polynucleotide is used to produce transformants for recombinant
CC production of the nitrile hydratase without expression of the associated
CC amidase.
XX
SQ Sequence 214 AA;
AAY53610 Length: 248 April 1, 2002 16:31 Type: P Check: 4816 ..
1 SQARNDBOE ZGHSQILKMF PSTWVYSQOT HERSMTIDOK NTNIDPREPH
51 HHPRQSQWE ARAKALESLS IEKGLSSDA IERVKHYEH ELGPMNGAKV
101 VAKAWTDPAF KQRLDEPET VLKELGYGL GEGHRYVEN TDYHNVVVC
151 TLCSCYPWPL LGLPSPWYKE PAYRARVKE PQVLEKEFL DLPDSVEIRV
201 WDSSEIRFM VLPORPECTE GMTHEELAKL VTRDSMIGVA KIEPLKLR
!!AA_SEQUENCE 1.0
ID AAM23571 standard; Protein; 157 AA.
XX
AC AAM23571;
XX
DT 12-OCT-2001 (first entry)
XX
DE Arabidopsis EST encoded protein SEQ ID NO: 1096.
XX
KW Human: sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition.
XX
OS Arabidopsis thaliana.
XX
PN W0200154477-A2.
PD 02-AUG-2001.
XX
PD 25-JAN-2001; 2001WO-US02687.
XX
XX 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;

XX MPI: 2001-476164/51.
DR N-PSDB; AAH98230.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX
PS Claim 20: Page 821-822; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention.
XX
SQ Sequence 157 AA;

AAH23571 Length: 191 April 1, 2002 16:31 Type: P Check: 7240 ..

1 SOARNDBQCE ZGHSQILKMF PSTWVVSQOT HERSMFVIAF LSPLSLFLA
51 KFLKKADTRD SRQACLAASL ALALNGVFTN TIKLIIGRPR PDFEYRCPFD
101 GLAHSDDLCT GDKDVNENGR KSPFSGHSF AFAGLAFAF YLAGLHCFT
151 POGRGKSWRF CAPLSPLFLA AVIALSRCTD YKHHMOGPPK W

!!AA_SEQUENCE 1.0
ID AAM40285 standard; Protein; 566 AA.

XX AAM40285;

XX 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 3430.

XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0634450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao Qa, Zhou P, Goodrich R, Drmanac RT;
XX MPI: 2001-442253/47.
DR N-PSDB; AAI59441.
XX Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -
XX
XX Example 5; SEQ ID NO 3430; 10078pp; English.
XX

CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with noctropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX

SQ Sequence 566 AA;

AAH40285 Length: 600 April 1, 2002 16:31 Type: P Check: 2082 ..

1 SOARNDBQCE ZGHSQILKMF PSTWVVSQOT HERSMDEGCT PLLPDSLIVYO
51 IFLSLGPAVY LAAGLVCRQW QAVSRDEFM REQFYTYOV ARDVRHRA
101 MSWYEEFORL YDTVPCVEVQ TLREHTDOVL HLFSSHGXQ FASCSKCTV
151 KIMSDLRTIS LLHSADMRPY NWSYQFSQF NKDDSLLLAS GVFLGPHNSS
201 SEEIVAVISD SFALLSRPN KPYDVEGCWL TETSLISGMV HRIGITSCS
251 VLMLNNAFOD VESERNVVK RLFKIONLNA STVRIVMAVD CSRFDPDL
301 LEAGPATSP CRIFDLGSDN EEVYAGPAPA HKEGRLRHL DYLEGRAP
351 QLSERMLETK VALLAQGHT KPERRSATGA KSYLIFFTG CLTYSPPHIG
401 IKOLLEPHONT TAGPYLGEGR GSDAFDLDL HYIDHGHII GMSLSPNRY
451 LVVNSRAMPN GAVVADPMQ PPIAEIDL VFDLKTREY RALRAHAY
501 TPNDCEFFIF LDVSRDFVAS GAEDRHGYM DRHYNICLAR LRHEVYNSV
551 VSPQEQELL LTASDDATIK AMRSPRTMY LQAPRRPRT PFSWLASORR

!!AA_SEQUENCE 1.0
ID AAM42450 standard; Protein; 85 AA.

XX AAM42450;

XX 22-OCT-2001 (first entry)

DE Human kidney related polypeptide SEQ ID NO 319.

XX Human; kidney antigen; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotrophic; cerebroprotective;
KW noctropic; neuroprotective; antibacterial; virocidic; fungicide;
KW ophthalmological; antiallergic; hepatotropic; antidiabetic;
KW antiinflammatory; antitumor; vulnerable; anticonvulsant; antiparasitic;
KW gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disease; infection.

XX Homo sapiens.

XX WO200155323-A2.

XX 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01343.

XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209457.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 18-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0234223.
PR 14-SEP-2000; 2000US-0234274.
PR 14-SEP-2000; 2000US-0234401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.

PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259676.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX WPI: 2001-488784/53.
XX N-PSDB: AAI63004.
PT New isolated nucleic acids and polypeptides, useful for diagnosing,

PT treating and/or preventing human diseases and disorders -
 XX
 XX Claim 11: SEQ ID NO 319; 564pp + Sequence Listing; English.
 XX
 CC The invention relates to novel kidney related polynucleotides
 CC (AA162971-AA163793) and the encoded polypeptides (AA42417-AA42691)
 CC collectively known as kidney antigens and the use of such kidney antigens
 CC for detecting disorders of the kidney, especially kidney cancer and
 CC kidney cancer metastases. The polynucleotides and proteins are also
 CC useful for preventing, treating or ameliorating medical conditions
 CC e.g. by protein or gene therapy. The genes are isolated from a range
 CC of human tissues disclosed in the specification. The nucleic acids,
 CC proteins, antibodies and (ant)agonists are useful in the diagnosis,
 CC treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer,
 CC and other cancers of the adrenal gland, bone, bone marrow, breast,
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders
 CC e.g. Addison's disease, allergies, autoimmune haemolytic anaemia,
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
 CC sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC (c) cardiovascular disorders such as myocardial ischaemia; (d) wound
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
 CC and (f) infectious diseases such as viral, bacterial, fungal and
 CC parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 85 AA:
 AA42450 Length: 119 April 1, 2002 16:31 Type: P Check: 7719 ..
 1 SQARNDBCEQ ZGHSQILKMF PSTWVYSQOT HERSKPSDLF ILESHYQKF
 51 PASQLAGITG HAPSWLAIEFC IFSRDVSPC MSGMSGNSRP QVDLPXNASQ
 101 SGWGFSTVGH PRPGYFVX
 11AA-SEQUENCE 1.0
 ID AAU12377 standard; Protein: 1184 AA.
 XX
 AC AAU12377;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human PRO1188 polypeptide sequence.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PE 01-DEC-2000; 2000WO-US32678.
 XX
 XX 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.

PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 PA (GENTECH) GENENTECH INC.
 XX
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerlitsen ME, Goddard A, Godowski PJ, Gurney AU, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 XX WP1: 2001-408281/43.
 DR N-PSDB; AAS21449.
 DR
 DR
 DR
 XX
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX
 PS Claim 12; Fig 412; 813pp; English.
 PS
 XX
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes, or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 SQ Sequence 1184 AA;
 AAU12377 Length: 1218 April 1, 2002 16:31 Type: P Check: 668 ..
 1 SQARNDBCEQ ZGHSQILKMF PSTWVYSQOT HERSWGTGA WFSFLVLEY
 51 TSVLGRQIML TOSVRRVQPG KKNPSIFAKP ADLESPEGW TTWFIIDIPG
 101 GKDYERLDA IRFYGDRCV ARPLRLAERT TMTFAGSTG QVHGSPREG
 151 FQCLNREORP GONCSNTYVR FLCPPGSLR DIERINSPMS PMSKSAACG
 201 QTCVOTRTPI CLAEVSLCS EASEEGCHM GDDCTACDLT CPMGVANADC
 251 DACMCOEML HGAVSLPGA PASGAAYLL TTPKLLTOT DSDGFRIRIG
 301 LCPDGSLIK ITKVFAPIV LTPPKTSLKA ATIKAEFVA ETPYVWNP
 351 TKARRAGQSV SLCKAIGKP RPDKIYWHN DTLIDPSLYK HESKIVLAKL
 401 OQHAGEYFC KAQSDAGAV SKVAQLITVA SDTPCNPVP ESYLIRLPHD

451 CFQNAATNSFY YDVGRCPVKT CAGQDNGIR CRDAVQNCQG ISKTEEREIQ
 501 CSGTYLPTKV AKESCCORCT EFRSIVRGVY SAADNGEPMR FGHYMGNSR
 551 VSMGYKATF TLHYPDTER LVLTFFVDRIQ KFNVTTKVLK FNKGSVFI
 601 EIKMLRKEP TLEAMETNI IPLGEVGED PMAELEIFSR SFYQNGEPEY
 651 IGKVASVTF LDPNISTAT AAQTDLNFIN DEGTFEPLRT YGMFSVDFRD
 701 EYTSPELNAK KVKYHLDSTQ VKMPEHISYV KMSLNPDIG LMEEGDFKE
 751 ENQRNRKRED RTFLVGNLEI RERRLFNLVY PESRCFVKV RAYSERPLP
 801 SEOIOGVVIS VINLEPRTGF LSNPRAMGRF DSVITGPNCA CVPACDDQS
 851 PDAYSAYVLA SLAGEELQAV ESSPKFNPNV IGVPPYLNK LMYRTIHED
 901 PRVKTAFOI SMAKPRPNSA EESNGPIYAF ENLRACEAP PSAAHFREYQ
 951 IEGDRYDNT VPFNEDDPMs WTEDYLAMP KMEFRACYI KVKIVGPLEV
 1001 NVRSNNMGT HRTVKGKLYG IRDVRSTRDR DQPNVSACL EFKSGMLYD
 1051 QDRVDRLVK VIPQSCSRA SVNPMLEHYL VNHPLAVANN DTSEYTMCLAP
 1101 LDPLGHNYGI YTVYDODPRT AKELALGRCF DQTSDGSSRI MKNVGVALT
 1151 FNCVERQYGR QSAFOYLOST PAQSPAAGTY QGRVPSRROQ RASRGQROG
 1201 GVVASLREPR VAQOPLIN

11AA-SEQUENCE 1.0
 ID AAG62768 standard; peptide: 11 AA.

AC AAG62768;
 DT 17-SEP-2001 (first entry)
 DE Amino acid sequence of substance P.
 KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 11
 FT /note- "amidated residue"
 XX
 PN WO200153336-A1.
 XX
 XX 26-JUL-2001.
 PD
 XX 17-JAN-2001; 2001WO-US01529.
 PF
 XX 19-JAN-2000; 2000US-0489667.
 PR
 XX (ALIR) ALLERGAN SALES INC.
 PA
 XX Donovan S;
 PI
 DR WPI: 2001-451900/48.
 XX
 XX Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety
 XX
 XX Disclosure: Page 61; 77pp; English.
 PS
 XX The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin

CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents substance P, and is used in the course of the invention.
 XX
 SO Sequence 11 AA;

AAG62768 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRKPQO FFGIM

11AA-SEQUENCE 1.0
 ID AAG62769 standard; peptide: 12 AA.

AC AAG62769;
 DT 17-SEP-2001 (first entry)
 DE Amino acid sequence of substance P precursor.
 KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 OS Unidentified.
 XX
 XX WO200153336-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 17-JAN-2001; 2001WO-US01529.
 PE
 XX 19-JAN-2000; 2000US-0489667.
 PR
 XX (ALIR) ALLERGAN SALES INC.
 PA
 XX Donovan S;
 PI
 DR WPI: 2001-451900/48.
 XX
 XX Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety
 XX
 XX Disclosure: Page 62; 77pp; English.
 PS
 XX The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents substance P precursor, and is used in the course of the
 CC invention.
 XX
 SO Sequence 12 AA;

AAG62769 Length: 46 April 1, 2002 16:31 Type: P Check: 3988 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRKPQO FFGIMG

11AA-SEQUENCE 1.0
 ID AAG62770 standard; peptide: 13 AA.

AC AAG62770;
 DT 17-SEP-2001 (first entry)
 DE Amino acid sequence of substance P precursor.
 KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 OS Unidentified.
 XX
 XX WO200153336-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 17-JAN-2001; 2001WO-US01529.
 PE
 XX 19-JAN-2000; 2000US-0489667.
 PR
 XX (ALIR) ALLERGAN SALES INC.
 PA
 XX Donovan S;
 PI
 DR WPI: 2001-451900/48.
 XX
 XX Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety
 XX
 XX Disclosure: Page 63; 77pp; English.
 PS
 XX The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents substance P precursor, and is used in the course of the
 CC invention.

OS Unidentified.
 XX WO200153336-A1.
 PN 26-JUL-2001.
 XX 17-JAN-2001; 2001WO-US01529.
 XX 19-JAN-2000; 2000US-0489667.
 XX (ALLR) ALLERGAN SALES INC.
 XX Donovan S;
 XX WPI; 2001-451900/48.
 DR Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety -
 XX Disclosure; Page 62; 77pp; English.
 PS The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents substance P precursor, and is used in the course of the
 CC invention.
 CC
 SQ Sequence 13 AA;
 AAG62770 Length: 47 April 1, 2002 16:31 Type: P Check: 7513 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMGR

IIA_SEQUENCE 1.0
 ID AAG62771 standard; peptide: 14 AA.
 XX AAG62771;
 XX 17-SEP-2001 (first entry)
 DE Amino acid sequence of substance P precursor.
 XX Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 KM Unidentified.
 OS
 XX WO200153336-A1.
 PN 26-JUL-2001.
 XX 17-JAN-2001; 2001WO-US01529.
 XX 19-JAN-2000; 2000US-0489667.
 XX (ALLR) ALLERGAN SALES INC.
 PA Donovan S;
 XX WPI; 2001-451900/48.
 DR Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety -
 XX Disclosure; Page 63; 77pp; English.
 PS The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected

CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents substance P precursor, and is used in the course of the
 CC invention.
 CC
 SQ Sequence 14 AA;
 AAG62771 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMGR

IIA_SEQUENCE 1.0
 ID AAG62772 standard; peptide: 12 AA.
 XX AAG62772;
 XX 17-SEP-2001 (first entry)
 DE Amino acid sequence of carboxy-ester substance P precursor.
 XX Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 KW Synthetic.
 OS Key Location/Qualifiers
 XX Modified-site 12
 FT /note="methylated residue"
 FT
 XX WO200153336-A1.
 PN 26-JUL-2001.
 XX 17-JAN-2001; 2001WO-US01529.
 XX 19-JAN-2000; 2000US-0489667.
 XX (ALLR) ALLERGAN SALES INC.
 PA Donovan S;
 XX WPI; 2001-451900/48.
 DR Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety -
 XX Disclosure; Page 64; 77pp; English.
 PS The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents a substance P precursor, and is used in the course of the
 CC invention.
 CC
 SQ Sequence 12 AA;
 AAG62772 Length: 46 April 1, 2002 16:31 Type: P Check: 3988 ..

1 SQARNDBCQE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMGR

IIA_SEQUENCE 1.0
 ID AAG62773 standard; peptide: 13 AA.
 XX

AC AAG62773;
XX
PR 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of carboxy-ester substance P precursor.
XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 13
FT /note= "methylated residue"
XX
PN W0200153336-A1.
XX
PD 26-JUL-2001.
XX
PE 17-JAN-2001; 2001WO-US01529.
XX
PR 19-JAN-2000; 2000US-0489667.
XX
PA (ALLR) ALLERGAN SALES INC.
XX
PI Donovan S;
XX
DR WPI; 2001-451900/48.
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX
PS Disclosure; Page 65; 77pp; English.
XX
CC The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P precursor, and is used in the course of the
CC invention.
XX
SQ Sequence 13 AA:
AAG62773 Length: 47 April 1, 2002 16:31 Type: P Check: 7513 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVSOOT HERSRPPQO FFGIMGK
11AA_SEQUENCE 1.0
ID AAG62774 standard; peptide: 14 AA.
XX
AC AAG62774;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of carboxy-ester substance P precursor.
XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 14
FT /note= "methylated residue"
XX
PN W0200153336-A1.
XX
PD 26-JUL-2001.
XX
PE 17-JAN-2001; 2001WO-US01529.
XX
PR 19-JAN-2000; 2000US-0489667.
XX
PA (ALLR) ALLERGAN SALES INC.
XX
PI Donovan S;
XX
DR WPI; 2001-451900/48.
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX
PS Disclosure; Page 65; 77pp; English.
XX
CC The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P precursor, and is used in the course of the
CC invention.
XX
SQ Sequence 14 AA:
AAG62774 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVSOOT HERSRPPQO FFGIMGK
11AA_SEQUENCE 1.0
ID AAG62775 standard; peptide: 12 AA.
XX
AC AAG62775;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of carboxy-ester substance P precursor.
XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 12
FT /note= "ethylated residue"
XX
PN W0200153336-A1.
XX
PD 26-JUL-2001.
XX
PE 17-JAN-2001; 2001WO-US01529.
XX
PR 19-JAN-2000; 2000US-0489667.
XX
PA (ALLR) ALLERGAN SALES INC.
XX
PI Donovan S;
XX
DR WPI; 2001-451900/48.
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX
PS Disclosure; Page 67; 77pp; English.
XX
CC The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin

XX
PR 19-JAN-2000; 2000US-0489667.
XX
PA (ALLR) ALLERGAN SALES INC.
XX
PI Donovan S;
XX
DR WPI; 2001-451900/48.
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX
PS Disclosure; Page 66; 77pp; English.
XX
CC The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P precursor, and is used in the course of the
CC invention.
XX
SQ Sequence 14 AA:
AAG62774 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..
1 SQARNDBCQE ZGHSQILKMF PSTWVSOOT HERSRPPQO FFGIMGK
11AA_SEQUENCE 1.0
ID AAG62775 standard; peptide: 12 AA.
XX
AC AAG62775;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of carboxy-ester substance P precursor.
XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 12
FT /note= "ethylated residue"
XX
PN W0200153336-A1.
XX
PD 26-JUL-2001.
XX
PE 17-JAN-2001; 2001WO-US01529.
XX
PR 19-JAN-2000; 2000US-0489667.
XX
PA (ALLR) ALLERGAN SALES INC.
XX
PI Donovan S;
XX
DR WPI; 2001-451900/48.
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX
PS Disclosure; Page 67; 77pp; English.
XX
CC The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin

CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents a substance P precursor, and is used in the course of the
 CC invention.
 XX
 SQ Sequence 12 AA;

AAG62775 Length: 46 April 1, 2002 16:31 Type: P Check: 3988 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMG

IIAA_SEQUENCE 1.0

ID AAG62776 standard; peptide; 13 AA.

AC AAG62776;

DT 17-SEP-2001 (first entry)

XX Amino acid sequence of carboxy-ester substance P precursor.

KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 13 /note="ethylated residue"

XX WO200153336-A1.

PD 26-JUL-2001.

XX 17-JAN-2001; 2001WO-US01529.

PR 19-JAN-2000; 2000US-0489667.

XX (ALLR) ALLERGAN SALES INC.

PA (ALLR) ALLERGAN SALES INC.

PI Donovan S;

DR WPI; 2001-451900/48.

XX Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety -
 XX
 PS Disclosure; Page 68; 77pp; English.

CC The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents a substance P precursor, and is used in the course of the
 CC invention.
 CC
 XX
 SQ Sequence 13 AA;

AAG62776 Length: 47 April 1, 2002 16:31 Type: P Check: 7513 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMG

IIAA_SEQUENCE 1.0

ID AAG62777 standard; peptide; 14 AA.

AC AAG62777;

DT 17-SEP-2001 (first entry)

XX Amino acid sequence of carboxy-ester substance P precursor.
 DE Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 XX
 KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers

FT Modified-site 14 /note="ethylated residue"

XX WO200153336-A1.

PD 26-JUL-2001.

XX 17-JAN-2001; 2001WO-US01529.

PR 19-JAN-2000; 2000US-0489667.

XX (ALLR) ALLERGAN SALES INC.

PA (ALLR) ALLERGAN SALES INC.

PI Donovan S;

DR WPI; 2001-451900/48.

XX Agent useful for treating pain comprises a clostridial neurotoxin (or
 PT component) attached to a targeting moiety -
 XX
 PS Disclosure; Page 69; 77pp; English.

CC The specification describes an agent, comprising a clostridial neurotoxin
 CC attached to a targeting moiety, where the targeting moiety is selected
 CC from transmission compounds, and compounds substantially similar to the
 CC transmission compounds. The agent may be used for treating pain, where
 CC the clostridial neurotoxin component is derived from botulinum toxin
 CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
 CC The targeting moiety comprises a light chain and an amine end segment of
 CC a heavy chain and comprises Substance P as the targeting moiety. The pain
 CC alleviating effects persist for 2-6 months. The present sequence
 CC represents a substance P precursor, and is used in the course of the
 CC invention.
 CC
 XX
 SQ Sequence 14 AA;

AAG62777 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMGR

IIAA_SEQUENCE 1.0

ID AAG62780 standard; peptide; 9 AA.

AC AAG62780;

DT 17-SEP-2001 (first entry)

XX Amino acid sequence of a substance P fragment.

KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.

PI Unidentified.

XX WO200153336-A1.

PD 26-JUL-2001.

XX 17-JAN-2001; 2001WO-US01529.

PR 19-JAN-2000; 2000US-0489667.

XX (ALLR) ALLERGAN SALES INC.

PA (ALLR) ALLERGAN SALES INC.

PI Donovan S;

DR WPI: 2001-451900/48.
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety -
XX
PS Disclosure; Page 72; 77pp; English.
XX
CC The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P fragment, and is used in the course of the
CC invention.
XX
SQ Sequence 9 AA;

AG62780 Length: 43 April 1, 2002 16:31 Type: P Check: 3913 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPPQO FFG

IIAA_SEQUENCE 1.0
ID AAG99353 standard; Protein; 129 AA.
XX
AC AAG99353;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human atypical tachykinin protein fragment SEQ ID NO: 63.
XX
KW Atypical tachykinin; ART; human; hypertension.
XX
OS Homo sapiens.
XX
PN WO200146415-A1.
XX
PD 28-JUN-2001.
XX
PF 21-DEC-2000; 2000WO-JP09083.
XX
PR 21-DEC-1999; 99JP-0362638.
PR 10-MAR-2000; 2000JP-0066714.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Itoh Y, Nishi K, Kitada C, Inatomi N;
XX
DR WPI: 2001-441676/47.
XX
PS Example 14; Page 143; 153pp; Japanese.
XX
CC The present invention relates to atypical tachykinin proteins of human
CC origin and their esters, amides, salts and partial peptides. These can be
CC used in the treatment, prevention and diagnosis of hypertension. The
CC present sequence is a protein fragment described in the exemplification
CC of the invention.
XX
SQ Sequence 129 AA;

AAG99353 Length: 163 April 1, 2002 16:31 Type: P Check: 5532 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVSQOT HERSMKIIVA LAVFLVSTQ

51 IFAEITIGAND DLNYSWMYD SDOIKELEPE PREHLQRTA RRPKQOFG
101 IMGKIDADS IEKQVALLKA LYGHGOISHK RKTDSFVLG MKRALNSVA

151 YERSAMQNYE RRR

IIAA_SEQUENCE 1.0
ID AAG99354 standard; Peptide; 11 AA.
XX
AC AAG99354;
XX
DT 25-SEP-2001 (first entry)
XX
DE Substance P peptide.
XX
KW Atypical tachykinin; ART; human; hypertension.
XX
OS Unidentified.
XX
PN WO200146415-A1.
XX
PD 28-JUN-2001.
XX
PF 21-DEC-2000; 2000WO-JP09083.
XX
PR 21-DEC-1999; 99JP-0362638.
PR 10-MAR-2000; 2000JP-0066714.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Itoh Y, Nishi K, Kitada C, Inatomi N;
XX
DR WPI: 2001-441676/47.
XX
PT Atypical tachykinin peptides of human origin and DNA encoding them for
PT screening potential agents for treatment of hypertension -
XX
PS Disclosure; Page 9; 153pp; Japanese.
XX
CC The present invention relates to atypical tachykinin proteins of human
CC origin and their esters, amides, salts and partial peptides. These can be
CC used in the treatment, prevention and diagnosis of hypertension. The
CC present sequence is a protein fragment described in the exemplification
CC of the invention.
XX
SQ Sequence 11 AA;

AAG99354 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPPQO FFGIM

IIAA_SEQUENCE 1.0
ID AAB84527 standard; peptide; 11 AA.
XX
AC AAB84527;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of human substance P.
XX
KW Substance P; cell toxin; Pseudomonas exotoxin; cell ablation;
KW NK-1 receptor; chronic pain; tumour; neurological dysfunction;
KW basal ganglia; cholinergic interneuron; Parkinson's disease.
XX
OS Homo sapiens.
XX
PN WO200131020-A1.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US29064.
XX
PR 22-OCT-1999; 99US-0161159.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX

PI Fitzgerald DJ, Iadarola MJ;
 DR WPI; 2001-417560/44.
 XX
 PT Making cell toxin to treat chronic pain, by forming substance
 CC P-pseudomonas exotoxin disulfide-linked conjugate, by reacting modified
 PT exotoxin and substance P having additional cysteine residue at its
 CC N-terminus
 XX
 PS Disclosure; Page 10; 54pp; English.
 XX
 CC The present sequence represents a human substance P. The peptide is
 CC used to produce a cell toxin. The cell toxin comprises a substance
 CC P-pseudomonas exotoxin disulfide-linked conjugate. The cell toxin is
 CC useful for ablating NK-1 receptor expressing cells, such as dorsal horn
 CC cell, a stratum cell or a brain parenchyma cell, for treating chronic
 CC pain in epineurium cells, perineurium cells, nerve ganglia, nerve
 CC sheathes, nerve linings, meninges, pia mater cells, arachnoid membrane
 CC cells, duramembrane cells, cells lining a joint or brain or spinal cord
 CC parenchymal cells, without significantly affecting basal nociceptive
 CC responses. The cell toxin is thus useful for treating chronic pain or
 CC tumours that binds substance P. It is also useful for neurological
 CC dysfunctions of the basal ganglia by targeting cholinergic interneurons
 CC that express substance P e.g. Parkinson's disease.
 CC
 SQ Sequence 11 AA;

AAB84527 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRPOQ FFGIM

!1AA-SEQUENCE 1.0
 ID AAB84528 standard; peptide; 12 AA.
 XX
 AC AAB84528;
 XX
 DT 05-SEP-2001 (first entry)
 XX
 DE Amino acid sequence of a modified substance P.
 XX
 KW Substance P; cell toxin; Pseudomonas exotoxin; cell ablation;
 KW NK-1 receptor; chronic pain; tumour; neurological dysfunction;
 KW basal ganglia; cholinergic interneuron; Parkinson's disease.
 XX
 OS Homo sapiens.
 XX Synthetic.
 XX WO200131020-A1.
 XX
 PD 03-MAY-2001.
 XX
 PF 20-OCT-2000; 2000WO-US29064.
 XX
 PR 22-OCT-1999; 9905-0161159.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Fitzgerald DJ, Iadarola MJ;
 DR WPI; 2001-417560/44.
 XX
 PT Making cell toxin to treat chronic pain, by forming substance
 CC P-pseudomonas exotoxin disulfide-linked conjugate, by reacting modified
 PT exotoxin and substance P having additional cysteine residue at its
 CC N-terminus
 XX
 PS Example 1; Page 10; 54pp; English.
 XX
 CC The present sequence represents a modified substance P. The peptide is
 CC used to produce a cell toxin. The cell toxin comprises a substance
 CC P-pseudomonas exotoxin disulfide-linked conjugate. The cell toxin is
 CC useful for ablating NK-1 receptor expressing cells, such as dorsal horn
 CC cell, a stratum cell or a brain parenchyma cell, for treating chronic

CC pain in epineurium cells, perineurium cells, nerve ganglia, nerve
 CC sheathes, nerve linings, meninges, pia mater cells, arachnoid membrane
 CC cells, duramembrane cells, cells lining a joint or brain or spinal cord
 CC parenchymal cells, without significantly affecting basal nociceptive
 CC responses. The cell toxin is thus useful for treating chronic pain or
 CC tumours that binds substance P. It is also useful for neurological
 CC dysfunctions of the basal ganglia by targeting cholinergic interneurons
 CC that express substance P e.g. Parkinson's disease.
 CC
 SQ Sequence 12 AA;

AAB84528 Length: 46 April 1, 2002 16:31 Type: P Check: 3910 ..

1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRPOQ QFGIM

!1AA-SEQUENCE 1.0
 ID AAG89279 standard; Protein; 180 AA.
 XX
 AC AAG89279;
 XX
 DT 11-SEP-2001 (first entry)
 XX
 DE Human secreted protein, SEQ ID NO: 399.
 XX
 KW Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
 KW GENSET.
 XX
 OS Homo sapiens.
 XX
 PN WO200142451-A2.
 XX
 PD 14-JUN-2001.
 XX
 PF 07-DEC-2000; 2000WO-IB01938.
 XX
 PR 08-DEC-1999; 9905-0169629.
 XX
 PR 06-MAR-2000; 2000US-0187470.
 XX
 PA (GENSET) GENSET.
 XX
 PI Dumas Milne Edwards J, Bougueleret L, Jobert S;
 DR WPI; 2001-367870/38.
 DR N-PDB; AAH64882.
 XX
 PT Full length GENSET human nucleic acids encoding potentially secreted
 PT proteins, useful in gene therapy and vaccination against a variety of
 PT diseases, and for diagnosis of those diseases
 XX
 XX Claim 21; Page 882-883; 921pp; English.
 XX
 CC The invention relates to full length GENSET human nucleic acids encoding
 CC potentially secreted proteins. The nucleic acids and the polypeptides
 CC they encode may be used in the prevention, treatment and diagnosis of
 CC diseases associated with inappropriate GENSET gene expression. For
 CC example, they be used to treat disorders associated with decreased
 CC GENSET gene expression by rectifying mutations or deletions in a
 CC patient's genome that affect the activity of GENSET or by supplementing
 CC the patient's own production of GENSET polypeptides. Conversely,
 CC antisense nucleic acid molecules may be administered to down regulate
 CC GENSET expression by binding with the cells' own genes and preventing
 CC their expression. The sense and antisense nucleic acids may also be
 CC used as DNA probes in diagnostic assays to detect and quantitate the
 CC presence of similar nucleic acid sequences in samples, and hence to
 CC determine which patients may be in need of restorative therapy.
 CC The GENSET polypeptides may be used as antigens in the production of
 CC antibodies and in assays to identify modulators (agonists and
 CC antagonists) of GENSET polypeptide expression and activity. The
 CC present sequence is a GENSET polypeptide of the invention.
 XX
 SQ Sequence 180 AA;
 AAG89279 Length: 214 April 1, 2002 16:31 Type: P Check: 9228 ..

XX 03-MAY-2001.
PD
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NEMF-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX WPI; 2001-397593/42.
DR
XX
XX
PT New chimeric peptides used for treating pain comprise opioïd receptor
PT binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 15; 34pp; English.
XX
XX The present invention describes a number of chimeric peptides comprising
CC an opioïd receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioïd receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 12 AA;
0

AAB98867 Length: 46 April 1, 2002 16:31 Type: P Check: 3988 ..

1 SQARNDBC0E ZGHSQILKMF PSTWVSQOT HERSRPPQO FFGIMG

IIAA_SEQUENCE 1.0
ID AAB98868 standard; Peptide; 13 AA.
XX

AC AAB98868;

DT 14-AUG-2001 (first entry)

DE Chimeric analgesic peptide #24.

KW Opioïd receptor binding; nociceptive receptor binding; analgesic;

KM pain; chimeric peptide.

OS Synthetic.

FT Key Location/Qualifiers

FT Modified-site 13
/label= OTHER
/note= "C-terminal amide"

PN WO200130371-A2.

PD 03-MAY-2001.

XX 27-OCT-2000; 2000WO-US29789.

XX 28-OCT-1999; 99US-0428692.

PA (NEMF-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

XX WPI; 2001-397593/42.

PT New chimeric peptides used for treating pain comprise opioïd receptor

PT binding group and nociceptive receptor binding group

PS Claim 10; Page 15; 34pp; English.

CC The present invention describes a number of chimeric peptides comprising
CC an opioïd receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioïd receptor based peptides alone, tolerance does not result from

CC their long-term use. The present sequence is one of the peptides of the
CC invention.

SQ Sequence 13 AA;

AAB98868 Length: 47 April 1, 2002 16:31 Type: P Check: 7513 ..

1 SQARNDBC0E ZGHSQILKMF PSTWVSQOT HERSRPPQO FFGIMG

IIAA_SEQUENCE 1.0
ID AAB98869 standard; Peptide; 14 AA.
XX

AC AAB98869;

DT 14-AUG-2001 (first entry)

DE Chimeric analgesic peptide #25.

KW Opioïd receptor binding; nociceptive receptor binding; analgesic;

KM pain; chimeric peptide.

OS Synthetic.

FT Key Location/Qualifiers

FT Modified-site 14
/label= OTHER
/note= "C-terminal amide"

PN WO200130371-A2.

XX 03-MAY-2001.

XX 27-OCT-2000; 2000WO-US29789.

XX 28-OCT-1999; 99US-0428692.

PA (NEMF-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

XX WPI; 2001-397593/42.

PT New chimeric peptides used for treating pain comprise opioïd receptor

PT binding group and nociceptive receptor binding group

PS Claim 10; Page 15; 34pp; English.

CC The present invention describes a number of chimeric peptides comprising
CC an opioïd receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioïd receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.

SQ Sequence 14 AA;

AAB98869 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..

1 SQARNDBC0E ZGHSQILKMF PSTWVSQOT HERSRPPQO FFGIMGR

IIAA_SEQUENCE 1.0
ID AAB98870 standard; Peptide; 12 AA.
XX

AC AAB98870;

DT 14-AUG-2001 (first entry)

DE Chimeric analgesic peptide #26.

KW Opioïd receptor binding; nociceptive receptor binding; analgesic;

KM pain; chimeric peptide.
OS Synthetic.

XX Key Location/Qualifiers
FH Modified-site 12
FT /label= OTHER
FT /note= "modified by Ome"
XX
XX WO200130371-A2.
XX
XX 03-MAY-2001.
XX
XX
XX 27-OCT-2000; 2000WO-US29789.
XX
XX 28-OCT-1999; 99US-0428692.
XX
XX (NEMO-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX WPI; 2001-397593/42.
XX
XX
XX New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group
XX
XX Claim 10; Page 15; 34pp; English.
XX
XX
XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
XX Sequence 12 AA;

AAB98870 Length: 46 April 1, 2002 16:31 Type: P Check: 3988 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRKPQO FFGLMG

!!AA_SEQUENCE 1.0

ID AAB98871 standard; Peptide: 13 AA.

AC AAB98871;

DT 14-AUG-2001 (first entry)

DE Chimeric analgesic peptide #27.

KW Opioid receptor binding; nociceptive receptor binding; analgesic;
pain; chimeric peptide.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 13

FT /label= OTHER

FT /note= "modified by Ome"

XX WO200130371-A2.

XX 03-MAY-2001.

XX 27-OCT-2000; 2000WO-US29789.

XX 28-OCT-1999; 99US-0428692.

XX (NEMO-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

XX WPI; 2001-397593/42.

XX New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group

XX Claim 10; Page 15; 34pp; English.
PS
XX
XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
XX Sequence 13 AA;

AAB98871 Length: 47 April 1, 2002 16:31 Type: P Check: 7513 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRKPQO FFGLMG

!!AA_SEQUENCE 1.0

ID AAB98872 standard; Peptide: 14 AA.

AC AAB98872;

DT 14-AUG-2001 (first entry)

DE Chimeric analgesic peptide #28.

KW Opioid receptor binding; nociceptive receptor binding; analgesic;
pain; chimeric peptide.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 14

FT /label= OTHER

FT /note= "modified by Ome"

XX WO200130371-A2.

XX 03-MAY-2001.

XX 27-OCT-2000; 2000WO-US29789.

XX 28-OCT-1999; 99US-0428692.

XX (NEMO-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

XX Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

XX WPI; 2001-397593/42.

XX New chimeric peptides used for treating pain comprise opioid receptor
PT binding group and nociceptive receptor binding group

XX Claim 10; Page 15; 34pp; English.

XX The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
XX Sequence 14 AA;

SQ

AAB98872 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..

1 SQARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRKPQO FFGLMGR

!!AA_SEQUENCE 1.0

ID AAB98873 standard; Peptide: 12 AA.

AC AAB98873;

DT 14-AUG-2001 (first entry)

```

XX DE Chimeric analgesic peptide #29.
XX KM Opioid receptor binding; nociceptive receptor binding; analgesic;
XX KM pain; chimeric peptide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 12
XX FT /label= OTHER
XX FT /note= "modified by Oeth"
XX PN W0200130371-A2.
XX PD 03-MAY-2001.
XX PF 27-OCT-2000; 2000WO-US29789.
XX PR 28-OCT-1999; 99US-0428692.
XX PA (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX DR WPI; 2001-397593/42.
XX PT New chimeric peptides used for treating pain comprise opioid receptor
XX PT binding group and nociceptive receptor binding group
XX PS Claim 10; Page 15; 34pp; English.
XX CC The present invention describes a number of chimeric peptides comprising
XX CC an opioid receptor binding moiety and a nociceptive receptor binding
XX CC moiety. These can be used as analgesics for the treatment of pain. Unlike
XX CC opioid receptor based peptides alone, tolerance does not result from
XX CC their long-term use. The present sequence is one of the peptides of the
XX CC invention.
XX SQ Sequence 12 AA;
AAB98873 Length: 46 April 1, 2002 16:31 Type: P Check: 3988 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMG
!!AA_SEQUENCE 1.0
ID AAB98874 standard; Peptide; 13 AA.
XX AC AAB98874;
XX DT 14-AUG-2001 (first entry)
XX DE Chimeric analgesic peptide #30.
XX KM Opioid receptor binding; nociceptive receptor binding; analgesic;
XX KM pain; chimeric peptide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 13
XX FT /label= OTHER
XX FT /note= "modified by Oeth"
XX PN W0200130371-A2.
XX PD 03-MAY-2001.
XX PF 27-OCT-2000; 2000WO-US29789.
XX PR 28-OCT-1999; 99US-0428692.
XX PA (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

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XX PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX DR WPI; 2001-397593/42.
XX PT New chimeric peptides used for treating pain comprise opioid receptor
XX PT binding group and nociceptive receptor binding group
XX PS Claim 10; Page 15; 34pp; English.
XX CC The present invention describes a number of chimeric peptides comprising
XX CC an opioid receptor binding moiety and a nociceptive receptor binding
XX CC moiety. These can be used as analgesics for the treatment of pain. Unlike
XX CC opioid receptor based peptides alone, tolerance does not result from
XX CC their long-term use. The present sequence is one of the peptides of the
XX CC invention.
XX SQ Sequence 13 AA;
AAB98874 Length: 47 April 1, 2002 16:31 Type: P Check: 7513 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMG
!!AA_SEQUENCE 1.0
ID AAB98875 standard; Peptide; 14 AA.
XX AC AAB98875;
XX DT 14-AUG-2001 (first entry)
XX DE Chimeric analgesic peptide #31.
XX KM Opioid receptor binding; nociceptive receptor binding; analgesic;
XX KM pain; chimeric peptide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 14
XX FT /label= OTHER
XX FT /note= "modified by Oeth"
XX PN W0200130371-A2.
XX PD 03-MAY-2001.
XX PF 27-OCT-2000; 2000WO-US29789.
XX PR 28-OCT-1999; 99US-0428692.
XX PA (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX DR WPI; 2001-397593/42.
XX PT New chimeric peptides used for treating pain comprise opioid receptor
XX PT binding group and nociceptive receptor binding group
XX PS Claim 10; Page 15; 34pp; English.
XX CC The present invention describes a number of chimeric peptides comprising
XX CC an opioid receptor binding moiety and a nociceptive receptor binding
XX CC moiety. These can be used as analgesics for the treatment of pain. Unlike
XX CC opioid receptor based peptides alone, tolerance does not result from
XX CC their long-term use. The present sequence is one of the peptides of the
XX CC invention.
XX SQ Sequence 14 AA;
AAB98875 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFGIMGR

```

```

11AA_SEQUENCE 1.0
ID AAB98878 standard; Peptide; 9 AA.
XX
AC AAB98878;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #34.
XX
KM Opioid receptor binding; nociceptive receptor binding; analgesic;
XX pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 9 /label= OTHER
FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
DR WPI; 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
XX binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 15; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 9 AA;
AAB98878 Length: 43 April 1, 2002 16:31 Type: P Check: 3913
1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFG
11AA_SEQUENCE 1.0
ID AAB98879 standard; Peptide; 11 AA.
XX
AC AAB98879;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #35.
XX
KM Opioid receptor binding; nociceptive receptor binding; analgesic;
XX pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT MISC-difference 2 /note= "D-form residue"
FT MISC-difference 7 /note= "D-form residue"
FT MISC-difference 9 /note= "D-form residue"
FT MISC-difference 9 /note= "D-form residue"

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FT Modified-site 11
FT /label= OTHER
FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
DR WPI; 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
XX binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 15; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 11 AA;
AAB98879 Length: 45 April 1, 2002 16:31 Type: P Check: 1410
1 SQARNDBQOE ZGHSQILKMF PSTWVVSQOT HERSRPRQO FFWLM
11AA_SEQUENCE 1.0
ID AAB98880 standard; Peptide; 12 AA.
XX
AC AAB98880;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #36.
XX
KM Opioid receptor binding; nociceptive receptor binding; analgesic;
XX pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT MISC-difference 2 /note= "D-form residue"
FT MISC-difference 7 /note= "D-form residue"
FT MISC-difference 9 /note= "D-form residue"
FT MISC-difference 9 /note= "D-form residue"
FT Modified-site 12 /label= OTHER
FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

```


DR WPI; 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 15-16; 34pp: English.
XX
CC The present invention describes a number of chimeric peptides comprising
an opioid receptor binding moiety and a nociceptive receptor binding
moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
their long-term use. The present sequence is one of the peptides of the
invention.
XX
SQ Sequence 12 AA;
AAB98880 Length: 46 April 1, 2002 16:31 Type: P Check: 4676 ..
1 SQARNDBQOE ZGHSQILKMF PSTWVYSOOT HERSRPKPQO FFWLMG
!!AA_SEQUENCE 1.0
ID AAB98881 standard; Peptide: 11 AA.
XX
AC AAB98881;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #37.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Misc-difference 11 /note= "D-form residue"
FT Modified-site 11 /label= OTHER
FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NEMO-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
DR WPI; 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 16; 34pp: English.
XX
CC The present invention describes a number of chimeric peptides comprising
an opioid receptor binding moiety and a nociceptive receptor binding
moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
their long-term use. The present sequence is one of the peptides of the
invention.
XX
SQ Sequence 11 AA;

AAB98881 Length: 45 April 1, 2002 16:31 Type: P Check: 2107 ..
1 SQARNDBQOE ZGHSQILKMF PSTWVYSOOT HERSRPKPQO FFWLMG
!!AA_SEQUENCE 1.0
ID AAB98882 standard; Peptide: 12 AA.
XX
AC AAB98882;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #38.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
pain; chimeric peptide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Misc-difference 12 /note= "D-form residue"
FT Modified-site 12 /label= OTHER
FT /note= "C-terminal amide"
XX
PN WO200130371-A2.
XX
PD 03-MAY-2001.
XX
PF 27-OCT-2000; 2000WO-US29789.
XX
PR 28-OCT-1999; 99US-0428692.
XX
PA (NEMO-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;
XX
DR WPI; 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 16; 34pp: English.
XX
CC The present invention describes a number of chimeric peptides comprising
an opioid receptor binding moiety and a nociceptive receptor binding
moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
their long-term use. The present sequence is one of the peptides of the
invention.
XX
SQ Sequence 12 AA;
AAB98882 Length: 46 April 1, 2002 16:31 Type: P Check: 5373 ..
1 SQARNDBQOE ZGHSQILKMF PSTWVYSOOT HERSRPKPQO FFWLMG
!!AA_SEQUENCE 1.0
ID AAB82070 standard; peptide: 11 AA.
XX
AC AAB82070;
XX
DT 22-JUN-2001 (first entry)
XX
DE Substance P.
XX
KW Antigen; immunostimulant; vaccine; pharmaceutical composition; antiviral;
viral infection; substance P.

OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 11
FT /note= "C-terminal amide"
XX
PN WO200124822-A2.
XX
PD 12-APR-2001.
XX
XX 02-OCT-2000; 2000WO-EP09657.
XX
XX 01-OCT-1999; 99AT-0001680.
XX
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
XX
PI Flettman J, Maltner F, Buschle M, Melling J;
DR WPI; 2001-290577/30.
XX
PT New pharmaceutical composition comprising an antigen, an
PT immunostimulating substance and a polycationic polymer, useful in
PT manufacturing vaccines .
XX
XX Example 3; Page 14; 20pp; English.
XX
CC The present invention relates to a pharmaceutical composition comprising
CC (a) an antigen; (b) an immunostimulating substance consisting of
CC neuroactive compounds, hormones, compounds having growth hormone activity
CC or their mixtures; and (c) a polycationic polymer. The composition is
CC useful in manufacturing vaccines. To illustrate the present invention, a
CC murine tyrosinase related protein-2 peptide (TRP-2 peptide; see
CC AAB82064), was used. Mice were injected subcutaneously with either the
CC TRP-2 peptide, TRP-2 peptide + poly-L-arginine 60 (pR60) or TRP-2 peptide
CC + pR60 + substance P (the present peptide). Animals were sacrificed 10
CC days post injection, and spleen tissue was harvested. Lymphocytes were
CC prepared from the spleen tissue and were re-stimulated with TRP-2 peptide
CC or with an ovalbumin-derived peptide (AAB82065), with the same major
CC histocompatibility complex (MHC) restriction serving as negative control.
CC Spots representing single T cells specific for the peptide used for
CC re-stimulation were counted. No spots were detected when the ovalbumin
CC derived peptide was used, while TRP-2 peptide + pR60 + substance P showed
CC the highest number of spots or single T cells.
XX
XX Sequence 11 AA:
SQ
AAB82070 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLM
11AA_SEQUENCE 1.0
ID AAB91402 standard; Peptide: 11 AA.
XX
AC AAB91402;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:578.
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US13576.
XX
XX 17-MAY-1999; 99US-0134406.
PR

PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
DR WPI; 2001-112059/12.
XX
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
PS Disclosure: Page 389; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (II) and a
CC reactive group (III) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stable therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 11 AA:
SQ
AAB91402 Length: 45 April 1, 2002 16:31 Type: P Check: 981 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSRPPQO FFGLM
11AA_SEQUENCE 1.0
ID AAB91409 standard; Peptide: 11 AA.
XX
AC AAB91409;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:585.
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US13576.
XX
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
DR WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT

PT -
XX
PS Disclosure; Page 391; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;
AAB91409 Length: 45 April 1, 2002 16:31 Type: P Check: 1520 ..
1 SQARNDBQCE ZGHSQILKMF PSTWYVSQOT HERSRPRQO FYGLM
11AA_SEQUENCE 1.0
ID AAB91410 standard; Peptide: 10 AA.
XX
AC AAB91410;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:586.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure; Page 391; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 10 AA;
AAB91410 Length: 44 April 1, 2002 16:31 Type: P Check: 7516 ..
1 SQARNDBQCE ZGHSQILKMF PSTWYVSQOT HERSRPRQO FYGLM
11AA_SEQUENCE 1.0
ID AAB91411 standard; Peptide: 11 AA.
XX
AC AAB91411;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:587.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure; Page 392; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specifically as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX

SQ Sequence 11 AA;
AAB91411 Length: 45 April 1, 2002 16:31 Type: P Check: 765 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFWLM
!!AA_SEQUENCE 1.0
ID AAB91412 standard; Peptide: 11 AA.
XX AAB91412;
AC
XX
DT 22-JUN-2001 (first entry)
XX
XX Tachykinins peptide SEQ ID NO:588.
DE
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimideyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS Synthetic.
XX WO200069300-A2.
PN
XX
XX 23-NOV-2000.
PD
XX 17-MAY-2000; 2000WO-US13576.
PF
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
PI WPI: 2001-112059/12.
DR
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX Disclosure; Page 392; 733pp; English.
PS
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimideyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
CC
SQ Sequence 11 AA;
AAB91412 Length: 45 April 1, 2002 16:31 Type: P Check: 1410 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFWLM
!!AA_SEQUENCE 1.0
ID AAB91413 standard; Peptide: 11 AA.
XX AAB91413;
AC
XX

DT 22-JUN-2001 (first entry)
XX
XX Tachykinins peptide SEQ ID NO:589.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimideyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS Synthetic.
XX WO200069900-A2.
PN
XX
XX 23-NOV-2000.
PD
XX 17-MAY-2000; 2000WO-US13576.
PF
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
PI WPI: 2001-112059/12.
DR
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX Disclosure; Page 392; 733pp; English.
PS
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimideyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
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CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
CC
SQ Sequence 11 AA;
AAB91413 Length: 45 April 1, 2002 16:31 Type: P Check: 2107 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPQO FFWLM
!!AA_SEQUENCE 1.0
ID AAB91414 standard; Peptide: 11 AA.
XX AAB91414;
AC
XX
DT 22-JUN-2001 (first entry)
XX
XX Tachykinins peptide SEQ ID NO:590.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimideyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS Synthetic.
XX

PM WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 392; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;
XX
AAB91414 Length: 45 April 1, 2002 16:31 Type: P Check: 1633 ..
1 SQARNDBOE ZGHSQILKMF PSTWVYSQOT HERSRKPPO WFWLL
ID AAB91415 standard; Peptide: 11 AA.
XX
AC AAB91415;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:591.
XX
KW Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification: succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.

XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 393; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;
XX
AAB91415 Length: 45 April 1, 2002 16:31 Type: P Check: 1109 ..
1 SQARNDBOE ZGHSQILKMF PSTWVYSQOT HERSRKPPO FFWLL
ID AAB91422 standard; Peptide: 10 AA.
XX
AC AAB91422;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:598.
XX
KW Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification: succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 395; 733pp; English.
XX

CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 10 AA;

AAB91422 Length: 44 April 1, 2002 16:31 Type: P Check: 7516 ..

1 SQARNDBCE ZGHSQILKMF PSTWYSQOT HERSRPPQQ FFLM

!!AA_SEQUENCE 1.0
ID AAB91423 standard; Peptide; 10 AA.

AC AAB91423;

DT 22-JUN-2001 (first entry)

DE Tachykinins peptide SEQ ID NO:599.

KM Protection: endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimide; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

DR WPI: 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure: Page 395; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
XX comprising a therapeutically active amino acid region (III) and a
XX reactive group (II) (e.g. succinimide and maleimido groups) attached to
XX a less therapeutically active amino acid region (IV), which covalently
XX bonds with amino/hydroxyl/thiol groups on blood components to form a
XX peptide stabilised therapeutic peptide composed of 3-50 amino acids.
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX factors and neurotransmitters, to protect them from peptidase activity
XX in vivo for the treatment of various disorders. Endogenous therapeutic
XX peptides are not suitable as drug candidates as they require frequent
XX administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 10 AA;

AAB91423 Length: 44 April 1, 2002 16:31 Type: P Check: 7257 ..

1 SQARNDBCE ZGHSQILKMF PSTWYSQOT HERSRPPQQ FFLG

!!AA_SEQUENCE 1.0
ID AAB91427 standard; Peptide; 10 AA.

AC AAB91427;

DT 22-JUN-2001 (first entry)

DE Tachykinins peptide SEQ ID NO:603.

KM Protection: endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimide; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.

OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

DR WPI: 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure: Page 396; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
XX comprising a therapeutically active amino acid region (III) and a
XX reactive group (II) (e.g. succinimide and maleimido groups) attached to
XX a less therapeutically active amino acid region (IV), which covalently
XX bonds with amino/hydroxyl/thiol groups on blood components to form a
XX peptide stabilised therapeutic peptide composed of 3-50 amino acids.
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX factors and neurotransmitters, to protect them from peptidase activity
XX in vivo for the treatment of various disorders. Endogenous therapeutic
XX peptides are not suitable as drug candidates as they require frequent
XX administration due to rapid degradation by peptidases in the body.
XX Modifying and attaching therapeutic peptides to albumin prevents or
XX reduces the action of peptidases to increase length of activity (half
XX life) and specificity as bonding to large molecules decreases
XX intracellular uptake and interference with physiological processes.
XX AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention.

XX Sequence 10 AA;

AAB91427 Length: 44 April 1, 2002 16:31 Type: P Check: 7257 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPKPOQ FEGL
!!AA_SEQUENCE 1.0
ID AAB91429 standard; Peptide; 11 AA.
XX
AC AAB91429;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:605.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
OS Homo sapiens.
OS Synthetic.
XX WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
XX WPI: 2001-112059/12.
DR
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 397; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;
AAB91429 Length: 45 April 1, 2002 16:31 Type: P Check: 1109 ...
1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPKPOQ FFPLM
!!AA_SEQUENCE 1.0
ID AAB91432 standard; Peptide; 10 AA.
XX
AC AAB91432;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:608.
XX

KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
OS Homo sapiens.
OS Synthetic.
XX WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
XX WPI: 2001-112059/12.
DR
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 398; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 10 AA;
AAB91432 Length: 44 April 1, 2002 16:31 Type: P Check: 7516 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVYSQOT HERSRPPKPOQ FFPLM
!!AA_SEQUENCE 1.0
ID AAB91434 standard; Peptide; 11 AA.
XX
AC AAB91434;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:610.
XX
KM Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
OS Homo sapiens.
OS Synthetic.
XX WO200069900-A2.
XX
PD 23-NOV-2000.
XX

PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 398; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy) and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SO Sequence 11 AA:
AAB91434 Length: 45 April 1, 2002 16:31 Type: P Check: 2062 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPKPOQ WFWLL
11AA_SEQUENCE 1.0
ID AAB91436 standard; Peptide: 11 AA.
XX
AC AAB91436;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:612.
XX
KW Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.

XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 399; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy) and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SO Sequence 11 AA:
AAB91436 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SOARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPKPOQ FFGLM
11AA_SEQUENCE 1.0
ID AAB91438 standard; Peptide: 11 AA.
XX
AC AAB91438;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:614.
XX
KW Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 399; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy) and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX
SQ Sequence 11 AA;
AAB91438 Length: 45 April 1, 2002 16:31 Type: P Check: 385 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVYSOOT HERSRPPQO FFGILM
!!AA_SEQUENCE 1.0
ID AAB91440 standard; Peptide: 14 AA.
XX
AC AAB91440;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:616.
XX
KW Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 400; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX
SQ Sequence 14 AA;
AAB91440 Length: 48 April 1, 2002 16:31 Type: P Check: 1449 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVYSOOT HERSRPPQO FFGILGKR
!!AA_SEQUENCE 1.0
ID AAB91444 standard; Peptide: 9 AA.
XX
AC AAB91444;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:620.
XX
KW Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 401; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX
SQ Sequence 9 AA;
AAB91444 Length: 43 April 1, 2002 16:31 Type: P Check: 3913 ..
1 SQARNDBCOE ZGHSQILKMF PSTWVYSOOT HERSRPPQO FFG
!!AA_SEQUENCE 1.0
ID AAB91449 standard; Peptide: 11 AA.

XX AAB91449;
AC
XX
DT 22-JUN-2001 (first entry)
XX
XX Tachykinins peptide SEQ ID NO:625.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200069900-A2.
XX
XX 23-NOV-2000.
PD
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI
XX WPI: 2001-112059/12.
DR
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX
PS Disclosure: Page 403; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX
SQ Sequence 11 AA;
AAB91449 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SCARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPPQO FFGLM
!!AA_SEQUENCE 1.0
ID AAB91450 standard; Peptide; 11 AA.
XX
XX AAB91450;
AC
XX
XX 22-JUN-2001 (first entry)
DT
XX
XX Tachykinins peptide SEQ ID NO:626.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX

OS Homo sapiens.
OS Synthetic.
XX
XX
XX WO200069900-A2.
PN
XX
XX 23-NOV-2000.
PD
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI
XX WPI: 2001-112059/12.
DR
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX
PS Disclosure: Page 403; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX
SQ Sequence 11 AA;
AAB91450 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..
1 SCARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPPQO FFGLM
!!AA_SEQUENCE 1.0
ID AAB91451 standard; Peptide; 10 AA.
XX
XX AAB91451;
AC
XX
XX 22-JUN-2001 (first entry)
DT
XX
XX Tachykinins peptide SEQ ID NO:627.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX
XX Homo sapiens.
OS Synthetic.
PN WO200069900-A2.
XX
XX 23-NOV-2000.
PD
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR

CC (1) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX Sequence 24 AA;

AAB92031 Length: 58 April 1, 2002 16:31 Type: P Check: 344 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSGWTLS AGYLGPAPK

51 PQGMFWLL

11AA_SEQUENCE 1.0

ID AAB70690 standard; Protein: 175 AA.

XX AAB70690;

DT 17-MAY-2001 (first entry)

DE Human hDPP protein sequence SEQ ID NO:7.

XX Human; hDPP; diacylglycerol pyrophosphate phosphatase; DPP; detection.

XX Homo sapiens.

XX CN1271009-A.

XX 25-OCT-2000.

PD 17-MAR-2000; 200QCN-0114952.

PF 17-MAR-2000; 200QCN-0114952.

PR 17-MAR-2000; 200QCN-0114952.

XX (SREN-) SOUTHERN RES CENT NAT HUMAN GENE GROUP.

XX LI N, Xiao H, Liu F;

XX WPI: 2001-081384/10.

DR N-PSDB; AAF74766.

XX New human diacyl glycerophosphatase phosphatase protein and its code

XX sequence -

XX Claim 4; Page 17; 19pp; Chinese.

XX The present invention describes a human diacylglycerol pyrophosphate

XX phosphatase (DPP) designated hDPP. hDPP is expressed in normal tissue

XX near cancerous liver cells of a human body. Also described are methods

XX for the preparation and detection of hDPP nucleotide and protein

XX sequences. The present sequence represents human hDPP, as given in the

XX present invention.

XX Sequence 175 AA;

XX AAB70690 Length: 209 April 1, 2002 16:31 Type: P Check: 4219 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSGWTLS AGYLGPAPK

51 KPMFVIAFLS PLSLIFLAKF LKKADTRDSR QACLAASLAL ALNGVFTNTI

101 KLIV3PRPD PFYRCFPDOL AHSILMCTGD KDVVNIGRKS FPGHSSFAF

151 AGIAPASFLI AGKLHCFTIPQ GRGSMRCA FLSPILFAAY IALSTCDYK

201 HHMOGPFEKW

11AA_SEQUENCE 1.0
 ID AAB49755 standard; peptide: 11 AA.

XX AAB49755;

DT 17-APR-2001 (first entry)

DE Complex sugar bound peptide (SBP) amino acid sequence.

XX Sugar peptide complex; SBP; sugar bound peptide; enzymatically stable.

XX Synthetic.

PN JP2000319297-A.

XX 21-NOV-2000.

PD 30-MAR-1999; 99JP-0088030.

PF 30-MAR-1999; 99JP-0088030.

PR 30-MAR-1999; 99JP-0088030.

XX (NOCK) ZH NOGUCHI KENKUSHO.

PA WPI: 2001-184996/19.

DR 17-MAR-2000; 200QCN-0114952.

XX A process for preparation of enzymically stable sugar peptide complex

XX Example 2; Page 3; 4pp; Japanese.

XX This invention relates to a process for the preparation of an

XX enzymatically stable sugar peptide complex, and includes an in vivo

XX stable inhibitor of peptide:N-glycanase (EC. 3.5.1.57). The process can

XX be used for the investigation of in vivo reciprocal recognition of

XX cell-cell and substrate-receptor interaction, and their metabolism. The

XX present sequence represents a complex sugar bound peptide (SBP) amino

XX acid sequence prepared by the process of the invention.

XX Sequence 11 AA;

AB49755 Length: 45 April 1, 2002 16:31 Type: P Check: 736 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVVSQOT HERSKRPQO FFGIM

51 AAB65180;

DT 02-APR-2001 (first entry)

DE Human PRO1188 (UNQ602) protein sequence. SEQ ID NO:124.

XX Human; secreted and transmembrane protein; PRO; cytosolic;

XX cell death; cancer; chromosomal mapping; gene mapping; tissue typing;

XX diagnostic assay.

XX Homo sapiens.

XX WO200073454-A1.

PD 07-DEC-2000.

PF 30-MAR-2000; 2000WO-US08439.

PR 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 07-JUL-1999; 99US-0143048.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 17-AUG-1999; 99US-0149396.

PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 08-OCT-1999; 99US-0158663.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US05884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi CJ, Gurney AL, Kijavini IU, Napier MA, Pan J, Paoni NF,
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
 PI Zhang Z;
 XX
 XX WPI: 2001-032160/04.
 DR N-PsDB: AAF44131.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 72; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 CC
 XX Sequence 1184 AA;
 SO
 AAB65180 Length: 1218 April 1, 2002 16:31 Type: P Check: 668 ..
 1 SOARNDBCOE ZGHSQILKMF PSTWYVSQOT HERSMYGTKA WVFSLVLEV
 51 TSVLGRQTM TQSVRRVOPG KKNPSITFAK ADLLESPGEM TFWFNIDIPG
 101 GKGDERLDA IREYYGDRVC ARPLRLBART TDWTPAGSTG QVHGSPPRG
 151 FWCINREORP GONCSNYTVR FLCPPGSLRR DTERIWPMS PWSKCSAAG
 201 QTVGVQTRRI CLAEVSLCS EASEGQHCN GQCTACDLT CPMGOVNADC
 251 DACMCOEML HGAVSLPGA PASGAAYLL TKTPKLLTOT DSDGRRRIIG
 301 LCPDGKSLK ITRVAFAPIV LTMPTSLKA ATIKAEFVRA ETPVWVMPDE
 351 TARRAGQSV SLCCATGKRP RPDKYFWYHN DTLLDSLYK HSKVLRLKL
 401 OOHQAGEYFC KAQSDAGAVK SKVAQLIVTA SDETPCNPVP ESYLIRLPHD
 451 CFQNAINSPY YDVGRCPVKT CAGQDNGIR CRDAVONCCG ISKTEBERIO

501 CSGYTLPTKV AKESCQRCET ETRSIYGRV SAADNBPBK FGHVYMGNSR
 551 VSKTGYKGTG TLHVPODTER LVLTFFVRLQ KEVNTTKULP FNKKSAAVPH
 601 EIKMLRRKEP ITLEAMETNI IPGEVVGED PMAELEIPSR SEYRONGEPY
 651 ICKVKSATFE LDPNISTAT AAQTDLMFIN DEGDTPPLRT YGMFVDFRD
 701 EYTSPELNG KVKVHLDSQ VKPEHISTV KLSLNPDTG LMEEGDKF
 751 ENORNRKRED RTFLVGNLEI RERLFNLDV PESRRCFVAV RAYRSERLP
 801 SQIQGVVIS VINLEPTGF LSNPRAGRF DSVITGPNGA CVPACDDQS
 851 PDAYSATVLA SLAGELOAV ESSPKFPNA IGVOPYLAK LMYRTDHD
 901 PRVKTAFQI SMAKRPNSA EESNGPIYAF ENLRACEAP PSAHFRFYQ
 951 IEGDRDYNT VPFNEDDEMS WTEDEYLAWP KPEFRACI KYKIGPLEV
 1001 NVSRNMGT HRTYGLYIG IRDYSTRDR DQPNVSAAC EFKSGMLYD
 1051 QDRVDRTLVK VIPQSCRRRA SYNPLHEYL VNHLPVANN DTSEYTM LAP
 1101 LDPIGHNYGI YTYVDQDPRT AKELALGRF DQTSDDSSRI MKNNGVALT
 1151 FNCVERQVR QSAFOYLOST PAOSPAAGTV QGRVPSRRQO RASRGQROG
 1201 GVVASLRFPR VAQOPLIN
 11AA_SEQUENCE 1.0
 ID AAB50544 standard; peptide: 11 AA.
 XX
 AC AAB50544;
 XX
 DT 16-MAR-2001 (first entry)
 XX
 DE Prolyl endopeptidase inhibitor substance P peptide.
 XX
 KW Prolyl endopeptidase inhibitor; PEP inhibitor; central nervous system;
 KW CNS; nootropic; brain function disorder; Alzheimer's disease; amnesia.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 11
 FT /note="amidated"
 PN WO200071144-A1.
 XX
 PD 30-NOV-2000.
 XX
 PF 16-MAY-2000; 2000WO-JP03135.
 XX
 PR 19-MAY-1999; 99JP-0138791.
 XX
 PA (DOME-) DOME INC.
 XX
 PI Kayahara H, Tsukahara K, Inagaki T;
 XX
 DR WPI: 2001-070833/08.
 XX
 PT Prolyl endopeptidase inhibitor comprises cereal extract including new
 PT ketone compound.
 XX
 PS Disclosure; Fig 1; 27pp; Japanese.
 XX
 CC The present invention describes prolyl endopeptidase (PEP) inhibitors
 CC comprising a cereal extract. Also described are:
 CC (i) a 7-octadecenyl-7,10-henecosadienyl ketone;
 CC (ii) germinating brown rice having prolyl endopeptidase inhibitory
 CC activity for preventing and/or relieving brain function disorders; and

CC (11) foods for preventing or relieving brain function disorders
CC comprising the above PEP inhibitor or the above germinated brown rice.
CC The PEP inhibitors can have central nervous system (CNS) and nootropic
CC activity. The PEP inhibitors can be used for preventing and relieving
CC brain function disorders including Alzheimer's disease and amnesia.
CC The present sequence represents a PEP inhibitor peptide given in the
CC exemplification of the present invention.

SO Sequence 11 AA:

AAB50544 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPKPOQ FFGLM

11AA_SEQUENCE 1.0

ID AAB50306 standard; peptide; 11 AA.

AC AAB50306;

DT 08-MAR-2001 (first entry)

DE Substance P.

KW Antibacterial; Botulinum toxin inhibitor; Bttxb;
KW previn; tetanus neurotoxin; buforinin; substance P.

OS Unidentified.

PN WO200069891-A2.

PD 23-NOV-2000.

PF 15-MAY-2000; 2000WO-US13215.

PR 17-MAY-1999; 99US-0134446.

PA (USSA) US DEPT OF THE ARMY.

PI Gordon RK, Moorad DR, Doctor BP, Garcia GE;

DR WPI: 2001-025001/03.

PT Novel Previn compounds useful for inhibiting the protease activity of
PT Botulinum B and tetanus toxins -

PS Claim 7; Page 29; 47pp; English.

CC The present sequence was investigated in the search for Botulinum
CC toxin inhibitors (Bttxb). Previn compounds which inhibit the enzymatic
CC activity of Bttxb and tetanus neurotoxins were isolated. Previn
CC may be used to construct compounds such as buforinins.

SO Sequence 11 AA:

AAB50306 Length: 45 April 1, 2002 16:31 Type: P Check: 722 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRPKPOQ FFGLM

11AA_SEQUENCE 1.0

ID AAB56000 standard; Protein; 128 AA.

AC AAB56000;

DT 08-MAR-2001 (first entry)

DE Skin cell protein, SEQ ID NO: 316.

KW Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;
KW nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine;
KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KW inflammation; neurological disease.

OS Ratus sf.

XX WO200069884-A2.

PD 23-NOV-2000.

PF 15-MAY-2000; 2000WO-N200075.

PR 14-MAY-1999; 99US-0312283.

PA (GENE-) GENESIS RES & DEV CORP LTD.

PI Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;

DR WPI: 2001-007495/01.

DR N-PSDB; AAC99699.

PT New isolated polynucleotide used in the identification of genetic
PT disorders and encoding polypeptides used for treating inflammatory
PT disease, cancer and neurological diseases -

PS Claim 4; Page 252-253; 352pp; English.

CC The present sequence is a polypeptide which is expressed in
CC mammalian skin cells. The polypeptide is useful for stimulating
CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC tumours, modulating skin inflammation, stimulating the growth of
CC epithelial cells, inhibiting the binding of human immunodeficiency virus
CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
CC neurological diseases. The polynucleotide can be used as a marker, in
CC the identification of genetic disorders, and for the design of
CC oligonucleotides for examining expression patterns.

SO Sequence 128 AA:

AAB56000 Length: 162 April 1, 2002 16:31 Type: P Check: 24 ..

1 SOARNDBCOE ZGHSQILKMF PSTWVSQOT HERSRAEFGT SCGMCNALG

51 AELGVAVLLF VAFIATELLP PFQRIQPEE LMIYRNPYE AXYFTGPMF

101 VIAELTPLSL IFFAKELRKA DAIDSKOACL AASLALALNG VFTNIKLIV

151 GRPRPDEFYR GF

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FINDPATTERNS on pir: * allowing 0 mismatches
1 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) April 1, 2002

1 SPHUB ck: 9307 len: 129 i neurokinin 1 precursor, beta splice form [V
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK
58: QRIAR RPKPOQFF

1 SPRTB ck: 239 len: 130 i substance P beta precursor - rat
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK
58: QRIAR RPKPOQFF

1 SPBOB ck: 421 len: 130 i neurokinin 1 precursor, beta splice form [V
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK
58: QRIAR RPKPOQFF

1 SPRBG ck: 1957 len: 115 i substance P gamma precursor - rabbit
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK
58: QRIAR RPKPOQFF

1 SPRTA ck: 2164 len: 112 i substance P alpha precursor - rat
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK
58: QRIAR RPKPOQFF

1 SPID ck: 4974 len: 11 i substance P - horse
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK
1: RPKPOQFF

1 AG0654 ck: 4974 len: 11 i substance P - guinea pig
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK
1: RPKPOQFF

1 S20901 ck: 1434 len: 6,805 i titin - rabbit (fragment)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(F)
VMDGE
6,200: IPVIG RRPRTFM

1 JCL1409 ck: 3357 len: 471 i glutamate--ammonia ligase (EC 6.3.1.2) - Ca
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(H)P-P-P(F)(F)
LYYDC
459: KOLQL RHPYEFY

1 SA7038 ck: 219 len: 130 i tachykinin 1 precursor - golden hamster
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK
58: QRIAR RPKPOQFF

1 SA7038 ck: 844 len: 115 i tachykinin 1 precursor - golden hamster
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK
58: QRIAR RPKPOQFF

1 T52526 ck: 430 len: 130 i neurokinin 1 precursor - mouse
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK
58: QRIAR RPKPOQFF

1 I62742 ck: 3920 len: 72 i tachykinin A gamma chain precursor - mou
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK
23: QRIAR RPKPOQFF

1 S12958 ck: 7129 len: 97 i tachykinin delta precursor - rat
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK
58: QRIAR RPKPOQFF

1 JC2412 ck: 7417 len: 63 i tachykinin gamma chain precursor - rat
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK
11: QRIAR RPKPOQFF

1 JC5455 ck: 4081 len: 72 i preprotachykinin-A gamma precursor - bo
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
GLMGK
23: QRIAR RPKPOQFF

1 JND029 ck: 4995 len: 11 i substance P - chicken
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(F)
GLMGK
1: RRPPOQFF

1 T408339 ck: 5542 len: 236 i haloacid dehalogenase-like hydrolase - f
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(H)P-P-P(F)(F)
IALKM
148: PVGRG KHPDIME

1 T13857 ck: 425 len: 3,828 i trithorax protein - fruit fly (Drosophi
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(K)P-P-P(F)(F)
GLATL
618: SDANG KPKKNYF

1 E862849 ck: 4011 len: 290 i hypothetical protein AAD39637.1 [Importe
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(F)
RCFPD
123: KDAVG RRPDPFW

1 E84421 ck: 2420 len: 302 i probable phosphatidic acid phosphatase (

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!!AA_SEQUENCE 1.0
 P1:SPHUB - neurokinin 1 precursor, beta splice form [validated] - human
 N:Alternate names: neurokinin A; neurokinin alpha; neuromedin L; neuropeptide K; preprotachykinin; substance K; substance P; tachykinin A
 N:Contains: neurokinin 1; neurokinin 1 precursor; alpha splice form; neurokinin 1 precursor, delta splice form; neurokinin 1 precursor, gamma splice form; neurokinin 2
 C:Species: Homo sapiens (man)
 C:Date: 12-Feb-1988 #sequence revision 26-May-1995 #text change 19-May-2000
 C:Accession: A24805; A60425; S00069; S03033; JC5451; JC5450; A59269; A59270; B59270; I62740; I84611
 R:Hamman, A.J.; Armstrong, A.; Pascall, J.C.; Chapman, K.; Rosie, R.; Curtis, A.; Goings, J.; Edwards, C.R.W.; Fink, G.
 FEBS Lett. 208, 67-72, 1986
 A:Title: cDNA sequence of human beta-preprotachykinin, the common precursor to substance P and neurokinin A
 A:Reference number: A24805; MUID:87030957
 A:Accession: A24805
 A:Molecule type: mRNA
 A:Residues: 1-129 <HAR>
 A:Cross-references: GB:M28109; EMBL:X54469; NID:929482; PIDN:CAA38351.1; PID:929483
 R:McGregor, G.P.; Conlon, J.M.
 Peptide 11, 907-910, 1990
 A:Title: Characterization of the C-terminal flanking peptide of human beta-preprotachykinin
 A:Reference number: A60425; MUID:91133994
 A:Accession: A60425
 A:Molecule type: protein
 A:Residues: 111-126 <MCG>
 A:Experimental source: neuroendocrine tumor of adrenal medulla
 R:Theodorsson-Morheim, E.; Joernvall, H.; Andersson, M.; Norheim, I.; Oberg, K.; Jacobsson, G.
 Eur. J. Biochem. 166, 693-697, 1987
 A:Title: Isolation and characterization of neurokinin A, neurokinin A(3-10) and neurokinin A(4-10) from a neutral water extract of a metastatic ileal carcinoid tumor
 A:Reference number: S00069; MUID:87275962
 A:Accession: S00069
 A:Molecule type: protein
 A:Residues: 98-107 <THE>
 R:Kage, R.; Thim, L.; Greutefeldt, W.; Conlon, J.M.
 Biochem. J. 253, 203-207, 1988
 A:Title: Post-translational processing of preprotachykinins. Isolation of preprotachykinin-(1-37)-peptide from human adrenal-medullary pheochromocytoma tissue
 A:Reference number: S03033; MUID:88339887
 A:Accession: S03033
 A:Molecule type: protein
 A:Residues: 20-30 <KAG>
 R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Iwell, R.
 Endocrinology 128, 2441-2448, 1991
 A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human and mouse testis
 A:Reference number: JC5450; MUID:91209287
 A:Accession: JC5451
 A:Status: translation not shown; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 36-73, 89-122 <CHI1>
 A:Cross-references: GB:M68907; NID:9190292; PIDN:AAA60160.1; PID:9553619
 A:Accession: JC5450
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 36-86, 'P', 88-122 <CHI2>
 R:Tan, A.; Too, H.P.
 submitted to GenBank, October 1995
 A:Reference number: A59269
 A:Accession: A59269
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-129 <TAN>
 A:Cross-references: GB:U37529; NID:91017792; PIDN:AAA79195.1; PID:91017793

A:Experimental source: tissue brain cortex
 R:Lai, J.P.; Douglas, S.D.; Rappaport, E.; Wu, J.M.; Ho, W.Z.
 submitted to GenBank, February 1998
 A:Description: Identification of a delta isoform of preprotachykinin mRNA in human mononuclear phagocytes and lymphocytes
 A:Reference number: A59270
 A:Accession: A59270
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 36-96, 'W', 116-118 <LAI1>
 A:Cross-references: GB:AF050656; NID:93098594; PIDN:AAC15702.1; PID:93098595
 A:Experimental source: alpha splice form; tissue blood; tissue brain; cell type monocytes/macrophages; cell type lymphocytes
 A:Accession: B59270
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 36-73, 89-96, 'W', 116-122 <LAI2>
 A:Cross-references: GB:AF050658; NID:93098598; PIDN:AAC15704.1; PID:93098599
 A:Experimental source: delta splice form; tissue blood; tissue brain; cell type monocytes/macrophages; cell type lymphocytes
 C:Comment: This protein is processed to produce the tachykinin peptide hormones neurokinin 1 (substance P) a paracrine factor, and neurokinin 2 (neurokinin A, neurokinin alpha, neuromedin L or substance K).
 C:Genetics:
 A:Gene: GDB:TAC1; TAC2; NKNA; PPT-A
 A:Cross-references: GDB:119452; OMIM:162320
 A:Map position: 7q21-q22
 C:Superfamily: substance P precursor
 C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin
 F:1-129/Product: neurokinin 1 precursor, beta splice form #status predicted <SPB>
 F:1-96, 'W', 116-118/Product: neurokinin 1 precursor, alpha splice form #status predicted <SPA>
 F:1-73, 89-129/Product: neurokinin 1 precursor, gamma splice form #status predicted <SPG>
 F:1-73, 89-96, 'W', 116-122/Product: neurokinin 1 precursor, alpha splice form #status predicted <SPD>
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
 F:58-68/Product: neurokinin 1 #status experimental <NK1>
 F:72-107/Product: neuropeptide K #status predicted <NEK>
 F:98-107/Product: neurokinin 2 #status experimental <NK2>
 F:101-107/Product: neurokinin 2(3-10) #status experimental <NK23>
 F:101-107/Product: neurokinin 2(4-10) #status experimental <NK24>
 F:111-126/Domain: carboxyl-terminal propeptide #status experimental <CTP>
 F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycine) #status experimental
 F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycine) #status experimental
 SPHUB Length: 129 April 1, 2002 16:31 Type: P Check: 9307 ..
 1 MKILVALAV FLYSTOLFAL EIGANDDLNY WSDWYDSQI KEELPEPFEH
 51 LIQRIARRPK PQPFGLMGK RDADSSIEKQ VALLKALYGH GQSHRHKHT
 101 DSFVGLMGKR ALNSVAYERS AMQNYERRR
 !!AA_SEQUENCE 1.0
 P1:SPHUB - substance P beta precursor - rat
 N:Alternate names: preprotachykinin beta; preprotachykinin gamma; substance K
 N:Contains: neurokinin A; substance P; substance P gamma precursor
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1988 #sequence revision 26-May-1995 #text change 18-Jun-1999
 C:Accession: A37163; A26590; C26590; A25067; JC2411
 R:Carter, M.S.; Krause, J.E.
 J. Neurosci. 10, 2203-2214, 1990
 A:Title: Structure, expression, and some regulatory mechanisms of the rat preprotachykinin gene encoding substance P, neurokinin A, neuropeptide K, and neuropeptide gamma
 A:Reference number: A37163; MUID:90331040
 A:Accession: A37163

A:Molecule type: DNA
 A:Residues: 1-130 <CAR>
 A:Cross-references: GB:M34159; GB:M34160; GB:M34162; NID:g206334;
 PIDN:AAA1926.1; PID:g206336; GB:M34163
 R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Hershey, A.D.
 Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987
 A:Title: Three rat preprotachykinin mRNAs encode the neuropeptides substance P and neurokinin A.
 A:Reference number: A94187; MUID:87118268
 A:Accession: A26590
 A:Molecule type: mRNA
 A:Residues: 1-130 <RA>
 A:Cross-references: GB:M15191; NID:g206341; PIDN:AAA1928.1; PID:g206342;
 GB:M35277
 A:Accession: C26590
 A:Molecule type: mRNA
 A:Residues: 1-73,89-130 <KR2>
 A:Cross-references: GB:M34183; NID:g206343; PIDN:AAA1929.1; PID:g206344
 R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
 Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
 A:Title: Sequence analysis of cloned cDNA for rat substance P precursor:
 existence of a third substance P precursor.
 A:Reference number: A25067; MUID:87025808
 A:Accession: A25067
 A:Molecule type: mRNA
 A:Residues: 1-73,89-130 <KAW>
 A:Cross-references: GB:M14312; NID:g206339; PIDN:AAA1927.1; PID:g206340
 R:Khan, I.; Collins, S.M.
 Biochem. Biophys. Res. Commun. 202, 796-802, 1994
 A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for
 substance P in the rat intestine.
 A:Reference number: JC2411; MUID:94324969
 A:Accession: JC2411
 A:Molecule type: mRNA
 A:Residues: 48-110 <KHA>
 A:Experimental source: Intestine
 C:Comment: Alternative splicing of the mRNA for substance P precursor yields
 the beta and gamma forms, presented in this entry, and the alpha form presented
 in SPRTA (Bx6590).
 C:Comment: The beta and gamma forms are processed to yield substance P and
 neurokinin A (substance K).
 C:Genetics: 41/3; 74/1; 89/1; 97/1; 115/1
 A:Introns: 41/3; 74/1; 89/1; 97/1; 115/1
 C:Superfamily: substance P precursor
 C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide;
 tachykinin
 F:1-130/Product: substance P beta precursor #status predicted <PREB>
 F:1-73,89-130/Product: substance P gamma precursor #status predicted <PREG>
 F:1-13/Domain: signal sequence #status predicted <SIG>
 F:58-68/Product: substance P #status predicted <SBP>
 F:98-107/Product: neurokinin A #status predicted <NKA>
 F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from
 following glycine) #status predicted
 F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from
 following glycine) #status predicted

SPRTB Length: 130 April 1, 2002 16:31 Type: P Check: 239 ..

1 MKLIVAVAF FLVSTQLFAE EIGANDDLN WSDMSDDQI KEAMPEFEH

51 LLIQRIARRR PQQFGLMGK RDADSSIEKQ VALIKALYGH GQISHRHKHT

101 DSFVGLMGKR ALNSVAYERS AMONERRRR

11AA_SEQUENCE 1.0

PI-SPDB - neurokinin 1 precursor, beta splice form [validated] - bovine

N:Alternate names: neurokinin A; preprotachykinin; substance K; substance P

N:Contains: neurokinin 1; neurokinin 1 precursor, alpha splice form; neurokinin

1 precursor, gamma splice form; neurokinin 2

C:Species: Bos primigenius taurus (cattle)

C>Date: 19-Feb-1984 #sequence, revision 19-Feb-1984 #text, change 16-Jun-2000

C:Accession: A05093; A01557; B25067; A61460; JC3454; I45966

R:Nawa, H.; Kotani, H.; Nakanishi, S.

Nature 312, 729-734, 1984

A:Title: Tissue-specific generation of two preprotachykinin mRNAs from one gene
 by alternative RNA splicing.
 A:Reference number: A05093; MUID:85086245
 A:Accession: A05093
 A:Molecule type: DNA
 A:Residues: 1-130 <NAM1>
 A:Cross-references: GB:X02351; GB:M14786; NID:g655; PIDN:CAA26206.1;
 PID:g1197197
 R:Nawa, H.; Hirose, T.; Takashima, H.; Inayama, S.; Nakanishi, S.
 Nature 306, 32-36, 1983
 A:Title: Nucleotide sequences of cloned cDNAs for two types of bovine brain
 substance P precursor.
 A:Reference number: A93118; MUID:84039802
 A:Accession: A01559
 A:Molecule type: mRNA
 A:Residues: 1-130 <NAM2>
 A:Cross-references: GB:X00075; NID:g758; PIDN:CAA24939.1; PID:g759
 A:Accession: A01557
 A:Molecule type: mRNA
 A:Residues: 1-96, 'M', 116-130 <NAM3>
 A:Cross-references: GB:X00076; NID:g762; PIDN:CAA24942.1; PID:g763
 R:Kawaguchi, Y.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.
 Biochem. Biophys. Res. Commun. 139, 1040-1046, 1986
 A:Title: Sequence analysis of cloned cDNA for rat substance P precursor:
 existence of a third substance P precursor.
 A:Reference number: A25067; MUID:87025808
 A:Accession: B25067
 A:Molecule type: mRNA
 A:Residues: 1-73,89-130 <KAW>
 R:McGregor, G.P.; Kage, R.; Tilm, L.; Conlon, J.M.
 J. Neurochem. 53, 1871-1877, 1989
 A:Title: Quantitation and characterization of peptides from the C-terminal
 flanking region of rat and bovine preprotachykinins.
 A:Reference number: A61460; MUID:90039314
 A:Accession: A61460
 A:Molecule type: protein
 A:Residues: 111-126 <MCG>
 A:Experimental source: corpus striatum
 R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
 Endocrinology 128, 2441-2448, 1991
 A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human
 and mouse testis.
 A:Reference number: JC5450; MUID:91209287
 A:Accession: JC5454
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 36-120, 'A', 122 <CHI>
 A:Cross-references: GB:M68911; NID:g163591; PIDN:AAA30724.1; PID:g552335
 C:Comment: The protein is processed to produce neurokinin 1 (substance P) and
 neurokinin 2 (neurokinin A or substance K).
 C:Genetics:
 A:Gene: PPT-A
 A:Introns: 41/3; 74/1; 89/1; 97/1; 115/1
 C:Superfamily: substance P precursor
 C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide;
 tachykinin
 F:1-130/Product: neurokinin 1 precursor, beta splice form #status predicted
 F:1-96, 'M', 116-130/Product: neurokinin 1 precursor, alpha splice form #status
 predicted <SPA>
 F:1-73,89-130/Product: neurokinin 1 precursor, gamma splice form #status
 predicted <SPG>
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
 F:58-66/Product: neurokinin 1 #status experimental <SBP>
 F:98-107/Product: neurokinin 2 #status predicted <NKA>
 F:111-126/Domain: carboxyl-terminal propeptide #status experimental <CTP>
 F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from
 following glycine) #status experimental
 F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from
 following glycine) #status predicted

SPROB Length: 130 April 1, 2002 16:31 Type: P Check: 421 ..

1 MKILVAVAVI FFIISTOLSAE EIGANDDFNY WSDWSDSDQI KEEMPEPEH

51 LLQRIARRPK PQOFFGLMGK RDADSTIEKO VALLKALYGH GOLSHKHKHT

101 DSFVGLMGKR ALNSVAVERS VMODYERRRR

!!AA_SEQUENCE 1.0

PI:SPRBS - substance P gamma precursor - rabbit

N:Alternate names: gamma-neuropeptide K; gamma-preprotachykinin I precursor; tachykinin I precursor

N:Contains: neuropeptide K; substance P

C:Species: *Oryctolagus cuniculus* (domestic rabbit)

C>Date: 10-Nov-1992 #sequence_revision 26-May-1995 #text_change 18-Jun-1999

C:Accession: JN0709; A60302; A60200; S18922

R:Megeert, H.J.; Heiland, A.; Rose, M.; Fotsmann, W.G.

Biochem. Biophys. Res. Commun. 195, 128-131, 1993

A:Title: Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.

A:Reference number: JN0709; MUID:93371392

A:Accession: JN0709

A:Molecule type: mRNA

A:Residues: 1-115 <MA2>

A:Cross-references: EMBL:X62994; NID:91565; PIDN:CAAA44728.1; PID:91566

R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.

Regul. Pept. 18, 346, 1987

A:Title: gamma-Neuropeptide K: a peptide isolated from rabbit gut that is derived from gamma-preprotachykinin.

A:Reference number: A60302

A:Accession: A60302

A:Molecule type: protein

A:Residues: 72-92 <KAG>

R:Kage, R.; McGregor, G.P.; Thim, L.; Conlon, J.M.

J. Neurochem. 50, 1412-1417, 1988

A:Title: Neuropeptide-gamma: a peptide isolated from rabbit intestine that is derived from gamma-preprotachykinin.

A:Reference number: A60200; MUID:88199570

A:Accession: A60200

A:Molecule type: protein

A:Residues: 72-92 <KA2>

C:Comment: The gamma alternatively spliced form is processed to yield substance P and neuropeptide A.

C:Superfamily: substance P precursor

C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin

F:1-15/Domain: signal sequence #status predicted <SIG>

F:38-68/Product: substance P #status predicted <SBP>

F:72-92/Product: gamma-neuropeptide K #status experimental <NPK>

F:83-92/Product: neuropeptide A #status predicted <NKA>

F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycine) #status predicted

F:92/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycine) #status experimental

SPRBS Length: 115 April 1, 2002 16:31 Type: P Check: 1957 ..

1 MKILVALAVL ALVSTQLFAE DIRANDLNY WSDWSDSDQI KEELPEPEH

51 LLQRIARRPK PQOFFGLMGK RDAGHGOISH KRHKTDSEVG LMGRALNSV

101 AYERSAMONY ERRRR

!!AA_SEQUENCE 1.0

PI:SPRRA - substance P alpha precursor - rat

N:Alternate names: preprotachykinin alpha

N:Contains: substance P

C:Species: *Rattus norvegicus* (Norway rat)

C>Date: 30-Jun-1988 #sequence_revision 26-May-1995 #text_change 18-Jun-1999

C:Accession: B26590

R:Krause, J.E.; Chirgwin, J.M.; Carter, M.S.; Xu, Z.S.; Hershey, A.D.

Proc. Natl. Acad. Sci. U.S.A. 84, 881-885, 1987

A:Title: Three rat preprotachykinin mRNAs encode the neuropeptides substance P and neuropeptide A.

A:Reference number: A94187; MUID:87118268

A:Accession: B26590

A:Molecule type: mRNA

A:Residues: 1-112 <KRA>

A:Cross-references: GB:M3184; NID:9206329; PIDN:AAA41925.1; PID:9206330

C:Comment: Alternative splicing of the mRNA for substance P precursor yields the alpha form, presented in this entry, and the beta and gamma forms presented in SPRBA (A26590).

C:Comment: The alpha form is processed to yield substance P.

C:Superfamily: substance P precursor

C:Keywords: alternative splicing; amidated carboxyl end; hormone; neuropeptide; tachykinin

F:1-112/Product: substance P alpha precursor #status predicted <PREA>

F:1-15/Domain: signal sequence #status predicted <SIG>

F:58-68/Product: substance P #status predicted <SBP>

F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from following glycine) #status predicted

SPRRA Length: 112 April 1, 2002 16:31 Type: P Check: 2164 ..

1 MKILVAVAVI FLVSTQLFAE EIGANDLNY WSDWSDSDQI KEEMPEPEH

51 LLQRIARRPK PQOFFGLMGK RDADSTIEKO VALLKALYGH GOISHKMAVE

101 RSAMONYERR RK

!!AA_SEQUENCE 1.0

PI:SEHO P substance P - horse

C:Species: *Equus caballus* (domestic horse)

C>Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996

C:Accession: A01558

R:Studer, R.O.; Tizack, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A:Title: Isolierung und Aminosäuresequenz von Substanz P aus Pferdedarm.

A:Reference number: A01558

A:Accession: A01558

A:Molecule type: protein

A:Residues: 1-11 <STU>

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; hormone

F:11/Modified site: amidated carboxyl end (Met) #status experimental

SEHO Length: 11 April 1, 2002 16:31 Type: P Check: 4974 ..

1 RKRPQOFFGL M

!!AA_SEQUENCE 1.0

PI:A60654 - substance P - guinea pig

C:Species: *Cavia porcellus* (guinea pig)

C>Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995

C:Accession: A60654

R:Murphy, R.

Neuropeptides 14, 105-110, 1989

A:Title: Primary amino acid sequence of guinea-pig substance P.

A:Reference number: A60654; MUID:90044685

A:Accession: A60654

A:Molecule type: protein

A:Residues: 1-11 <MPR>

C:Superfamily: substance P precursor

C:Keywords: amidated carboxyl end; neuropeptide; tachykinin

F:11/Modified site: amidated carboxyl end (Met) #status experimental

A60654 Length: 11 April 1, 2002 16:31 Type: P Check: 4974 ..

1 RKRPQOFFGL M

!!AA_SEQUENCE 1.0

PI:IS20901 - ttfm - rabbit (fragment)

C:Species: *Oryctolagus cuniculus* (domestic rabbit)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999

C:Accession: S20901; I46520

R:Labell, S.; Gautel, M.; Lakey, A.; Trinick, J.

EMBO J. 11, 1711-1716, 1992

A:Title: Towards a molecular understanding of titin.
A:Reference number: S20897; MUID:92258380
A:Accession: S20901
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-6805 <LAB>
A:Cross-references: EMBL:X64696
A:Note: the nucleotide sequence was submitted to the EMBL Data Library,
February 1992
R:Label: S.; Barlow, D.P.; Gautel, M.; Gibson, T.; Holt, J.; Hsieh, C.L.;
Francke, U.; Leonard, K.; Wardale, J.; Whiting, A.; Trinick, J.
Nature 345, 273-276, 1990
A:Title: A regular pattern of two types of 100-residue motif in the sequence of
titin.
A:Reference number: 146520; MUID:90238553
A:Accession: 146520
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 4235-5250 <LA2>
A:Cross-references: EMBL:X17329; NID:q1756; PIDN:CAA35207.1; PID:930251
C:Superfamily: titin; fibronectin type III repeat homology; immunoglobulin
homology; protein kinase homology
C:Keywords: muscle

S20901 Length: 6805 April 1, 2002 16:31 Type: P Check: 1434 ..

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1  RRLKSTDM RVHKSICKET HYLVDKCVEN QIEFVQTK NEGESDVK
51  TEEVYVKEKL OKPVLDLKL GVLTVKAGET IRLEAGVRGK PPEVYVWKD
101  KDAIDETRSP RAKIDTSADS SKFSLTKRKR SDGKYVYVTA TWTAGSFVAY
151  ATYVNLDKPG PVRLNKIPDV SSDRCTIRWD PREDGGCEI QVYLIEKCS
201  KKKWMTYSA TVLTPTGTVT RLIGNEYIF RYAKENKIGT GPPTSKPVI
251  AKTKYDRGR PDPEVTVKS KEEMTVVWSP PEYDGGKSIT GYLLEKEKH
301  SVRWVYVNS AIPERLKVQ NLIPGHEYOF RYKAENDIGV GEPSPSRPV
351  VAKDPIEPFG PPINKAVDT TKSSITLSWG KPYVDGAPL IGYVVEVRK
401  IADASPEEGM KRCNAAQOLV RTEFTVSLD ENQVEFRVC AQNOVGIGRP
451  AELKEAIKPK ELIPEPEIDL DASMRLVVY RAGCPTRLFA IYRGPRPVY
501  TTRKVGIDNV VRKGVLDVLD TMAFLVLPNS TRDDSGKYSL TLVNAGEKA
551  VEVNVRVLDT PGVSDLKVS DVTKTSCHVS WAPENDGGS QVTHYIVERR
601  DAEIKTWISIV NPEVKTSCQ VTNLVPGNEY YFRVTVANEX GPGVPADVPK
651  PVLASDGLSE PDPPKKEVLT EMTKNSATLA WLPELDDGA KIDGYIISTR
701  EEDQPADRWY EYSVVKDSL VITGLKEGKK YKFRVAARNA VGSVLPREAE
751  GYVFAKEQOLI PKILMPEQI TIKAGKKLR EAHVYGRPOP ICKMKKGEDD
801  VVTISHLAVH KAESSILITI KDVTTRKDSGY YSLTAENSSG TDTQIKIYIV
851  MDRPGPPPP FDISDIDADA CSLSMHIPLE DGGSNTINYI VEKCDVSRCD
901  WYTLALASVTK TSCRIGKLIIP GQEVFVRVA ENRFGISEPL QSPKMLAOP
951  FGVISEPKNA RVTKVNDCCI FVANDRPDSD GGSPTGYLI ERKGRNSLWM
1001  VRANDTAVNS TEYPCAGLVE GLEYSFRIYA LNKAGSSPPS KTEYVYART
1051  PVDIPGKPEV IDVTKSTVSL IMARPKHDG SKIIGYFVEA CLKLPDKNVR
1101  CNTTPHQIPH EBYVTGLEE NAQYQRAIA KTAVNISOPS ELRTPTVTHA
1151  ENVPFRIDLS VAMKSLTVK AGTVNCDAT VEGKPMPTVS WKKEGTVLKP
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1201  AEGIKMAMQR NCTLELFSV NRKDSGVTI TAENSSGSKS ATIKLKVLDR
1251  PGPPASVAKIN KMYSDRAMLS WEPPLEDGGS EITNYIYDKR EYSSRNMAOV
1301  SANVPITSCS VEKLIEGHEY QFRICAENKY GAVDPVFTEP AIAKNPYDPP
1351  GRCDPPIVSN VTKDMTVSW KPPADDGSGP ITGYLLEKRE TVAVNMTKYN
1401  RKVIERITIK ATGLOEGTEY EFRVTAINKA GPGKPSDASK AVYADPLYP
1451  PGPPAPPKVY DTRSSVSLS WGRPAYDGS PIIGYLVEX RADTDNMYAC
1501  NLPOKLQKTR FEVTGLMENT EYQFRVYAVN KVGYSPPSDV POKHCPKDL
1551  IPEGELDAD LKRTILIRAG VTMRLYPVK GRPPKTIWS KRNVLRELI
1601  GLDIKSTDFD TFLRCENYK YDAGKYILTL ENSCGKKGYT IYKVLDPFG
1651  PPVNVTVKEI SRDSAYITWD PPIVDGSGPI INVVEKROA ERKSNSTVTT
1701  ECKTISFRVS NIEBKSYFF RYVAENEXGI GDEGTRDAY KASETPGPVY
1751  DLKVLTVTKS SCNIGMKRPR SDGGSRTIGY VDFLTEENK WQVWKSLSL
1801  QYSTKDLNEG KQYTFRVSAE NENEGTPE ITVVAKDDVY APDLDKDLR
1851  DICYLAKENS NFRKLIPOG KPAHSVYWK GEPLATDTR VVESSAVNT
1901  TLVVYDCQKS DAGKYITLK NVAGTKEGTL SIKVGCKPGI PTGPRIKFEV
1951  TAEAITLKMG PKDDGSEI TNYLLEKRS VNNKWTCAS AVQKTFRVT
2001  RLHEGMEYTF RYSAENKYG V GEGLSKPIV AKRPVDPDA PPPNIVDYR
2051  HDSVSLTWTD PKTGGSPTT GYHIEFKERN SLLMKRANKT PIRMKDFKYT
2101  GLTEGLEVEF RVMAINLAGV GKPSLPSBP VALDPIDPPG KEVINVTFRN
2151  SVTLITEPK YDGGHKLITGY IVEKRDLPSK TMMKANHINV POCATYVDL
2201  VEGKYEFRPI RAKNTAGALS APSESTGTII CKDEYEAPTI VLDPTIKDGL
2251  TIKAGDTIVL NALSILGKPL PKSSMSKAG DIRPSDITQ TSTPSSMLT
2301  VKYASRKDAG EYTTATNPF GTKEEHYAVT VLDVPGBPGR IETSNVSAK
2351  ATLWTTPLE DGGSPIKSYV LEKRETSRLI WTVVAEDIOS CRHVVTKLIQ
2401  GNEYLFRVSA VNHYGKEPV QSEPVKMYDR FGPGRPGKP EYSVNTKNTA
2451  TVSMKRPTDD GGSSETITGYV ERREKKGLRW VRATKTPVSD LACKYTGLOE
2501  GNTYEFVSA ENRAGIGPPS DASNYVLMDK VAYAPGPPSN ARVTDITKKS
2551  ASLAWGKPHY DGLLETIGV VEHQVGDDET WVDQTTGPAI RTEFVVPDL
2601  HTRKEKNFRI SAINDAGVE PAVLPDVEIV ERMADPFEL DAELRRTLVY
2651  RAGLSIRIFV PIKGRPAEV TWTKDINLK TRANIENTES FTLLIIPCN
2701  RYDTGKFVMT IENPAGKKS FVNVRLDTP GPVLNLRPD ITKDSVTLHM
2751  DLPLIDGSR ITNYIVERRE ATRKSYSTVT TKCHKCTYAK TGLSGCEYF
2801  FRVMAENEGY IGEPSETKEP VKASEAPSP DSLINIDITK STVSLAMPKP
2851  KHDGSKITG YVIEQORKGS DQWTHITVK GLECVARNLT BEEETTFQW
2901  AVNSAGRSAP RESRPVIVE QTMLPELDR GIYQKVLIAK AGDNIKVEIP
2951  VLGRRPPTVT WKKGDVILQ TORVNVENTA TSTILNISBC VASDGGPYPL
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3001 TAKNIVEGVG DVITIIVHDI PGPPGPIKF DEVSSDFVTF SWEPPENDGG
 3051 VPISNVIEIM RQDSTTWVE LATTVIIRTY KATRLTGVVE YQFVKAQNR
 3101 YGVGGIISA SIVANYPEKV PGPPGPQVOT AVTKDSMTIS WHEPISDGG
 3151 PILGVHEVK ERNGILMOIV SKALVPGNIF KSSGLTDGIA YEFRVIAEM
 3201 AGSKSPKPS EPVLALDPID PGKPIPLNI TRHTVTLKMA KREYTGFEKI
 3251 TSYIVEKROL PNGRWLKANF SNILENFIV SGLTEDAAYE FRVIAKNAG
 3301 AISPSEBSD AITCRDVEA PRILVDYREK DTVIILKAGA EKLEADVSGR
 3351 PPPTMEWTKD GKELEGTKL EIKIADFSY LINKDSSRRD SGAYILTATD
 3401 PGGFAKHIFN KVVLDRGPP EGPLAVSEVT SEKCVLSMIP PLDDGAKIE
 3451 HIYOKRETS RLAMTNVASE VOYTKLKVTK LKGNEXIFR VMAVNRKYGVG
 3501 EPLESEPVLA VNPYGPPDP KNEVTTITK DSMVVCWGHF DSDGSEIIN
 3551 YIVERRDAG QRMVCKNKKT VTDLRFKVSF LTBGHEYEFR IMAENAAGIS
 3601 ABSRTSPFYK ACDAVEKPPG PGNPRVLDTIS RRSISIAMNK PIYDGSSEIT
 3651 GYVMEIALPE EDEWKIVTPP AGLKATSYTI TNLVNOEYK IRIVAMNSBG
 3701 LGEPALVPOT PKADRMILPP EIELDADLRK LVVIRACCTL RLFVPIKGRP
 3751 DPEVKTREH GESLDKASIE STSSYILLIV GNVNRPDSK YILTVENSSG
 3801 SKSAFVNVRV LDTPGPPQDL KKEVTKTSV TLTWDPPLD GSKIKNTYIV
 3851 EKRESTRKAY STVATNCHKT SMKVDOLOEG SSYIFRVLAE NEXYGLAPAE
 3901 TAESVKASER PLPPGKITLV DVTRNSVLSL WEKPEHDGGS RILGYIVEMO
 3951 SKGSDKMATC ATVKVTEATI TGLIQGDEYS FRVSAQNEKG ISDPQLSVYV
 4001 VJAKDLVIRP AFKLEFNFTF VIAGEDLKID VPRIGRPTI VYMHDDVVL
 4051 KOTTRVNAES TENSSLSLIK EACREDVGHY VVXLSNAGE ATELTNAIL
 4101 DKPGPTGVV KMEVTAADI TISWEPKYD GSSINNIYIV EKROSTTTTW
 4151 QIVSATVART TIKASRLKTG CEYQFRTAAE NRYGKSTYLN SEPIYAQYVF
 4201 KVPGPPTPE VTLSSRDSME VOMNEPVNDG GSRVIGYHLE RKERSIILWV
 4251 KLNKPIPIOT KFKTTGLEEG IEVEFRVSAE NIVGIGKPSK VSECYVARDP
 4301 CDPGPRPEKI IVTRNSVTLO WKKPTYDGS KITGYIVEKK ELPPDGRMKA
 4351 SFTNIMDTQF EVTGLVEDHR YEFRVIAARNA AGVESSEPS TSALTARDEI
 4401 DEPRISMDBK YKDTIVHAG ESFRIDADIY GKPIPTQWI KQDQELSNIA
 4451 RLEIKSTDA TSLSKYKAFR VDSGNIVYKA QNVAGERSVT VAVKVLDRG
 4501 PPGPIVJSG VTAEKCTIAM KPPLQDGS D IINYIVERRE TSRLVWTJVD
 4551 ANVQTLSCV TKLEGENEYI FRVAVVNRKYG VGEPLSEPV IAKNPFVVPD
 4601 ARKARECTIV TKDSMIYVME RPASDGSSEI LGVLEKRDK BEIRTRCHK
 4651 RLIGELRLV TGLIENHAYE FRVSAENAG LSEPPSPAY QKACDPIYKP
 4701 GPPNPKVMD ITRSSVFLSM SKPIYDGCCE IQGYIVEKCD VSGEWMTJCT
 4751 PPTGINKTNI EVERKLEKHE YNFRICAVNK AGVGDHADV GPVIVBEKLE
 4801 APDIDIDEL RKIINIRAG SLRLVPKIG RPTPEVWKWK VDGEIRDAAI

4851 IDSTSSFTSL VLDNVRNRYDS GKYLTLLENS SGTKSAFVTV RYLDTPSPPV
 4901 NLKVTEITKD SVSITMEPPL LDGSGKIKNY IVEKROSTRK SYAAVNTNCH
 4951 KSSWKIDOLO EGCSYFFRVT AENEXGICLP ARTADPIKVA EYDPPGKIT
 5001 VDDVTRNSVS LSWTRKPEHDG GSKIIQIYVE MOAKHSEKMS EGARVKSLEA
 5051 VITNLQOGEE YLFRVAVNE KGRSDPRSLA VPIVAKLVI EPDVKRAFSS
 5101 YSVQVQDLK IEVPISGRPK PTTWTKDGL PLKQTRINV ASDLITLIS
 5151 IKETHKDDSG HYGITVANYV GQKTASIEII TLDPDPPKG PKFDEVSAB
 5201 SITLSMNPPL YTGCGQITNY IVHKRDITTT VMDVVSATVA RYTLKATKLK
 5251 TGTEYQFRIF PENRYQOSFA LDSEPIYAQY PYKEPGEPT PVTATSKDS
 5301 MVYQWHEPIN NGSPILIGYH LERKERNIL WTKVDSIIH DTQFKALNLE
 5351 EGIEYEFRVY AENIVGVKA SKNSECYAR DPCDPPGTE AIIVKNEIT
 5401 LQWTKFVYDG GMITGYIVE KRDLPEGRWM KASFTNVIET QFTVSGLTED
 5451 QRYEFRVIAK NAAGTMSKPS DSTGPITAKD EVELPRISM PFRDITVYN
 5501 AGEFTFLEAD VAGKPLPTIE WLRGDKEVEE SARCEINNTD FKALLVXKA
 5551 IRIDGQOYIL RASNAGSKS FPVNVKVLDR PGPEGEVOV TGVTCCKCTL
 5601 TWSPPLQDGG SDIPHYVEK RETSLAMTV VASEVYNSL KITKLEGNE
 5651 YIFRIAMVNK YGVGEPLESA PVLKKNPFVY PGPPKSLVET NIAKDSMTJC
 5701 WNRPDGSGGS EITGYIVEKR DRSGIRWIKC NKRRVTDLRF RYTGLEDHE
 5751 YEFRVSAENA AGVGEPPSPAT VYKACDPVF KPGPPTNAVH VDTKNSITL
 5801 AMGKPIYDGG SEVLGYIIEI CKADEEMOI VTPOGTGLKAN REIISLIEH
 5851 QEYKIRVICAL NKVGLGEAAS VPGTVKPEDK LEABELDLS ELRKGIIVRA
 5901 GGSARIIHP KGRPTPDITW SREGEFTDK VOUEKGVNFT QLSIDCDRN
 5951 DACKIYKLE NSSGKTAFV TVKVLDTGPP PONAIVAEVK KDSAVLWMB
 6001 PIIDGAKYR NYVIDKREST RKAYANVSSK CNKTFEVEN LIEGAIYFR
 6051 VMAENERGVG VPETVDAVK AAEPSPPGK VTLTDVQOTS ASIMWEPKH
 6101 DGSRVLGIV VEMQPKCTEK MSYVAESKVC NAVVTGJSSG HEQOFVKAY
 6151 NEKGKSDPRV LGVPVIAKDL TIQPSFKLP KRVSQAGED LKIEPIVIGR
 6201 PREPIFWKD GEPLRQTRV NVEETATSTI LHIKSSKDD FGKYITITAN
 6251 SACTATENLS VYLEKPPGP VGPVAFDEIS ADFVLSWEP PATYGGCQIS
 6301 NYIVERKDDT TTTWHIVSAT VARTTIKVTK LKTGSEYQFR IYAEINRYGS
 6351 TSIDSXRVIV QYFKEPGEPP GTPEVTSYVR DOMLVQWHEP VNDGSGKVLG
 6401 YHLEQKEKNS IIMVAVNKTL IQDRFKFTG LDGLEYEFK VSAENIVGIA
 6451 SLAKCPNAFV ARDPCDPPGR PEALVITRNN VTLKMKRPAY DGSKITTYI
 6501 VERKDLPPDGR WMKASETNVL ETEFTVSGLV EDQRYEPRVI ARNAAGNLSE
 6551 PSSESGAITA RDEIDAPNAS LDPKYKDVIV VHAGETVLE ADIRGAPID
 6601 VVWLKDGKEL BETTARMEIK STIOKTTLVV KDCIRTDGGO YVILKSNVGG

6651 TNSLPTTVK IDRPGPPEP LKVSQVTAEK CYLAMPPELO DGCASISHYI
6701 IEKRETSRLS WTOVSTEOVA LNYKVTLLP GNEYIFRVA VMKYIGPEPL
6751 ESEPVYACNP YKPPGPSTP EASAITKDSM VYTWARVYD GGAIEGYIL
6801 EKRDK
!!AA_SEQUENCE 1.0
P1:JC1403 - glutamate--ammonia ligase (EC 6.3.1.2) - Calothrix sp. (PCC 7601)
N:Alternate names: glutamine synthetase
C:Species: Calothrix sp.
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: JC1403
R:Elmoujani, K.; Liotenberg, S.; Houmard, J.; de Marsac, N.T.
Biochem. Biophys. Res. Commun. 189, 1296-1302, 1992
A>Title: Molecular characterization of the gene encoding glutamine synthetase
in the cyanobacterium Calothrix sp. PCC 7601.
A:Reference number: JC1403; MOID:93129187
A:Accession: JC1403
A:Molecule type: DNA
A:Residues: 1-471 <EIM>
A:Cross-references: EMBL:L05609; NID:g144935; PIDN:AAA23288.1; PID:g144936
C:Genetics:
A:Gene: glna
C:Superfamily: glutamate--ammonia ligase
C:Keywords: ligase; phosphoprotein
F:399/Binding site: AMP (Tyr) (covalent) #status predicted
JC1403 Length: 471 April 1, 2002 16:31 Type: P Check: 3357 ..

1 MTPQEVKLK IQDKIQIMD LKFIIDPQTW QHLYVYQNI DSSFTDGPV
51 FDCSSIRGKM GTEESDMTMV LDPNTAWDP FMKEPTLSTI CSIKERTGE
101 WYHRCPRVIA OKAIDYLVST GLGDTAFEGP EAEFFIFDDA RPDQTNASGY
151 YVDSVEGRW NSGKDEGPNL AYKPRFKEGY FVPAPTDTFQ DMRTMLTLM
201 AACGVPIERQ HHEVATNGOC ELGFRFGCLI EAADWMTYK YVKKNAKKY
251 GRVVTMPKP IFGDNGSMH CHOSIWKDK PLFGGDKYAG LSDMALYYIG
301 GLIKHAPALL GITNPTNSY KRLVGYEAR VNLAYSOGNR SASVRIPLSG
351 TNEKARLER RCPDATSNPY LAFAMLCAG IDGIKKNIHP GEPLDNIIE
401 LSEELAKVP STPGSLLEAL EALENDHAFI TEGVFTEDF IONWIEYKLV
451 NEVQQLQLRP HPEFYLYYD C
!!AA_SEQUENCE 1.0
P1:S47038 - tachykinin 1 precursor - golden hamster
C:Species: Nesocricetus auratus (golden hamster)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S47038
R:Heltebrand, A.; Krühoffer, M.; Juergen Maegerl, H.J.; Forssmann, W.G.
submitted to the EMBL Data Library, July 1994
A:Reference number: S47038
A:Accession: S47038
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <HEI>
A:Cross-references: EMBL:X80662; NID:g520917; PIDN:CAA56691.1; PID:g520918
C:Superfamily: substance P precursor
S47038 Length: 130 April 1, 2002 16:31 Type: P Check: 219 ..

1 MKLIVAVAF FLYSTQLSAE EIGANDDLNY WSDWSDSDQI KEALPEPFERH
51 ILQRIARRPK PQQFGLMGK RDADSSIEKQ VALLKALYGH GQISHRHHT
101 DSFVGLMGKR ALNSVAVERS AMQYERRRR

!!AA_SEQUENCE 1.0
P1:S47039 - tachykinin 1 precursor - golden hamster
C:Species: Nesocricetus auratus (golden hamster)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S47039
R:Heltebrand, A.; Krühoffer, M.; Juergen Maegerl, H.J.; Forssmann, W.G.
submitted to the EMBL Data Library, July 1994
A:Reference number: S47038
A:Accession: S47039
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-115 <HEI>
A:Cross-references: EMBL:X80663; NID:g520938; PIDN:CAA56692.1; PID:g520939
C:Superfamily: substance P precursor
S47039 Length: 115 April 1, 2002 16:31 Type: P Check: 844 ..

1 MKLIVAVAF FLYSTQLSAE EIGANDDLNY WSDWSDSDQI KEALPEPFERH
51 ILQRIARRPK PQQFGLMGK RDAGHGQISH KRHTDSFVG LMGKRALNSV
101 APEFSAMQNT ERRRR

!!AA_SEQUENCE 1.0
P1:I52526 - Neurokinin 1 precursor - mouse
N:Alternate names: neurokinin A; preprotachykinin; substance K; substance P
N:Contains: neurokinin 1; neurokinin 2
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 26-May-2000
C:Accession: I52526; JCS452; I62741
R:Kako, K.; Muneakata, E.; Hosaka, M.; Murakami, K.; Nakayama, K.
Biomed. Res. 14, 253-259, 1993
A>Title: Cloning and sequence analysis of mouse cDNAs encoding preprotachykinin
A and B.
A:Reference number: I52526
A:Accession: I52526
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-130 <KAK>
A:Cross-references: GB:D17584; NID:g407345; PIDN:BA04508.1; PID:g435121
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Iwell, R.
Endocrinology 128, 2441-2448, 1991
A>Title: Tachykinin (substance-P) gene expression in Leydig cells of the human
and mouse testis.
A:Reference number: JCS450; MOID:91209287
A:Accession: JCS452
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 36-122 <CHT>
A:Cross-references: GB:M68908; NID:g200467; PIDN:AAA39969.1; PID:g554260
C:Genetics:
A:Gene: PPT-A
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-57/Domain: amino-terminal propeptide #status predicted <PRO>
F:58-68/Product: neurokinin 1 #status predicted <NK1>
F:98-107/Product: neurokinin 2 #status predicted <NK2>
F:111-126/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from
following glycine) #status predicted
F:107/Modified site: amidated carboxyl end (Met) (amide in mature form from
following glycine) #status predicted

I52526 Length: 130 April 1, 2002 16:31 Type: P Check: 430 ..
1 MKLIVAVAF FLYSTQLFAE EIDANDDLNY WSDWSDSDQI KEALPEPFERH
51 ILQRIARRPK PQQFGLMGK RDADSSVEKQ VALLKALYGH GQISHRHHT
101 DSFVGLMGKR ALNSVAVERS AMQYERRRR

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11AA_SEQUENCE 1.0
F1:162742 tachykinin A gamma chain precursor - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: J03453
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human
and mouse testis.
A:Reference number: JC5450; MUID:91209287
A:Accession: 162742
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-72 <RES>
A:Cross-references: GB:M68909; NID:9200469; PIDN:AAA39970.1; PID:9554261
C:Comment: This protein contains two tachykinin peptide hormone substance-P
and neurokinin-A (substance-K).
C:Genetics:
A:Gene: gamma-PPT-A
C:Superfamily: substance P precursor
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-33/Product: substance-P #status predicted <STP>
F:48-57/Product: neurokinin-A #status predicted <NKA>

162742 Length: 72 April 1, 2002 16:31 Type: P Check: 3920 ..

1 DSDQIKEMP EPFHLORI ARRPQOFF GLMGRDAGH GOLSHKRKHT
51 DSFVGLMGKR ALNSVAYERS AM

11AA_SEQUENCE 1.0
F1:112958 tachykinin delta precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S12958; JC2413
R:Harman, A.J.; Hyde, V.; Chapman, K.
FEBS Lett. 275, 22-24, 1990
A:Title: Identification and cDNA sequence of delta-preprotachykinin, a fourth
splicing variant of the rat substance P precursor.
A:Reference number: S12958; MUID:91085565
A:Accession: S12958
A:Molecule type: mRNA
A:Residues: 1-97 <HAR>
A:Cross-references: GB:X56306; NID:956067; PIDN:CAA39752.1; PID:956068
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994
A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for
substance P in the rat intestine.
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2413
A:Molecule type: mRNA
A:Residues: 48-92 <KHA>
A:Cross-references: GB:S72369; NID:9632805; PIDN:AAB31499.1; PID:9632806
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:59-68/Product: substance P #status predicted <SUP>
F:68/Modified site: amidated carboxyl end (Met) (amide in mature form from
following glycine) #status predicted

S12958 Length: 97 April 1, 2002 16:31 Type: P Check: 7129 ..

1 MKILVAVVF FLVSTQLFAE ELGANDLINY WSDWMSDOI KEAMPEPEH
51 LLQRIARRPK PQQFFGLMGK RDAGHGOISH KMAVERSAMQ NYERRRK

11AA_SEQUENCE 1.0
F1:JC2412 tachykinin gamma chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1995 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: JC2412
R:Khan, I.; Collins, S.M.
Biochem. Biophys. Res. Commun. 202, 796-802, 1994

A:Title: Fourth isoform of preprotachykinin messenger RNA encoding for
substance P in the rat intestine.
A:Reference number: JC2411; MUID:94324969
A:Accession: JC2412
A:Molecule type: mRNA
A:Residues: 1-63 <KHA>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end
F:12-21/Product: substance P #status predicted <SUP>
F:21/Modified site: amidated carboxyl end (Met) (amide in mature form from
following glycine) #status predicted

JC2412 Length: 63 April 1, 2002 16:31 Type: P Check: 7417 ..

1 FEHLQRIARR RPKQOFFGL MGKRDAGHGO ISHKKRKIDS FVGLMGKRAL
51 NSVAYERSAM QNY

11AA_SEQUENCE 1.0
F1:JC5455 preprotachykinin-A gamma precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 16-Jul-1999
C:Accession: JC5455; I45967
R:Chiwakata, C.; Brackmann, B.; Hunt, N.; Davidoff, M.; Schulze, W.; Ivell, R.
Endocrinology 128, 2441-2448, 1991
A:Title: Tachykinin (substance-P) gene expression in Leydig cells of the human
and mouse testis.
A:Reference number: JC5450; MUID:91209287
A:Accession: JC5455
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-72 <CHI>
A:Cross-references: GB:M68912; NID:9163593; PIDN:AAA30725.1; PID:9552336
C:Comment: This protein contains two tachykinin peptide hormone substance-P
which is involved in a local feedback reaction and acts as a paracrine factor,
and neurokinin-A (substance-K).
C:Genetics:
A:Gene: PPT-A
C:Superfamily: substance P precursor
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-33/Product: substance-P #status predicted <STP>
F:48-57/Product: neurokinin-A #status predicted <NKA>

JC5455 Length: 72 April 1, 2002 16:31 Type: P Check: 4081 ..

1 DSDQIKEMP EPFHLORI ARRPQOFF GLMGRDAGH GOLSHKRKHT
51 DSFVGLMGKR ALNSVAYERS AM

11AA_SEQUENCE 1.0
F1:JN0023 substance P - chicken
C:Species: Gallus gallus (chicken)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997
C:Accession: JN0023
R:Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.
Regul. Pept. 20, 171-180, 1988
A:Title: [Arg3]substance P and neurokinin A from chicken small intestine.
A:Reference number: JN0023; MUID:88204263
A:Accession: JN0023
A:Molecule type: protein
A:Residues: 1-11 <CON>
C:Superfamily: substance P precursor
C:Keywords: amidated carboxyl end; tachykinin
F:11/Modified site: amidated carboxyl end (Met) #status predicted

JN0023 Length: 11 April 1, 2002 16:31 Type: P Check: 4995 ..

1 RRPQOFFGL M

11AA_SEQUENCE 1.0
F1:T40833 haloacid dehalogenase-like hydrolase - fission yeast
(Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe

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C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: I40833
R:Oliver, K.; Harris, D.; Wood, V.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, May 1998
A:Reference number: 221950
A:Accession: I40833
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-236 <OLIT>
A:Cross-references: EMBL:AL023518; PIDN:CAI18995.1; GSPDB:GN00068;
SPDB:SPCC1023.07
A:Experimental source: strain 972h-; cosmid c1020
A:Genetics:
A:Gene: SPDB:SPCC1020.07
A:Map position: 3
A:Insertions: 11/3; 26/1; 47/1
C:Superfamily: hypothetical protein b2690

T140833 Length: 236 April 1, 2002 16:31 Type: P Check: 5542 ..

1 MIPACLFDM DGLVDTESI YTKSTNIIK RYKGFESME VKAKMGRTS
51 KEASHIFIDW SGIDLCEBY IALQRETQAE LMRHTKPLFG VMNLSIKLS
101 LNIPIALATS SDTHNEFKS AHLSHLFDFH DGNIIITGDDP RLPVGRGKPH
151 PDIVFIALKM INDKRAQOG AEILPENCIV FEDSITGVGS GRAGMKVVM
201 VPDVNIIEFF SLSPQAAADK HITKVLSEEN PDVTKY
11AA_SEQUENCE 1.0
P1:T13857 - trithorax protein - fruit fly (Drosophila virilis)
C:Species: Drosophila virilis
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13857
R:Mazo, A.
submitted to the EMBL Data Library, July 1995
A:Reference number: 217801
A:Accession: T13857
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-3828 <MAZ>
A:Cross-references: EMBL:Z50038; NID:9899253; PID:9899254; PIDN:CAA90349.1
C:Genetics:
A:Cross-references: FlyBase:FBgn0014844
A:Insertions: 337/3; 529/1; 721/1; 791/1; 3668/2; 3713/1; 3771/3
C:Superfamily: Drosophila trithorax protein
C:Keywords: DNA binding; transcription regulation; zinc finger

T13857 Length: 3828 April 1, 2002 16:31 Type: P Check: 425 ..

1 MGRSFFPQNP SKSINRRKIS VIOLEDEAAS AAAAAAATA ATTEDHOOSE
51 QSAUSSASRE KGNCCDDDD DNAPSGAITS GNRGASSGAS DAAPGGSY
101 GNGSSTGSKT TNGGNVNGS HHKSATAPAE LKECKNQNO IEPNNCIAAE
151 PDGETDTNND DDDSSNDKK PTAATAAAAA AAFVPGPSAL QRARKGKK
201 FKNINLARPE VMLPSTSKLQ QQQQQOQLQN CPSASASSIS SAAAAAATA
251 APTTTTTAS ASATLTATAT STSTSSLPCT PLSVIAGGGG GAAAAALLLA
301 NPFLASVETKV VEVNAATAA ATAAATAAG AGEDVGMLKA STEMANEGL
351 EAPVAVAKSS GSSPNNHNP NAVAGSTSA AAGAPATKQ KKYVTFKNIL
401 ETSDDKSVK RYFNDNRVP LVSIMKDSL NRPLVYCRGS EPIVPSILS
451 KILKNSMID KLSLKRFSV HASSNSIOES SSTTNLBS GLSRAFGAPI
501 DDEAVSGGV TFRKQEPQHK TPEDNDDGS ASSDAIEDDE DIDDAAEEN

551 EBAASEKSAE TTASVDEKEA DDROLVMDKH FVLPRKSTRS SRIIPKRL
601 LEVGGICSKR SPSPANGKPK PKNYFGLATL PAKCTPRRRR SAATLALSOKL
651 GKETFASEAT AKVNSFVLR QPRLQFOTDK SRSEVSAKPT LPTTVLPAS
701 SSAITSANVL SFGALNNANS AVAAASTCAV CSAFVNNKDA PLARKYGVIA
751 CEVCKRFNFR MTKISKLSLP MHSNPSTSTA QSQOQLKCID GNCCLLSLK
801 SOLKNEKLY KERCKACWLK KCLATLQIPA GHRSRLSAIL PASMREAVP
851 KDKCPBELLS PTASLRFAP TSSASGTTI KMKSAETAV NSIKSNPLAE
901 NNVTGCGTFL LRPALLEKPL FLKIGSDNKK AKSKKALGL SVVPSSEAA
951 VAPGKTTTRA KODEKAREL EAEKPLSPNA KKTTEANTPE TOKDQOPAST
1001 TTVSAASSS TSHTSAAATN SSOLETTAEA NASAVPDNLK RQRLDKGPR
1051 VHHVCRSASI VLQGPLATFG DEBELAAE AGAPTTTTT TTSPEVILIK
1101 PKSPQPMQMI IDENDNCASC ILPTTEATAE AQPAVKSVLE SRSKSNQT
1151 EAKKTPATG SSKGVTTTRN ATAVTSVAS SLVATKKORH IEVSSISS
1201 QAAATQSRRA LAKEVNRILA LISTDFWENY DPAEVOQTGF GLIVETVAAQ
1251 RALCFLOGST GLDPLIFCAG CCEBYHOYCV LDEYNLKHSS FEDTLMTSL
1301 ETSNNACATS AATNTALNQL TORLNLCPR CTVCYTCNMS SSKYKQKOC
1351 QKNYHSTGCG TSKRLGADR PLICVNLCK KSCATTKVSK FGNLPMCTA
1401 CFFLRKKGNF CPICOKCYTD NDFDLKMEC GDCNQVHSHK CEGLSDEQYN
1451 LLSLTPESIE FICKKCARC DVSRRKADEN RQAVMEFKS SLXSVLKLIS
1501 KSRQACALLK LSPRKNMRC SAGAQPAKAH SQGLQPKAL QTYNGLSGD
1551 GESQNSDDLY EFKQHSTNR KPSTPVPCSC LQPLSOSPSP SLVDIKOKIA
1601 SNAVYSIAEF NYDMSOVIQ SNCELDIAY KELLSQFPW FQNETKACTD
1651 ALEEDMFESC GYEELKESPT TYAEHHTASQ APRTGLLDIP LDDVDLDGSC
1701 AKTRLDTRY CLFCRKGEG LSGBEARLLY CGHDCVNHIN CAMSAEVE
1751 EIDGSLQNVH SAVARGMIK CTVCGNRGAT VGCNVKSGE HYHYPCARTI
1801 DCAFLTKSM YCPAHARNAL KANGSPSVTY ESNFEVSRVP YVELBRKRRK
1851 LIIPAKVOFH IGSVAVROLG SIVPRSDSF EALVPLNPLC SRLYSSKEP
1901 WKIVETVART TIQNSYSTL TLDAGNFTV DHTNPNCISLV QGLAQIARW
1951 HSLARSDLL DTDMAEFPNS YVPADENTEE EPQNMADLP PEIKOAFED
2001 LPHELLDGIS MLDIFMYEDL GDKTELFAMS EDSKDGTTAT SOAGASAYII
2051 CDEDTRNMS LNKHLVLSNC CTASNPDVDA MLCARSSSQ EKECGDVLYK
2101 TDTAPTFRSWP KLDGGSVAAF KRRRLSNIA EGYLISLNR SKKEAVTVAG
2151 ITRROSVGGS SELPAEGSAT MTKSFTWSA AKCLEFKNS REEPKLTIM
2201 QMDGVDDSIY EYRIIGSDN LSTAQFTGOV KERCOCOTYR NYDSFORHLG
2251 SCEPMSTSES ESEFATGTAQ LSAESLNELO KQALAATIS NTGGLNYLOT
2301 SFPVOYNIAT LGQFGVOGLQ GLQTLQLOP SLGNGFFLSQ PNAQAATNSG
2351 NDVLQLYANS LQNLAA NLGG GFTLTQPTMS TQAPOLIAL STNPDTQOF

2401 IQLPSNGAT TQLLTATAPL RCNATYOTLQ ATNSDKIVL LFLAGDPLQ
 2451 EYVTAQAOA TAAAHOKOL SGHGVRIQA KIAGQOOOOR HQOHQOHOH
 2501 QOOOQOOOQO QOOOQOPIVY AQHGTTQLL GONLLOPOLL FOSNAPOTO
 2551 QLLLPOTQAO NISFVTGDG SQNOPIQYIS IPTTDFKPO QTSPTFELT
 2601 AFGGATFLQ TDASGNMLT TAPANSGLM LIGQLOTOPO VIGTLIQOT
 2651 LQLTGADGT QTATAOPLI LGATGGGTT GLEFATAPV ILATPMYTG
 2701 LETIVQNTVM SSQOFVSTAM PGVLSNSSF SATTTQVFOA SKIEPIVLP
 2751 AGVVLNNAV DASGNTSWLQ QSQTQATDDA TALLONMAG QPQTPTTST
 2801 QOTMSTDPAP PLVVTAKVP VAOIKRNTNA NKSPIVLSK VOPPOQSOV
 2851 VAKVLPNTVI QOOOQOOOQO QOOOQOQMPK OOLAGNANLK LSGFOROQO
 2901 ANELKNKQAA GQOTGTCGA PPSIASKPLQ KTNILRPH KVEVPKIMK
 2951 QAPKLATSAA SMOHQQOOS PAALNVAKY ALLQORLAPA POPQOQEPQ
 3001 EQOHLHQOQO QOOOQOOHMQ OHQOQOOQLS MPQLRAQOP IISIVTAEP
 3051 QAAQPFVIRP ALQAAQPIQ LOEQOSQOQ QQPAEOLING KAARLQRYAS
 3101 NSLPTNVNP LQOQRCASAN NSSNSVNTQO NSTIINSRP TNRVLPQOOR
 3151 QEPPLSNDV VVOSPTPKP IEEVPAGAS TOKPIVKCYA QLEKSPGYE
 3201 TELKNTITLD NLEQTNSTTT MOLOQPOQRP IYGEQIFPEQ SBAQVQLEKP
 3251 KHNIMLLLEA TSCQOQOQOQ OHMEMVNDG FOLTSNESCL LEKHGENVEA
 3301 VMQDIEDHYA SMKNGSGGA AEGIGQVDA EDEDDDDDE SLKMATSAQN
 3351 DHEMDSEEP AVKEKISKIL DNLITNDQSD STATATVEA SAGYQOMVED
 3401 VLATTAAGSV STDETTAT AEAVEAASY INEMAHLE OLKOLQAGVE
 3451 IDLKRPKLDV PQOQPDVVP NVVPTAAPQ QPPMRDPK ISGPHLYEI
 3501 QSEDEFTYS SSIAIWEKV PEAVQARRA HGLTPLEPG LADMGVQMT
 3551 GLKTNALKYL IEOLPGVEKC VKYTPKYHRK NGNVSTAAG GHARTAGSNP
 3601 AALAGAEEL IDYSGDQEL QENAYECARC EPVVSSEVD MFSMLASRR
 3651 KPIQVFPVOP SDNELVPRRG TGSMLPAMK YTLKETKID YGVFRSHIH
 3701 GGLYCTKDI EAGEWIEYA GELIRSTLTD KREYVDSRG IGCYMFKIDD
 3751 NLVVDATMG NAARINHC EPNCYSKVD ILGHKHIIF ALRRIQGE
 3801 LTYDKPFPE DEKIPSCGS KRCKRYLN

!!AA_SEQUENCE 1.0
 PI:E86284 -hyothetical protein AAD39637.1 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: E86284
 R:Theologos, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White,
 O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.;
 Chan, A.; Chao, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.;
 Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Egu, P.;
 Feldblum, T.V.; Feng, J.; Fong, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.;
 Haas, B.; Hansen, N.E.; Hughes, B.; Huizart, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.D.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin,
 E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.;

Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.;
 Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, A.; Millscher, J.;
 Miranda, M.; Nguyen, M.; Niemman, W.C.; Osborne, B.L.; Pal, G.; Peterson, J.;
 Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.;
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
 Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken,
 S.; Vaysberg, M.; Vysotskaia, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.;
 Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719
 A:Accession: E86284
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-290 <STO>
 A:Cross-references: GB:AE005172; NID:g5103807; PIDN:AAD39637.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

E86284 Length: 290 April 1, 2002 16:31 Type: P Check: 4011 ..

1 MPEIHGAHT IRSHGVTVAR FHMMDWILL LLIVIEVLN VIEPFRFVG
 51 EDMITDLRNP LQDNTIPEWA VPLIAVLPF AVICVYFIR NDVYDLHHAI
 101 LGLFSLVLT GVITDAIKDA VGRPRDFEW RCPFDGIGIF HNTKKNVLT
 151 GAKDVKEGH KSPFGHTSM SFAGIGFLSL YLSKIRVDF QRHVAKLCI
 201 VILPLVAL VGSVRVDYW HHMODVEGGA IIGLTVAFC YLOFPPPYD
 251 PDGMPHAYF QMLADSRNDV QDSAGMHLIS VRQTELESVR

!!AA_SEQUENCE 1.0
 PI:E84421 -probable phosphatidic acid phosphatase [imported] - Arabidopsis
 thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: E84421
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;
 Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblum, T.V.;
 Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.;
 Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.;
 Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.;
 Copenhaver, G.P.; Preuss, D.; Niemman, W.C.; White, O.; Eisen, J.A.; Salzberg,
 S.L.; Fraser, C.M.; Venter, J.C.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana.
 A:Reference number: A84420; MUID:20083487
 A:Accession: E84421
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-302 <STO>
 A:Cross-references: GB:AE002093; NID:g4262225; PIDN:AAD14518.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: AT2g01180
 A:Map position: 2

E84421 Length: 302 April 1, 2002 16:31 Type: P Check: 2420 ..

1 MQEIDLSVHT IKSHGGRVAS KHKHDMITLV ILIAIEGLN LISPFYRVG
 51 KDMMTDLKTP FQDNTVPTMS VPVAVALLPI IVEYCFYLRK TCYYDLHHST
 101 LGLFAVLIT GVITDSIKVA TGRPRNFW RCPFDGKELY DALGVVCHG
 151 KAAEVEGKH SPFGHTSMS FAGLFLSLY LSGKIKAFNN EGHVAKLCV
 201 IFPLAACLV GISRDVDYH HMODYFACAL IGLTVAFCY RQTPPYRHE
 251 EGMGPYAYFK AAOERGVPVT SSONGDALRA MSLOMDSTSL ENNESGTSTA
 301 PR

11AA_SEQUENCE 1.0
PI:T33064 - hypothetical protein F56C3.9 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T33064
R:Stonking, T.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of *C. elegans* cosmid F56C3.
A:Reference number: 221276
A:Accession: T33064
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-206 <STO>
A:Cross-references: EMBL:AF067214; PIDN:AC17009.1; GSPDB:GN00028; CESP:F56C3.9
A:Experimental source: strain Bristol N2; clone F56C3
C:Genetics:
A:Gene: CESP:F56C3.9
A:Map position: X
A:Introns: 43/2; 87/1; 116/1; 141/2; 184/3
T33064 Length: 206 April 1, 2002 16:31 Type: P Check: 3281 ..
1 MTQOKHMFSTETALKKFOI NTQSDTIYV LNTLAEISEY FHILRTGYS
51 EMTAEKYNLN DYFAEDLYVF LSYVCPDGE FDRITNOHNI TPLVPSDRLL
101 VEPWVKEVH KYLNSEAFON EIDYELLVQ LCYLHSONY SELDVYFKKI
151 ALDNLVVD RLVOEITDSD VQSFETKIL QYRPYTEKPR PQMFEDMDHT
201 PYSAVY
11AA_SEQUENCE 1.0
PI:T09484 - cartilage intermediate layer protein precursor - human
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09484
R:Lorenz, P.; Neame, P.; Sommarin, Y.; Heinigard, D.
J. Biol. Chem. 273, 23469-23475, 1998
A:Title: Cloning and deduced amino acid sequence of a novel cartilage protein (CILP) identifies a proteom including a nucleotide pyrophosphorylase.
A:Reference number: Z16689; MUID:98389785
A:Accession: T09484
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1184 <LOR>
A:Cross-references: EMBL:AF035408; NID:93513502; PIDN:AC33838.1; PID:93513503
A:Experimental source: tissue type articular cartilage
C:Genetics:
A:Note: CILP
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-1184/Product: cartilage intermediate layer protein #status predicted <MAT>
T09484 Length: 1184 April 1, 2002 16:31 Type: P Check: 4681 ..
1 MVGTRAVES FLVLETVSVL GRQFMLTQSV RRVOPGKKNP SIPAKPADTL
51 ESFGEMTTLF NIDYPGKGD YERLDARFY YGDRVCARPL RLEARTDWT
101 PAGSTQVVH GSPREGFWCL NREORPGNC SNYTVRFCL PGSLRDTFR
151 IWSWSPWSK CSAAGQGVV QTRTRICLAE MSLSCSEASE EGOHCWGDC
201 TACDLCPMG QVNADOCACM CODEMLHGV SLFGAPASG AATYLLTKTP
251 KLITQDSOG RFRIGLCPD GKSLIKITKV KEAPVLTMP KTSLKAAITK
301 AEFVRAETPV MVMNPETKAR RAGQSVSLCC KATGKPRDK YFWYHNDTLL
351 DPLUYHESK LVLRKLQOHQ AGEYFCKAQS DAGAVSKVA QLVYASDET
401 PCNPVESYL IRLPHDCFON ATNSFYDVG RCPVKTCAQ ODNGIRCDA

451 VONCGISKT EEREIQCSGY TLPTKAKEC SCQCTETRS IYGRVSAAD
501 NGEMRFGHV YMGNSRVSM GYKGTFTLHV PODERLVLV FVRLQKFN
551 TTKVLPENKK GSAVFHEIKM LRKEPTILE AMETNIPLG EYGEDPMAR
601 LEIRSRSFYR QNGEPIGVK KASVTFIDPR NISTATAQT DLNFINDEGD
651 TFLRTYGMF SVDFREVTIS EPLNAGKAV HLDSTQKMP EHSYTKIMS
701 LNPDTGLMEE EGDKEFNOR RNKREDRTFL VGNLEIRRR LFNLDVPESR
751 RCFVKVAYR SERFLPSEDI QGVVISYVNL EPTGFLSNP RAMGRDSVI
801 TGPAGACVPA FCDQSPDAY SAYVLASLAG EELDAVESP KFPNAGVP
851 QPYLNKLINR RIDHEDPRVK KTAFOISMAR PRPSAESN GPIYAFENLR
901 ACEAPPSAA HPRFYIEGD RYDNTVPFN EDDPMSTED YLAWMPKPMR
951 FRACIYVKI VGPLEYNVS RNMGTHTRT VGKLYGIRDV RSTRDRDPN
1001 VSAACLEFKC SGMLYDQDRV DTLVKVLPQ GSCRRASVNP MLHELYVNL
1051 PLAVNNDTSE YTMALAPLPL GHNYGITYVT DQDRTAKEI ALGRCPDGT
1101 DGSSRIKSN VGVALTFNCV EROVGRQSAF QYLDOSTAQS PAAGTQGRV
1151 PSRRQQRASR GGORQSGVVA SLRFPVAAQ PLIN
11AA_SEQUENCE 1.0
PI:A84089 - hypothetical protein BH3513 [imported] - *Bacillus halodurans*
(strain C-125)
C:Species: *Bacillus halodurans*
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirama, C.; Nakamura, Y.; Ogasawara, N.; Kuhara, S.; Horikoshi, K.
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis*.
A:Reference number: A83650; MUID:20263314
A:Accession: A84089
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-957 <STO>
A:Cross-references: GB:AP001519; GB:BA000004; NID:910176109; PIDN:BA07232.1; GSPDB:GN00137
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3513
A84089 Length: 957 April 1, 2002 16:31 Type: P Check: 4652 ..
1 MKFISWTLNE PSNAQFAEYA TEVSPGEWRI LNPDAKRMWG GNQKNFMLAF
51 MNHDKITGV GLHDEGVNAD GTIYSKAGE GYPLNDEET AIRMMWRDSL
101 RFLVDHPNI KWSLQWVCFD PSRVEPIIDN VNGAQDTFVR QLKKAIEVLY
151 NREPGRIKGI EMDFEKTSR PRSAQEPKY RDLRLRVKDE VCPRLGLEIR
201 VNLHAMTGEY NPSWYMTNV STIAADLDE YQIUSYFSA GNAPRPSRP
251 VMMLEVLVDH VRNVLPEPKT FIGNAAYGR WSLNRDRIGT ALAYWQLLOW
301 QNGLFKHNAG ORNDQSEFTI FDQSFIPYCG FHDESGEY TELHCYDRFQ
351 ARFARLIPYN NSQVYRGTY RNAEYTSYS KHQAKFTGI QRLTEATST
401 SGHISDAHSV WEKDDLPY TFGYNTLPQ QYLYDEATNS CVRASAIGQ

451 DGRVYSPSL STPTGYRLIA TVEFPYLNCR IPINWGVYD VIGEDIDPMY
501 PEFVNPSPHF FDCGTFSFST SNTITGVATQ DSAQIMGFVI CRDEHNGSG
551 GEVEYNWVLQ VPKKRGSVLD GAVTKVDADM PDEVTLTIEL IRRHPPAIF
601 WEDLEFPAPD QEVENLTETN YVORALTGFR APNGPYVDG ACRGPLONIG
651 YSNGTWRPVA ASGDEAHVY COARNSAQL VLNREFSFA HIEADIRALD
701 SNAITGIRFY ARNDGVYNG VYLAQLYRNR TVRLYESGG SSQVLAIPAM
751 SETLANGIS RHITLIRVN GRIKILVAV EYINYSGLP GSLSGAHGV
801 YANCRIRCY RHITATNDY EPEKYSALV DGREVALLE DRPSYDELG
851 YLYVSGENPD EGLDIDIDND YDNFPIVNP SWVGEKNIRI RLVDAGWLR
901 NFVYDGEFY SIAMNSDLEG FITTLGFIKN YGCKGVGMWT IGEDPRVFT
951 YLPPEND

!!AA_SEQUENCE 1.0
PI:G96806 ? unknown protein T5M16.25 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96806
R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White,
O.; Alonso, J.; Altif, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.;
Chen, A.; Cho, Q.; Chen, H.; Cheuk, R.F.; Chin, C.W.; Chung, M.K.; Conn, L.;
Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Dunn, P.; Etgu, P.;
Feldblum, T.V.; Feng, J.; Ford, B.; Fujii, C.Y.; Gill, J.E.; Goldsmith, A.D.;
Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin,
E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.;
Langin-Hooper, S.; Lee, A.; Lee, J.M.; Lenz, C.A.; Li, J.H.; Li, Y.; Lin, X.;
Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani, A.; Miltischer, J.;
Miranda, M.; Nguyen, M.; Nierman, W.C.; Osborne, B.I.; Pal, G.; Peterson, J.;
Pham, P.K.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
Tallon, L.J.; Tamburiga, G.; Tortum, M.J.; Town, C.D.; Utechtack, T.; van Aken,
S.; Vaysberg, M.; Vysotskaya, V.S.; Walker, M.; Wu, D.; Yu, G.; Fraser, C.M.;
Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: G96806
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-421 <STO>
A:Cross-references: GB:AE05173; NID:96382510; PID:AAF07796.1; GSPDB:GN00141
C:Genetics:
A:Gene: T5M16.25
A:Map position: 1

G96806 length: 421 April 1, 2002 16:31 Type: P Check: 8387

1 MSQKLTITQ SSLRSSPTI RSSIQSLSTI TECDDFNES HHRRODLEA
51 GEKEKORRR KPVKSGSMN RIKPGLAFTL ACLSLSLSS FLFFVDEIF
101 TSENLLGLI FVALALFPAS RNMAVINQV IAIKOIRVS RIKHPRPVQ
151 WYIGDSKEP IKEETRLVY KEGVQFFNSG DYEGEFNG KCNGSVYYY
201 YVNGRYEGDW INGRYDGYI ECWSKSGSKYX GOYKQGLRHG FGYYWYTGCD
251 SYSGEMFNQ SHRGVOTCA DGSSFVGEFK FGKXHLGASY HFRNDKYAG
301 EYFGKINGF GYVHFANGHY YEGAMHGRK OGTYTTRFT GDINSGEHD
351 GNLVNHFLD SDPVRAVOS ARERANGVN ORRIDEQVIR AVAANKAAT

401 AARVAARAV ONOMDKICD N

!!AA_SEQUENCE 1.0
PI:S29344 ? protein kinase KIN3 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein O5220; protein YOR233w
C:Species: Saccharomyces cerevisiae
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Sep-1999
C:Accession: S29344; S67126; S24707
R:Kambouris, N.G.; Burke, D.J.; Creutz, C.E.
Yeast 9, 141-150, 1993
A:Title: Cloning and genetic analysis of the gene encoding a new protein kinase
in Saccharomyces cerevisiae.
A:Reference number: S29344; MUID:93220392
A:Accession: S29344
A:Molecule type: DNA
A:Residues: 1-800 <KAM>
A:Cross-references: EMBL:X67916; NID:95514; PID:CAA48115.1; PID:95515
R:Boyer, J.; Fairhead, C.; Gallion, L.; Gallison, F.; Michaux, G.; Thierry, A.;
Dujon, B.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67104
A:Accession: S67126
A:Molecule type: DNA
A:Residues: 1-800 <BOY>
A:Cross-references: EMBL:Z75141; NID:91420534; PID:CAA99453.1; PID:e252094;
PID:g1420535; MIPS:YOR233w
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:KIN4; KIN3; KIN31
A:Cross-references: SGD:S0005759; MIPS:YOR233w
A:Map position: 15R
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein
kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
E:44-313/Domain: protein kinase homology <KIN>
E:52-60/Region: protein kinase ATP-binding motif

S29344 length: 800 April 1, 2002 16:31 Type: P Check: 2811

1 MASVRRKHY GGNVYTDNR HSLORNEIL HPHKQRKH ATFGYITGS
51 TLGESEFGKV KLGWTKASS NEVPKQYAK LIRRDITKRD ADKEIKIYRE
101 INALKHLTHP NIYLEEVLQ NSKYIGIVLE FVSGGEFYK IQRRRLKES
151 SKCRLEAQLI SGVNMHTKG LVHRDLKEN LLLDKHENLV ITDFGFVNEF
201 PEDNELMKTG CGSPDYAPE LVVSTKAYEA RKADVWSCGV ILYAMLAGYL
251 PWDDHENTP GDLARLEKY ITOTPLKFFE YITPIPRDL RLILVNPFR
301 RINLOTIKRH VMLKPHENFL SIQPNYDEH LQKRRKPPN KQDVGRHSY
351 SSSASSYSKS RDRNSLIES TLBOHRMSPQ LATSRPASPT FSTGSKVVLN
401 DFKNMKEEN INGERTSASC RYTRDSKNG QVQIEGVYAR HSSRQNKHTS
451 VAGLVITIPS PTTARTNAP SKLITEHYKD SSTSTSTQOE FHRIGNHYV
501 RSRPRTSYV PGLSRNADN SLADIPVNL GSNRGLTDAK DVPPLAITHD
551 TKATISNNS IMLSECPAA KTSFVDHYA IGDNLHGDKP ITEVIDKINK
601 DLTHRAENG FPRESIDPS TSTILVKEP TNSITDEHYE SOLENGHSS
651 NKSDASSDKD SKTIYKRRF SFMSLYSSLN GSRSTVESRT SKGNAPVSS
701 RMPGSGSNS NIKITQOOPR NLSDRPVNDP KKINDRIRD NAPSVAESBN
751 PGRSVRASVW VSTLRENRK ELSNEGNVVE AQTSTARKVL NFKRSMRY

!!AA_SEQUENCE 1.0
PI:S23308 ? substance P - rainbow trout

C:Species: *Oncorhynchus mykiss* (rainbow trout)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
 C:Accession: S23308
 R:Jensen, J.; Conlon, J.M.
 Eur. J. Biochem. 206, 659-664, 1992
 A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.
 A:Reference number: S23308; MUID:92298992
 A:Accession: S23308
 A:Molecule type: protein
 A:Residues: 1-11 <LEN>
 A:Experimental source: brain
 C:Function:
 A:Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions
 A>Note: substance P is derived by post-translational processing of preprotachykinin A
 C:Superfamily: unassigned animal peptides
 C:Keywords: neuropeptide; amidated carboxyl end (Met) #status predicted
 F:11/Modified site: amidated carboxyl end (Met) #status predicted

S23308 Length: 11 April 1, 2002 16:31 Type: P Check: 4943 ..

1 KRPHOFFGL M

!!AA_SEQUENCE 1.0
 P1:F65524 } 3uvs type protein [imported] - Chlamydia pneumoniae (strain J138)
 C:Species: *Chlamydia pneumoniae*, *Chlamydia pneumoniae*
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
 C:Accession: F65524
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ishii, K.; Hattori, M.; Kuhara, S.; Nakazawa, T.
 Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of *Chlamydia pneumoniae* J138.
 A:Reference number: A66491; MUID:20330349
 A:Accession: F65524
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-286 <STO>
 A:Cross-references: GB:BA000008; NID:98978644; PIDN:BA098460.1; GSPDB:GN00142
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: ywlc

F65524 Length: 286 April 1, 2002 16:31 Type: P Check: 9351 ..

1 MPKKAQITF SLPEYMSAIH QGKIVALPTD TYGFLVLSLY ASEAEERLYA
 51 LKDRPSKAF ALVYNSIEDI ENISGYPLSP TAKKLAQLFP GAITLVVNR
 101 NRPFKETLA FRIVDSVVR EIVDHGCTLI GTSANLSEFP SALTQDELFA
 151 DFADHDLCTF DGPCSHGLES TVVASDPLYI YREGLISRSV IENIAGTEAK
 201 IFHRTSHAES KHIKIYTVKN QEQLVSFLSG SLDFKGVCE HPRKPNFYTR
 251 LREALKKTRP SIVFIYDINT SDPELEPFL SPYIIE

!!AA_SEQUENCE 1.0
 P1:F85107 } hypothetical protein AT4g10370 [imported] - Arabidopsis thaliana
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
 C:Accession: F85107
 R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor, Washington University in St Louis and PE Biosystems
 Nature 402, 769-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.
 A:Reference number: A85001; MUID:20083488
 A:Accession: F85107
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-676 <STO>
 A:Cross-references: GB:NC_001268; NID:97267734; PIDN:CAB78160.1; GSPDB:GN00140
 C:Genetics:
 A:Gene: AT4g10370
 A:Map position: 4

F85107 Length: 676 April 1, 2002 16:31 Type: P Check: 7623 ..

1 MDENLFFVK LTQDPTSS GEVLAMSTG DDQPLDQPLE LCPDARIKH
 51 KKIQRDGD IFDYDFKHP YISSPHPSK RSGDQGGESI LDCDEGJCK
 101 LPVPLFWCN NKESDSREFQ CGGCRDSMLS ASYVACLOE KKFHRECVES
 151 PLEIKHPTL FHSRLYYHP APEFCIOCK EYVMIFYHCL TONLSMHPVC
 201 AMKRVPEFID HPSKHPHPLT FEPTQASLVC HFCALIKKLD PLYCTKCVF
 251 VHKGCIGFP HVIRISRTH RISFTSSLPC GKLSGVCVHQ QVDNDYGAYS
 301 CKKDAVEFH SKCALGRHW DGNLEVEPE EDDMIDGER FKRIDGILL
 351 HPHSHNLHL QTTAYDENT YCRGALPIY EGOFYSCIES DFLHEHCAN
 401 APRMKRPHL PHPLTLVVAT RGPENEGTF QCDACHRKGT GFYEHHTDQ
 451 ENIFMDIHC ASIFEPFOYQ GHEHPLFLPS EPRKMKRCQM CYEYEVNLT
 501 NCLECDYILC FHCATLPYKV RYKHDSHFLK ICNGKRANNO SYWCEICECK
 551 IEGTERAFY NTPKRDTSFY KGNACCTTLH QRCLGIDTY MKPGETVDY
 601 LSIKXASEG QSKESITDVO ILNNSPTR ICRCRCRCR PFIFKGNHT
 651 IFCSDCVED SAMRSYORLL YSLWLG

!!AA_SEQUENCE 1.0
 P1:G84527 } hypothetical protein At2g15340 [imported] - Arabidopsis thaliana
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: G84527
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umeyan, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Coppenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A84420; MUID:20083487
 A:Accession: G84527
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-85 <STO>
 A:Cross-references: GB:AE002093; NID:94544379; PIDN:AA022250.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g15340
 A:Map position: 2

G84527 Length: 85 April 1, 2002 16:31 Type: P Check: 8684 ..

1 MALSGQKKR RGAGVLYTAT AGDGDLMALA PLPOAOVOLL VIQTLAVOTL
 51 EVRIIVLVLP LGLDGGVGD PTALGARPHR MLTYEF

!!AA_SEQUENCE 1.0
 P1:B4054 } orf2 protein - Junonia coenia densovirus
 C:Species: *Junonia coenia densovirus*
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
 C:Accession: B4054

R.Dumas, B.; Jourdan, M.; Pascaud, A.M.; Bergoin, M.
 Virology 191, 202-222, 1992
 A:Title: Complete nucleotide sequence of the cloned infectious genome of
 Junonia coenia densovirus reveals an organization unique among parvoviruses.
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: A44054; MUID:93033112
 A:Reference number: A44054
 A:Accession: B44054
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-545 <DUM>
 A:Cross-references: GB:S47266; MID:9257675; PIDN:AB23699.1; PID:9257677

B44054 Length: 545 April 1, 2002 16:31 Type: P Check: 1211 ..

1 MANGDTNRET DSTTRPNQDI IRSSSGRTSP SECCSVAVAM SKRRMSHG
 51 RCTMASIAKE SOENFOYAE ELEKMGSEFF GYVTGOSIKP SSAYISDYII
 101 LRDIDLRODC LDVLEYGERS RRNGLFGFSE EGDHIVIH D CSYTRNSCRD
 151 IMISQVKPRG SVQTKGKPVK FIMEFKRTDW YDVEIFEFR KRGEAIIYR
 201 GSGKIPSD ECVNTRFEK EREWVSSDC TDYEECOE HKISRRSDAG
 251 SNGRLYEKK AYSAGKEFAYI RKTKALLRK YVSPVSAIC DYPERRDDL
 301 LCDPKRDIY QAACDDFGKD LNMASLEIY NLITEDYNFT DEQELNPYAL
 351 FISSMKYDNL ENSLNIITEL LKFOCNDDED LIVEFLTNLY NVLDRIIPKL
 401 NAFLLISPPS AGKNFFPDM FGLLSYCOL GOANRHNLFA FOEAPNRYL
 451 LNNEPVESS LTDITKMEG GDPYTVAVKN RMDAHYKRP VILLNNYVP
 501 FMYEAFSDR IIOYKMNAP FLKDYELKPH PMTFILLSK YNITF

!!AA_SEQUENCE 1.0
 PIR:70605 hypothetical protein RV3567c - Mycobacterium tuberculosis (strain
 H37RV)

C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C:Accession: E70605
 R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
 Gordon, S.V.; Eigmeier, K.; Gao, S.; Barry III, C.E.; Tekala, F.; Badcock, K.;
 Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.;
 Felwell, T.; Genies, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagsels, K.;
 Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail,
 M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.;
 Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the
 complete genome sequence.
 A:Reference number: A70500; MUID:98295987
 A:Accession: E70605
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-187 <COI>
 A:Cross-references: GB:292774; GB:AL123456; MID:93261729; PIDN:CA60741.1;
 PID:9306707; PID:91877298
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: RV3567c

E70605 Length: 187 April 1, 2002 16:31 Type: P Check: 8381 ..

1 MSAQIDPRTF RSVLGQCTG ITVITTVHDD VPVGFAQSH AALSLPEPLY
 51 LCPPTKVSRS WQALEASGRF CVNVLTREKQK DVSAREGSKE PKKFGIDMR
 101 PSLGSPITTE GSLAIIDCTV ASVHDGDFH VVFGAVESLS EYPAVKPRPL
 151 LFYRGDYGTGI EPKPTPAHW RDLLEAFILIT TTQDTWL

!!AA_SEQUENCE 1.0
 PIR:T36591 - hypothetical protein SCH24.26c - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T36591
 R:Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream,
 M.A.
 submitted to the EMBL Data Library, May 1999
 A:Reference number: T36591
 A:Accession: T36591
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-373 <OLI>
 A:Cross-references: EMBL:AL049826; PIDN:CA642732.1; GSPDB:GN00070;
 SCOEDB:SCH24.26c
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SCH24.26c

T36591 Length: 373 April 1, 2002 16:31 Type: P Check: 1196 ..

1 MSLLTFTSR EOHLYIYSL PASHMCPA WADYKAWMS ENLGNFDDRT
 51 GELVAGALV YKOLPKIKRY LAYLPEGPVI NMFAPILQDW MEPMALHLKQ
 101 QGAFSVKMP PYIIRMDAT SIKKGIODPD VKRLRIEND HIEPRAFEVA
 151 DKIRRMGOO GEDGAGFGD VQPRYPQVP LANRSLEEVH KNFNOLMRN
 201 IKKAERAGVE VVOGGYHLE EMORLYEITA VRDHFRPRPL SYFOEMMAL
 251 NNEDPRMRL YFARHNGVNL SAATMLVVG HWVYSYGASD NIGREVRSN
 301 ANQMAMLRDS YALGATVYDL RGISDSIDES DHLFGLQK VETGGOAAY
 351 LGEMDFPLNK LHKALDIYM SRR

!!AA_SEQUENCE 1.0
 PIR:T04052 hypothetical protein F24G24.170 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
 C:Accession: T04052
 R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.;
 Mayer, K.F.X.; Scheller, C.
 submitted to the Protein Sequence Database, March 1999
 A:Reference number: T04052
 A:Accession: T04052
 A:Molecule type: DNA
 A:Residues: 1-705 <BEV>
 A:Cross-references: EMBL:AL049488
 A:Experimental source: cultivar Columbia; BAC clone F24G24
 C:Genetics:
 A:Map position: 4
 A:Note: F24G24.170

T04052 Length: 705 April 1, 2002 16:31 Type: P Check: 9930 ..

1 GEKERNRITK IQPIYVAMS SVGVFHVEM DENLYYVYKL TQTDYPTSSG
 51 EYLANDSTGD DQPLDPLFL CPDARIKFKH LKIQREDDGI FDYDEKFNHY
 101 ISSPHFPSKR SGDQGESIL DCDEDDGICKL PVPPLRWGNN KESDSREPC
 151 GGCDSMLSA SYACLOCEK KEHKECVESP LEIKHPTHLF HSLRLYHDA
 201 PERCLOCKTE VMPIFYHCLT CNLSMHPVCA MRKVPEFIDH PRSHPHPLTF
 251 PFTQASLVGH FCALLKKIDP TYICTKCVF IHKGCGIGFPH VARISRHTHR
 301 ISFTSSLPFG KSCGVCQHOQ VNDYGAIVSC KQDAYFVHS KCAIORHWMD
 351 GKDLSEVPPEE DDMIDGEPF KRIADGIIH PFSHNLHIQ TRAYDENTY

401 CRGALPIYE GQFYSCIESD FILHEHCANA PRMKRHLPH HPLTLVATR
 451 GPCNEEGTQ CDACHKCTG FFEYHHTDQ NIEMLDIHA SIFEPQYQG
 501 HEHPLFPE PRKMGRCMC TYEVNINLN CLECDYILCE HCATLPIYVR
 551 YKDSHFLKI CNGKEANDOS YWCEICEGKI EECTERAFYN TPKKDTSFYK
 601 CNACCTTHQ RCLLIGIDTYM KPGETVKDYL SSIKVASEG SKESITDQI
 651 LNSSSTRPI CTRCLCRCPF PIFKGHNTI FCSMDCVEDS AMRSTQRLLY
 701 SFLMG

11AA_SEQUENCE 1.0
 PI:T51199 hypothetical protein B7N4.60 [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C>Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
 C:Accession: T51199
 R:Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.;
 Nyakatura, G.; Mewes, H.W.; Mannhaupt, G.
 submitted to the Protein Sequence database, July 2000
 A:Reference number: 225286
 A:Accession: T51199
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-422 <SCH>
 A:Cross-references: EMBL:AL390218; GSPDB:GN00116; NCSP:B7N4.60
 A:Experimental source: BAC clone B7N4; strain OR74A
 C:Genetics:
 A:Gene: NCSP:B7N4.60
 A:Map position: 6

T51199 Length: 422 April 1, 2002 16:31 Type: P Check: 9296
 1 MDNLNRMGAR GGGGLPGHL DRLFPFEMD TAMEARVRA LMAEFGTPG
 51 RYGRSDSLE RLREERAQRQ RQANDRYRE RRAEYQGYR LRGGSDDDA
 101 DAERGSMEER RSSRVEIQS TSQASPCIQ RYTVVRSQS RSRSSRRRR
 151 RPSDNDQTS SSQDRKPPDL HVRETSCTKH PKRRSSAVL SCKRPAYTK
 201 CHTKFEDYSC LEPPHPIPTS CHSRPRPKTP VVAKCOPPKR KPAYTPCLP
 251 PGHPTSPFS PYPARAOTCH PRASSQVCH SSKPRKATY RRRPRPRPC
 301 GPYKSRPERI YREVPYHET PYREIREVEV EYVRYVEVY EYVRYVEV
 351 PYEVNYPARY PYHVPVHVYV PQPYVYHGG GGGGXYGYG GYGHGGRYG
 401 ARADEGPRYP FKAVTWQSGP PF

11AA_SEQUENCE 1.0
 PI:T18785 hypothetical protein B0564.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T18785
 R:Lightning, J.
 submitted to the EMBL Data Library, May 1996
 A:Reference number: Z19021
 A:Accession: T18785
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-912 <MIL>
 A:Cross-references: EMBL:Z73422; PIDN:CAA97769.1; GSPDB:GN00022; CESP:B0564.7
 A:Experimental source: Clone B0564
 C:Genetics:
 A:Gene: CESP:B0564.7
 A:Map position: 4
 A:Introns: 33/1; 61/3; 144/1; 187/2; 415/2; 517/3; 546/3; 591/3; 639/3; 675/2;
 712/2; 747/3; 818/1; 852/2

T18785 Length: 912 April 1, 2002 16:31 Type: P Check: 558
 1 MMSRGLPTLC RTIPORFSV AAQAGAPAE IDDFLSHIA APQKLVKNR
 51 TYLESTEEFF KMLEONPIKS IDQFITAQM AITVKTEDN KAFSIIDIA
 101 KVLKPEYEN FGPKETVDAL REVLOLNSKG KYSTDIQNF LEKISQSDL
 151 QTVPEDTLV IIRKSSSID QNVIESIATS LISRIEKELA NPADLLAILA
 201 GDGYEKSKAF HNEAFLEKAE RLVAVMGMAE KCALLKHMV NKORRQLLG
 251 AINMAISSSS QVLTVSQITS VTGSCALTY YPPKIARKIS NDLEKSNVL
 301 AQMDVLSIA DSFIRMGRD QKSNLLVRY ALENVQAHP ARLSKFSGL
 351 ARIGPSSGRP LAKALKPFLV KERASTNNW LNIVFSLAF QELEAVHADS
 401 VLNKSEVDQI MNSTWEIHDR LRKAMTLMT SSAKAVDMOG KYEGFTVKE
 451 TFARFGIND AKTIRNARQL KYSSNHSEC RYFLKSLFKL APQDTRCOLP
 501 NWEDGAFVD AYVMDPNSN LLVNTSOMGS KKRPLFFYG WLQTKONTET
 551 SGEINTVQGE QLGRLMBSA GFDPVVEFKT ELDYCSIED QOKFQNMVI
 601 TPFPADGVDP KPVCIYADI FETWTARKI HFSIYIYFK NVELAEPFKL
 651 LYTTEKKNAV HLDGSAVADF GLPMTKDDG QRPADLSRQK NDYILDFET
 701 NINNPEDGFS YCMTDCISTK NTTWVPRQLM PPSKRSKMLY LLLPYEESNI
 751 MYLSEKAYS LQLMKKHRKM GQPPQVGCY INENCOTSKY MEGCHVYCE
 801 QCLNSWNDKP CSVCLKPYTS EPTQKLROG PCGFDCSRP SSTMTIVLIP
 851 CGCHVWCQNL EDAYERNKHH LEPLIEIKY CPPEPCRIYV RKLKRFWHQ
 901 QDKHTLEMN SA

11AA_SEQUENCE 1.0
 PI:T32912 hypothetical protein C54G6.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T32912
 R:Tim-Wollam, A.; Graves, T.; Ozeraky, P.
 submitted to the EMBL Data Library, January 1998
 A:Description: The sequence of C. elegans cosmid C54G6.
 A:Reference number: Z21245
 A:Accession: T32912
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-173 <TIN>
 A:Cross-references: EMBL:AF043698; PIDN:AAB97561.1; GSPDB:GN00019; CESP:C54G6.3
 A:Experimental source: strain Bristol N2; clone C54G6
 C:Genetics:
 A:Gene: CESP:C54G6.3
 A:Map position: 1
 A:Introns: 17/2; 51/3; 94/1; 169/2

T32912 Length: 173 April 1, 2002 16:31 Type: P Check: 8718
 1 MALLKVRDEC TKLVGYOFLN SHICLSISL QLLVCCMAVA QHVNYSYTHS
 51 KILKDFLEEG SLPLEAVDAV IFDRLRHYL WGRGCAVEE LDGGGRLLM
 101 CVSHCLTVF SIPVTFISHP KPCLFWPLLF QVSWLKKFGK KLFNPFKKA
 151 QWDFRPLPLT TAWFESAWL EKF

11AA_SEQUENCE 1.0
 PI:S33300 probable substance P - smaller spotted catshark
 C:Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted

dogfish)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999
 C:Accession: S33300
 R:Maugh, D.; Wang, Y.; Hazou, N.; Balment, R.J.; Conlon, J.M.
 Eur. J. Biochem. 214, 469-474, 1993
 A>Title: Primary structures and biological activities of substance-P-related peptides from the brain of the dogfish, *Scyliorhinus canicula*.
 A:Reference number: S33300; MUID:93292508
 A:Accession: S33300
 A:Molecule type: protein
 A:Residues: 1-11 <MAU>
 A:Experimental source: brain
 C:Function:
 A:Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions
 A>Note: substance P is derived by post-translational processing of preprotachykinin A
 C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
 F:11/Modified site: amidated carboxyl end (Met) #status predicted

S33300 length: 11 April 1, 2002 16:31 Type: P Check: 4938 ..

1 KPRGQFRL M

!!AA_SEQUENCE 1.0
 P1:C72098 -Sua5/Yrc10 family protein CP0489 [imported] - Chlamydomonas pneumoniae (strains CML029 and AR39)
 C:Species: Chlamydomonas pneumoniae; Chlamydia pneumoniae
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
 C:Accession: C72098; B81572
 R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lamell, C.; Fan, J.; Olinger, L.; Grimwood, J.; Davis, R.W.; Stephens, R.S.
 Nature Genet. 21, 385-389, 1999
 A>Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 A:Reference number: A72000; MUID:99206606
 A:Accession: C72098
 A:Molecule type: DNA
 A:Residues: 1-286 <ARN>
 A:Cross-references: GB:AE001612; GB:AE001363; NID:g4376541; PIDN:AAD18419.1; PID:g4376543
 A:Experimental source: strain CML029
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, E.R.; Peterson, J.; Uterback, T.; Berry, K.; Bass, S.; Linher, K.; Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser, C.M.
 Nucleic Acids Res. 28, 1397-1406, 2000
 A>Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.
 A:Reference number: A81500; MUID:20150255
 A:Accession: B81572
 A:Molecule type: DNA
 A:Residues: 1-286 <REA>
 A:Cross-references: GB:AE002210; GB:AE002161; NID:g7189400; PIDN:AAF38319.1; PID:g7189407; GSPDB:GN00122; TIGR:CP0489
 A:Experimental source: strain AR39, HL cells
 C:Genetics:
 A:Gene: ywIC; CP0489

C72098 length: 286 April 1, 2002 16:31 Type: P Check: 9351 ..

1 MPDKKAQITF SLPEYMSAIH QGKIVALPTD TYGFLVLSLY ASEAEERLYA
 51 LKDRPSKAP ALVYNSIEDI ENISGYPLSP TAKKLAQLP GAITLVKHR
 101 NRPFKETLA FRIVDSYVR EIVDHCCTLI GTSANLSEFP SALTAQELFA
 151 DFADHLCIF DQPCSHLES TVVSDPLYI YREGLSRSY IENAGTEAK
 201 IFRRTSHAS KHKIITYVN QEQLVSLSG SLDFKGVCE HPPKNFYTR
 251 LREALKKTP SIVFIYDINT SDYPELFPFL SPYIE


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1 FINDPATTERNS on swp: * allowing 0 mismatches
1 1 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) April 1, 2002
1 GLNA_FREDI ck: 2021 len: 470 i P33035 fremyella diplosiphon (calothrix pcc
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(H)P-P-P(F)(F) LYDC
1 458: KOLOL
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(H)P-P-P(F)(F)
1 KINA_YEAST ck: 2811 len: 800 i Q01919 saccharomyces cerevisiae (baker's ye
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(Y)(Y) PGLSR
1 503: HVPRS
SERO_GALME ck: 3636 len: 167 i O76192 gallieria mellonella (wax moth). serc
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(K)P-P-P(F)(F) NGISV
1 103: DIKNI
KPRPGQFF
1 TKNL_BOVIN ck: 421 len: 130 i P01289 bos taurus (bovine). protachykinin 1
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F) GLMCK
1 58: ORIAR
RPRKQQFF
1 TKNL_HUMAN ck: 9307 len: 129 i P20366 homo sapiens (human). protachykinin
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F) GLMCK
1 58: ORIAR
RPRKQQFF
1 TKNL_MESAU ck: 219 len: 130 i Q60541 mesocricetus auratus (golden hamster
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F) GLMCK
1 58: ORIAR
RPRKQQFF
1 TKNL_MOUSE ck: 430 len: 130 i P41539 mus musculus (mouse). protachykinin
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F) GLMCK
1 58: ORIAR
RPRKQQFF
1 TKNL_RABIT ck: 1957 len: 115 i P41540 oryctolagus cuniculus (rabbit). prot
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F) GLMCK
1 58: ORIAR
RPRKQQFF
1 TKNL_RAT ck: 239 len: 130 i P06767 rattus norvegicus (rat). protachykin
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F) GLMCK
1 58: ORIAR
RPRKQQFF
1 TKNA_CHICK ck: 4995 len: 11 i P19850 gallus gallus (chicken). substance P
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(F) GLM
1 1:
RPRKQQFF
1 TKNA_HORSE ck: 4974 len: 11 i P01290 equus caballus (horse), and cavia
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F) GLM
1 1:
RPRKQQFF
1 TKNA_ONCMY ck: 4943 len: 11 i P28499 oncorhynchus mykiss (rainbow trou
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(F)(F) GLM
1 1:
KPRPHQFF
1 TKNA_SCYCA ck: 4938 len: 11 i P41333 scyllorhinus canicula (spotted do
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(F)(F) GLM
1 1:
KPRPGQFF
1 TRX_DROVI ck: 425 len: 3,828 i Q24742 drosophila virilis (fruit fly). t
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(K)P-P-P(Y)(Y) GLM
1 1:
KPRKKNYF
1 618: SDANG
GLATL
1 VNCS_DSQNV ck: 3506 len: 545 i O71153 diatraea saccharalis densovirus (
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(H)P-P-P(F)(F) LLSK
1 528: KDVEL
KPHMTEF
1 VNCS_JCDNV ck: 1211 len: 545 i Q90054 junonia coenia densovirus (jcdnv)
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(K)P-P-P(F)(F) LLSK
1 528: KDVEL
KPHMTEF
1 Y192_HUMAN ck: 6689 len: 2,124 i Q93074 homo sapiens (human). hypothetica
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(Y)(Y) LEPLP
1 1,678: YHTHL
RPRPRAYY
1 Q9X8U0 ck: 1196 len: 373 i Q9x8u0 streptomyces coelicolor. hypothet
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(Y)(F) QRMMA
1 236: VRDHF
RPRPLSYF
1 P96849 ck: 8381 len: 187 i P96849 mycobacterium tuberculosis. hypot
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(K)P(R)P-P-P(F)(Y) RGDYT
1 146: EVPAV
KPRPLLYF
1 Q9Z8R8 ck: 9351 len: 286 i Q9Z8r8 chlamydia pneumoniae (chlamydophi
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(H)P(K)P-P-P(F)(Y) TRLRE
1 241: GVCE
HPRKKNYF
1 Q9L541 ck: 2826 len: 214 i Q9L541 bacillus sp. br449. nitrile hydra
(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(F)

```

1	18: RFRPH	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(F)(W) HPRPQSEW	EARAK	
1	Q9K760	ck: 4652 len: 957 1 Q9K760 bacillus halodurans. bh3513 protein. (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(F)(W) HPRRAIFW	EDLFG	
1	594: ELIRR	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(F)(W) KPHPDIFW	IALKM	
1	Q59760	ck: 5542 len: 236 1 Q59760 schizosaccharomyces pombe (fission y (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(F)(F)		
1	148: PVGRG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(F)(F) KPRPDIFW		
1	Q9P3B8	ck: 9296 len: 422 1 Q9P3B8 neurospora crassa. conserved hypochr (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(F)(Y)	PGLRP	
1	339: KCOPP	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(F)(Y) KPRPXTYX		
1	Q13512	ck: 4657 len: 551 1 Q13512 homo sapiens (human). protein b. 6/2 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(F)(W) KPRPLTYW	KDVLV	
1	251: DHEPV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(F)(Y) KPRPLTYW		
1	Q15410	ck: 7370 len: 652 1 Q15410 homo sapiens (human). cagha5. 11/199 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPRPRXYX	LEPLP	
1	203: YHTHL	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPRPRXYX		
1	Q75557	ck: 6311 len: 2,023 1 Q75557 homo sapiens (human). opa-containing (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPRPRXYX	LEPLP	
1	1,578: YHTHL	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPRPRXYX		
1	Q9Y6V5	ck: 8014 len: 128 1 Q9Y6V5 homo sapiens (human). wugsc:h_dj0841 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F) RPRPQQFF	GLMCK	
1	58: QRIAR	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F) RPRPQQFF		
1	Q15740	ck: 4695 len: 551 1 Q15740 homo sapiens (human). b protein. 6/2 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(F)(W) KPRPLTYW	KDVLV	
1	251: DHEPV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(F)(W) KPRPLTYW		
1	Q75339	ck: 4681 len: 1,184 1 Q75339 homo sapiens (human). cartilage inte (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(F)(F) KPRPDKYF	WYHND	
1	335: CKATG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(F)(F) KPRPDKYF		
1	Q9UND7	ck: 7074 len: 2,023 1 Q9UND7 homo sapiens (human). opa-containing (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y)		
1	1,578: YHTHL	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPRPRXYX	LEPLP	
1	Q9UNV6	ck: 8071 len: 2,212 1 Q9UNV6 homo sapiens (human). thyroid hor (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPRPRXYX	LEPLP	
1	1,766: YHTHL	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPRPRXYX		
1	Q9Y494	ck: 3943 len: 72 1 Q9Y494 homo sapiens (human). gamma prepr (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F) RPRPQQFF	GLMCK	
1	23: QRIAR	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F) RPRPQQFF		
1	Q9H6A8	ck: 4809 len: 566 1 Q9H6A8 homo sapiens (human). cdna: flj22 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F) RPRPRTFE		
1	551: VLQAP	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F) RPRPRTFE	SMLAS	
1	Q9HB06	ck: 4523 len: 159 1 Q9HB06 homo sapiens (human). hypotheticala (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F) RPRPRTFE	SMLAS	
1	144: VLQAP	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F) RPRPRTFE		
1	Q9BY45	ck: 3438 len: 175 1 Q9BY45 homo sapiens (human). hcpap. 6/20 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPRPDEFY	RCPFD	
1	72: KLIYG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPRPDEFY		
1	Q9BT44	ck: 1992 len: 649 1 Q9BT44 homo sapiens (human). trinulecti (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPRPRXYX	LEPLP	
1	203: YHTHL	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPRPRXYX		
1	Q9BSU8	ck: 5292 len: 433 1 Q9BSU8 homo sapiens (human). unknown (pr (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F) RPRPRTFE	SMLAS	
1	418: VLQAP	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F) RPRPRTFE		
1	Q44981	ck: 8718 len: 173 1 Q44981 caenorhabditis elegans. c5496.3 p (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(F)(W) HPRPCLFW	PLLFQ	
1	119: VTEIS	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(F)(W) HPRPCLFW		
1	Q61761	ck: 3281 len: 206 1 Q61761 caenorhabditis elegans. f56c3.9 p (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(F)(F) KPRPQMEF	DMDHT	
1	188: RPYTE	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(F)(F) KPRPQMEF		
1	P91767	ck: 6396 len: 1,264 1 P91767 manduca sexta (tobacco hawkmoth) (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(F)(W) HPRKRVYW	MLOGD	
1	157: EPPDG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(F)(W) HPRKRVYW		

1 09L1Q7 ck: 92 len: 374 1 09L1q7 vigna unguiculata (cowpea). phosphat
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(R)P-D-P(F)(Y)
178: KNGVG RRPDPFW RCFPD

1 09LJQ8 ck: 3777 len: 307 1 09Ljq8 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(R)P-D-P(F)(Y)
123: KDAVG RRPDPFW RCFPD

1 09L1S4 ck: 4935 len: 221 1 09L1s4 prunus dulcis (almond) (prunus amygd
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(K)P(R)P-D-P(F)(Y)
30: RTKCS KRPPLQYF TINGL

1 09FV11 ck: 8335 len: 322 1 09fv11 vigna unguiculata (cowpea). phosphat
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(R)P-D-P(F)(Y)
123: KDGVC RRPDPFW RCFPD

1 09FVJ1 ck: 7946 len: 162 1 09fvj1 prunus dulcis (almond) (prunus amygd
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(K)P(R)P-D-P(F)(Y)
19: RTKCS KRPPLQYF TINGL

1 09FVJ0 ck: 5836 len: 172 1 09fvj0 prunus dulcis (almond) (prunus amygd
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(K)P(R)P-D-P(F)(Y)
21: KRPCS KRPPLQYF TINGL

1 09FM61 ck: 7091 len: 685 1 09fm61 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(H)P(H)P-D-P(F)(Y)
230: DHPRS HPHPLSFF PTQAS

1 09CAP2 ck: 8387 len: 421 1 09cap2 arabidopsis thaliana (mouse-ear cress)
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(K)P(K)P-D-P(W)(Y)
145: SRIRH KRPVQWY IGDSK

1 09AWT8 ck: 2435 len: 362 1 09awt8 oryza sativa (rice). putative phosphat
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(R)P-D-P(F)(Y)
126: KNAV G RRPDPFW RCFPD

1 088542 ck: 415 len: 2,074 1 088542 mus musculus (mouse). opa-containing
(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(R)P-D-P(F)(Y)
1,638: YHTHL RRPRAFY LEPLP

1 09D788 ck: 7438 len: 158 1 09d788 mus musculus (mouse). 2310022a04rik

1 (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)
(R)P(R)P-D-P(F)(Y)
RRPDPFW RCFPD

109: KLIVG

Databases searched:
SWISS-PROT, Release 39.2, Released on 24Aug2001, Formatted on 27Aug2001
SPRINT, Release 17.0, Released on 1Jun2001, Formatted on 26Jun2001

Total finds: 73
Total length: 182,937,156
Total sequences: 573,564
CPU time: 16:28.16

11AA_SEQUENCE 1.0 STANDARD: PRT: 470 AA.
 ID_GINA_FREDDI_3
 AC_P33035;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE-AMMONIA LIGASE).
 GN_GINA.
 OS_Fremyella diplosiphon (Calothrix PCC 7601).
 OC_Bacteria; Cyanobacteria; Nostocales; Rivulariaceae; Fremyella.
 OX_NCB1_TaxID=1197;
 RN [1]
 RP_SEQUENCE FROM N.A.
 RX_MEDLINE=93129187; PubMed=1362348;
 RA_Elmerjani K., Liotenberg S., Houmad J., de Marsac N.T.;
 RT "Molecular characterization of the gene encoding glutamine synthetase
 in the cyanobacterium Calothrix sp. PCC 7601.";
 RL_Biochem. Biophys. Res. Commun. 189:1296-1302(1992).
 CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + GLUTAMINE +
 ORTHOPHOSPHATE.
 CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
 HEXAGON.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR_EMBL: L05609; AAA3288.1; -
 DR_PIR: JCI403; JCI403.
 DR_HSSP: P06201; 2LGS.
 DR_InterPro: IPR001691; GLN_synth.
 DR_InterPro: IPR001637; Glna_adenyltn.
 DR_Pfam: PF00120; gln-synt; 1.
 DR_ProDom: PD001057; Glna_adenyltn; 1.
 DR_PROSITE: PS00180; GlnA_1; 1.
 DR_PROSITE: PS00181; GlnA_ATP; 1.
 DR_PROSITE: PS00182; GlnA_ADENYLATION; 1.
 DR_Ligase.
 KW_INIT MET 0 0 BY SIMILARITY.
 FT_SEQUENCE 470 AA; 52919 MW; ADD7B49A7789E832 CRC64;
 SO_GINA_FREDDI Length: 470 April 1, 2002 16:32 Type: P Check: 2021 ..

DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE SERINE/THREONINE-PROTEIN KINASE KIN4 (EC 2.7.1.1).
 GN_KIN4 OR KIN31 OR KIN3 OR YOR233W OR O5220.
 OS_Saccharomyces cerevisiae (Baker's yeast).
 OC_Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC_Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX_NCB1_TaxID=4932;
 RN [1]
 RP_SEQUENCE FROM N.A.
 RX_MEDLINE=93220392; PubMed=8465601;
 RA_Kandouris N.G., Burke D.J., Creutz C.E.;
 RT "Cloning and genetic analysis of the gene encoding a new protein
 kinase in Saccharomyces cerevisiae.";
 RL_Yeast 9:141-150(1993).
 RN [2]
 RP_SEQUENCE FROM N.A.
 RC_STRAIN=S288C / FY1679;
 RX_MEDLINE=97127829; PubMed=8972580;
 RA_Boyer J., Michaux G., Fairhead C., Gallion L., Dujon B.;
 RT "Sequence and analysis of a 26.9 kb fragment from chromosome XV of
 the yeast Saccharomyces cerevisiae.";
 RL_Yeast 12:1575-1586(1996).
 CC -1- FUNCTION: THIS PROTEIN IS PROBABLY A SERINE/THREONINE PROTEIN
 KINASE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR_EMBL: X67916; CAA4815.1; -
 DR_EMBL: Z75141; CAA39453.1; -
 DR_PIR: S29344; S29344.
 DR_HSSP: S63450; 1A06.
 DR_SGD: S0005759; KIN4.
 DR_InterPro: IPR000719; Euk_pkinase.
 DR_InterPro: IPR002290; Ser_thr_kin_actsite.
 DR_Pfam: PF00069; pkinase; 1.
 DR_SMAP: SM00220; S_TKc; 1.
 DR_PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR_PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR_PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW_Transferase; Serine/threonine-protein kinase; ATP-binding.
 FT_DOMAIN 46 313 PROTEIN KINASE.
 FT_NP_BIND 52 60 ATP (BY SIMILARITY).
 FT_BINDING 80 80 ATP (BY SIMILARITY).
 FT_ACT_SITE 175 175 BY SIMILARITY.
 SO_SEQUENCE 800 AA; 90087 MW; 655B5B5EB0BACF65 CRC64;
 KIN4_YEAST Length: 800 April 1, 2002 16:32 Type: P Check: 2811 ..

1 MASVPRKHTY GGNVYIDRRD HSLORNNEL HPHKNRKH ATFGPIIGS
 51 TLGEGFGRV KLGWTKASS NEVPKQVAIK LIRRDITKID ADKEIKYRE
 101 INALKHLTHP NIIVLEEVQ NSKYGIYVE FVSGGEFYKY IQKRRLKES
 151 SACRLFAQLI SGVNYMHYKG LVHRDLKLEN LLDKHNLY IDDFGVNER
 201 FEDNELKRTS GSPCYAAPE LVSTKAYEA RKADWVSCGV IIVAMLGYL
 251 PMDDHNPPT GDIARLYKY ITQPLKPEE YTFPIPDLL RRLVNPBR
 301 RINLQITKRH VWLKPHEAFL SIQPNYWDEN LQKERPRPN KGVYGHSTY
 351 SSSASSYSKS RDRNSLIIES TLEQHRMSPQ LATSRAASPT FSTGSKVVLN
 401 DTKNDKESN INERTSASC RYTRDSKNG QTOIEGVASR HSSRGKHTS

451 VAGLVITPGS PTTARTRNAP SSKLTHEVND SSQTSFTQEE FHRIGNVHV
 501 KSRRPRTSYR PGLSRNTADN SLADIPVKNL GSNRLIDAK DPLPLAIHD
 551 TNKATISNNS IMLESGPAA KTSPPVHYA IGDINHDKP ITEVIDKINK
 601 LETHKAENG FPRESIDPES TSTILVTEKP TNSDEDEHVE SOLENVGHSS
 651 NKSASSDKD SKKIYEKKRF SPMLSYSSIN GSRSTVESRT SKKNAPPVSS
 701 RNPSSGNSRS NIKITQOQPR NISDRVPND KKIINDRIKD NADVAESEN
 751 PGRSVRASVM VSTLRENSRS ELSNEGNNVE AQTSTARKVL NFKRRSMRV

11AA SEQUENCE 1.0
 ID SERO_GALME 3 STANDARD; PRT: 167 AA.
 AC 076192;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DE SEROIN PRECURSOR (SILK 23 KDA GLYCOPROTEIN).
 OS Galleria mellonella (wax moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Pyralidae; Pyralidae; Galleriinae; Galleria.
 OX NCBI_TaxID=7137;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-31.
 RC TISSUE=SILK gland;
 RX MEDLINE=98288272; PubMed=9624126;
 RA Zurovec M., Yang C., Kodrik D., Sehna F.;
 RT "Identification of a novel type of silk protein and regulation of its
 expression.";
 RL J. Biol. Chem. 273:15423-15428(1998).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- TISSUE SPECIFICITY: PRODUCED BY BOTH THE POSTERIOR (PSC) AND
 CC MIDDLE (MSG) SECTIONS OF SILK GLANDS.
 CC -1- DEVELOPMENTAL STAGE: SEROIN MRNA IS HIGH IN THE SILK GLANDS OF
 CC FEEDING LARVAE, DECLINES AT ECDYSIS, REACHES A MAXIMUM DURING
 CC COOON SPINNING, AND THEREAFTER RAPIDLY DROPS TO AN UNDETECTABLE
 CC LEVEL.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF009828; AAC25171.1;
 KW SILK; Glycoprotein; Signal; Repeat.
 FT CHAIN 1 167 SEROIN.
 FT REPEAT 18 167 1-1.
 FT REPEAT 38 46 1-2.
 FT REPEAT 56 64 2-1.
 FT REPEAT 76 78 2-2.
 FT REPEAT 79 81 2-3.
 FT REPEAT 82 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 167 AA; 18088 MW; 27A6ABEB62774EB9 CRC64;

SERO_GALME Length: 167 April 1, 2002 16:32 Type: P Check: 3636

1 MAYKILFILS FVALSSAGFV WYDDNNNSFP KLRLVYVPL POPPLPLNIP
 51 GLQGPPLPQ PPLPLGFDFS PILPLPPLP IPPLPLPPF INIPAPEDIK
 101 NIKPKPGQFF NGISVSRSG YALDKGNRV KTGSTAVLIN DNGEVNETHV
 151 GDNPKPFES RKSSSN

11AA SEQUENCE 1.0
 ID TKNL_BOVIN 0 STANDARD; PRT: 130 AA.
 AC P01289; P01291; P04091; P20773;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ I PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TAC1 OR NKA OR TAC2 OR NKA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RX MEDLINE=85086245; PubMed=6083453;
 RA Nawa H., Kotani H., Nakanishi S.;
 RT "Tissue-specific generation of two preprotachykinin mRNAs from one
 RT gene by alternative RNA splicing.";
 RL Nature 312:729-734(1984).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RX MEDLINE=84039802; PubMed=6195531;
 RA Nawa H., Hirose T., Takashima H., Inayama S., Nakanishi S.;
 RT "Nucleotide sequences of cloned cDNAs for two types of bovine brain
 RT substance P precursor.";
 RL Nature 306:32-36(1983).
 RN [3]
 RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
 RC TISSUE=Hypothalamus;
 RX MEDLINE=91209287; PubMed=1708336;
 RA Chivakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
 RA Ivell R.;
 RT "Tachykinin (substance-P) gene expression in Leydig cells of the
 RT human and mouse testis.";
 RL Endocrinology 128:2441-2448(1991).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA: ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X00075; CAA24939.1; -
 DR EMBL: X00075; CAA24940.1; -
 DR EMBL: X00075; CAA24941.1; -
 DR EMBL: X00075; CAA24942.1; -
 DR EMBL: X00076; CAA24943.1; ALT_SEQ.
 DR EMBL: X02351; CAA26206.1; -
 DR EMBL: X01396; CAA26206.1; JOINED.
 DR EMBL: X01397; CAA26206.1; JOINED.
 DR EMBL: X01398; CAA26206.1; JOINED.
 DR EMBL: X01399; CAA26206.1; JOINED.
 DR EMBL: X01400; CAA26206.1; JOINED.
 DR EMBL: M68911; AAA30724.1; -
 DR EMBL: M68912; AAA30725.1; -
 DR PIR: A01557; SPBOA.
 DR PIR: A01559; SPBOB.
 DR PIR: A05093; A05093.
 DR PIR: B25067; B25067.
 DR InterPro: IPR003580; Protachykinin.

DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR ProDom: PD005598; Protachykinin; 1.
 DR SMART: SM00203; TK; 2.
 DR PROSITE: PS00267; TACHYKININ; 2.
 DR Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 RW Amidation; Alternative splicing; Signal; Neurotransmitter.
 FT SIGNAL 1 19
 FT PROPEP 20 56 POTENTIAL.
 FT PEPTIDE 58 68 SUBSTANCE P.
 FT PEPTIDE 72 107 NEUROPEPTIDE K.
 FT PEPTIDE 72 107 NEUROPEPTIDE GAMMA 1ST PART.
 FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 2ND PART.
 FT PEPTIDE 98 107 NEUROKININ A.
 FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
 FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
 FT MOD_RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
 FT VASPLIC 74 88 MISSING (IN ISOFORM GAMMA AND ISOFORM
 FT VASPLIC 97 114 MISSING (IN ISOFORM ALPHA AND ISOFORM
 FT VASPLIC 115 115 DELTA).
 FT VASPLIC 115 115 V -> M (IN ISOFORM ALPHA AND ISOFORM
 FT CONFLICT 121 121 DELTA).
 FT CONFLICT 121 121 V -> A (IN REF. 3).
 SQ SEQUENCE 130 AA; 15076 MW; CE2A28572305DEB7 CRC64;
 TKNL_BOVIN Length: 130 April 1, 2002 16:32 Type: P Check: 421 ..

1 MKILVAVAVI FFISTQLSAE EIGANDDEFY WSDWSDSDOI KEENPEPEH
 51 ILQRIARRRK PQOFFGLMGR RDADSSIEKQ VALLKALYGH GOLSHRRHKT
 101 DSFVGLMGR ALNSVAYERS VMQDYERRR

11AA-SEQUENCE 1.0 STANDARD; PRT; 129 AA.
 AC -P20366; Q00072; Q06000; Q06001;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE PROTACHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
 DE (NKA) (SUBSTANCE K) (NEUROKININ I); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
 DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
 GN TAC1 OR NKKA OR TAC2 OR NKA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 OX [1]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RX MEDLINE=87030957; PubMed=3770210;
 RA Hartman A.J., Armstrong A., Pascual J.C., Chapman K., Rosie R.,
 RA Curtis A.J., Goling J., Edwards C.R.W., Fink G.;
 RT "cDNA sequence of human beta-preprotachykinin, the common precursor
 RT to substance P and neurokinin A.";
 RL FEBS Lett. 208:67-72(1986).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM BETA).
 RC TISSUE=Brain;
 RA Tan A., Too H.P.;
 RL Submitted (Oct-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
 RC TISSUE=Testis;
 RX MEDLINE=91209287; PubMed=1708336;
 RA Chivakata C., Brackmann B., Hunt N., Davidoff M., Schlize W.,
 RA Iveli R.;
 RT "Tachykinin (substance-P) gene expression in Leydig cells of the
 RT human and mouse testis.";
 RL Endocrinology 128:2441-2448(1991).
 RN [4]
 RP SEQUENCE OF 98-107.
 RX MEDLINE=87275962; PubMed=3038549;

RA Theodorsson-Norheim E., Joernvall H., Andersson M., Norheim I.,
 RA Oeberg K., Jacobsson G.;
 RT "Isolation and characterization of neurokinin A, neurokinin A(3-10)
 RT and neurokinin A(4-10) from a neutral water extract of a metastatic
 RT ileal carcinoid tumour.";
 RL Eur. J. Biochem. 166:693-697(1987).
 RN [5]
 RP SEQUENCE OF 36-118 FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Blood, and Brain;
 RA Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;
 RT "Identification of a delta isoform of preprotachykinin mRNA in human
 RT mononuclear phagocytes and lymphocytes.";
 RL Submitted (Feb-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 111-126.
 RC TISSUE=Adrenal medulla;
 RX MEDLINE=9113394; PubMed=2284201;
 RA McGregor G.P., Conlon J.M.;
 RT "Characterization of the C-terminal flanking peptide of human
 RT beta-preprotachykinin.";
 RL Peptides 11:907-910(1990).
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -!- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA, BETA (SHOWN HERE),
 CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
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 CC or send an email to license@sib-sib.ch).
 CC -----

DR EMBL: X54469; CAA8351.1; -;
 DR EMBL: U37529; AAA79195.1; -;
 DR EMBL: M68906; AAA60159.1; -;
 DR EMBL: M68907; AAA60160.1; -;
 DR EMBL: AF050656; AAC15702.1; -;
 DR EMBL: AF050658; AAC15704.1; -;
 DR PIR: A24805; A24805.
 DR PIR: S00069; S00069.
 DR MIM: 162320;
 DR InterPro: IPR003580; Protachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR ProDom: PD005598; Protachykinin; 1.
 DR SMART: SM00203; TK; 2.
 DR PROSITE: PS00267; TACHYKININ; 2.
 DR Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 KW Amidation; Alternative splicing; Signal; Neurotransmitter.
 FT SIGNAL 1 19
 FT PROPEP 20 56 POTENTIAL.
 FT PEPTIDE 58 68 SUBSTANCE P.
 FT PEPTIDE 72 107 NEUROPEPTIDE K.
 FT PEPTIDE 72 107 NEUROPEPTIDE GAMMA 1ST PART.
 FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 2ND PART.
 FT PEPTIDE 98 107 NEUROKININ A.
 FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE.
 FT MOD_RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
 FT MOD_RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
 FT VASPLIC 74 88 MISSING (IN ISOFORM GAMMA AND ISOFORM
 FT VASPLIC 97 114 MISSING (IN ISOFORM ALPHA AND ISOFORM
 FT VASPLIC 115 115 DELTA).
 FT VASPLIC 115 115 V -> M (IN ISOFORM ALPHA AND ISOFORM
 FT CONFLICT 87 87 L -> P (IN REF. 4).
 FT CONFLICT 87 87 L -> P (IN REF. 4).
 SQ SEQUENCE 129 AA; 15003 MW; 51412C1692368DE4 CRC64;

TKNL_HUMAN Length: 129 April 1, 2002 16:32 Type: P Check: 9307 ..

1 MKILVALAE FLVSTQLFAE EIGANDDLNY WSDWYSDQI KEELPEPFH
51 ILORIARRPK POOFGLMGK RDADSSIEKQ VALLKALYGH GQISHRHHT
101 DSFVGLMGKR ALNSVAFERS AMONERRR

11AA_SEQUENCE 1.0 STANDARD; PRT; 130 AA.
ID TKNL_MESAU
AC 060541; P49110;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTECHKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
(NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
GN TAC1 OR NKMA OR TAC2 OR NKA.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS BETA AND GAMMA).
RC STRAIN=AUFA; TISSUE=Brain;
RA Heiland A., Kruehoffer M., Juegen Maegert H.J., Forssmann W.G.;
RL Submitted (Jul-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: ALPHA, BETA (SHOWN HERE),
CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X30662; CAAS6691.1; -
DR EMBL: X30663; CAAS6692.1; -
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR ProDom: PD005598; Protachykinin; 1.
DR SMART: SM00203; TK; 2.
DR PROSITE: PS00267; TACHYKININ; 2.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Alternative splicing; Signal; Neurotransmitter.
FT SIGNAL 1 19
FT PROPEP 20 56
FT PEPTIDE 58 68 SUBSTANCE P.
FT PEPTIDE 72 107 NEUROPEPTIDE P.
FT PEPTIDE 72 107 NEUROPEPTIDE K.
FT PEPTIDE 72 73 NEUROPEPTIDE GAMMA 1ST PART.
FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 2ND PART.
FT PEPTIDE 89 107 NEUROKININ A.
FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
FT MOD.RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
FT MOD.RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
FT VARSPLIC 74 88 MISSING (IN ISOFORM GAMMA).
SQ SEQUENCE 130 AA; 14907 MW; CC92E937A646F2E CRC64;

TKNL_MESAU Length: 130 April 1, 2002 16:32 Type: P Check: 219 ..

1 MKILVALAE FLVSTQLFAE EIGANDDLNY WSDWYSDQI KEELPEPFH
51 ILORIARRPK POOFGLMGK RDADSSIEKQ VALLKALYGH GQISHRHHT

101 DSFVGLMGKR ALNSVAFERS AMONERRR

11AA_SEQUENCE 1.0 STANDARD; PRT; 130 AA.
ID TKNL_MOUSE
AC P41539; Q00073;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PROTECHKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A
(NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE
DE GAMMA; C-TERMINAL FLANKING PEPTIDE].
GN TAC1 OR NKMA OR TAC2 OR NKA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=ICR; TISSUE=Brain;
RA Kato K., Muekata E., Hosaka M., Murakami K., Nakayama K.;
RT Cloning and sequence analysis of mouse CDNA encoding
RT preproachykinin A and B.
RL Biomed. Res. 14:253-259(1993).
RN [2]
RP SEQUENCE OF 36-122 FROM N.A. (ISOFORMS BETA AND GAMMA).
RC TISSUE=Brain;
RX MEDLINE=91209287; PubMed=1708336;
RA Chivakata C., Brackmann B., Hunt N., Davidoff M., Schulze W.,
RA Iwell R.;
RT Tachykinin (substance-P) gene expression in Leydig cells of the
RT human and mouse testis.
RL Endocrinology 128:2441-2448(1991).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: ALPHA, BETA (SHOWN HERE),
CC GAMMA AND DELTA; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D17584; BAA04508.1; -
DR EMBL: M68908; AAA39969.1; -
DR EMBL: M68909; AAA39970.1; -
DR MGD: MGI:98474; TACL.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR ProDom: PD005598; Protachykinin; 1.
DR SMART: SM00203; TK; 2.
DR PROSITE: PS00267; TACHYKININ; 2.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Alternative splicing; Signal; Neurotransmitter.
FT SIGNAL 1 19
FT PROPEP 20 56
FT PEPTIDE 58 68 SUBSTANCE P.
FT PEPTIDE 72 107 NEUROPEPTIDE P.
FT PEPTIDE 72 73 NEUROPEPTIDE K.
FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 1ST PART.
FT PEPTIDE 89 107 NEUROPEPTIDE GAMMA 2ND PART.
FT PEPTIDE 89 107 NEUROKININ A.
FT PEPTIDE 111 126 C-TERMINAL FLANKING PEPTIDE (POTENTIAL).
FT MOD.RES 68 68 AMIDATION (G-69 PROVIDE AMIDE GROUP).
FT MOD.RES 107 107 AMIDATION (G-108 PROVIDE AMIDE GROUP).
FT VARSPLIC 74 88 MISSING (IN ISOFORM GAMMA).
SQ SEQUENCE 130 AA; 15045 MW; 7BE8DA15FE272F8 CRC64;

TKN1_Mouse Length: 130 April 1, 2002 16:32 Type: P Check: 430 ..

1 MKILVAVAF ELVSTQLFAE EIDANDLNV WSDMSDSDOI KEAPEPEEH

51 LLQRIARRPK PQQFFGLMGK RQADSSVERQ VALLKALYGH GOISHKRHKT

101 DSFVQMGKR ALNSVAYERS AMONYERRRK

11AA_SEQUENCE 1.0 STANDARD: PRT: 115 AA.

1D_TKN1_RABIT 4 STANDARD: PRT: 115 AA.

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PROTAHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A

DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE GAMMA; C-TERMINAL

DE FLANKING PEPTIDE].

GN TACT OR NKNA OR TAC2 OR NKA.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=93371392; PubMed=8363593;

RA Maegret H.J., Heltland A., Rose M., Forssmann W.G.;

RT "Nucleotide sequence of the rabbit gamma-preprotachykinin I cDNA.";

RL Biochem. Biophys. Res. Commun. 195:128-131(1993).

RN [2]

RP SEQUENCE OF 72-92.

RA Kage R., McGregor G.P., Thim L., Conlon J.M.;

RT "Gamma-neuropeptide K: a peptide isolated from rabbit gut that is

derived from gamma-preprotachykinin.";

RL Regul. Pept. 18:346-346(1987).

RN [3]

RP FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,

EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND

SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH

MUSCLES.

CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: ALPHA, BETA (SHOWN HERE),

CC GAMMA AND DELTA, ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

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DR EMBL; X62994; CAA44728.1; -

DR PIR; S18922; S18922.

DR InterPro; IPR003580; Protachykinin.

DR InterPro; IPR002040; Tachykinin.

DR Pfam; PF02202; Tachykinin.1.

DR ProDom; PD005598; Protachykinin.1.

DR SMART; SM00203; TK.2.

DR PROSITE; PS00267; TACHYKININ.2.

KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;

AMAdation: Alternative splicing; Signal; Neurotransmitter.

FT SIGNAL 1 19 POTENTIAL.

FT PEPTIDE 20 56 SUBSTANCE P.

FT PEPTIDE 58 68 NEUROPEPTIDE GAMMA.

FT PEPTIDE 72 92 NEUROPEPTIDE GAMMA.

FT PEPTIDE 83 92 NEUROKININ A.

FT PEPTIDE 96 111 C-TERMINAL FLANKING PEPTIDE.

FT MOD_RES 68 68 AMADATION (G-69 PROVIDE AMIDE GROUP).

FT MOD_RES 92 92 AMADATION (G-93 PROVIDE AMIDE GROUP).

SO SEQUENCE 115 AA; 13370 MW; 5E76F7C9B10E1C CRC64;

TKN1_RABIT Length: 115 April 1, 2002 16:32 Type: P Check: 1957 ..

1 MKILVALAVL ALVSTQLFAE DIRANDLNV WSDMSDSDOI KEAPEPEEH

51 LLQRIARRPK PQQFFGLMGK RQAGHGQISH KHKKIDSFVG LMGKRALNSV

101 AYERSAMONY ERRRK

11AA_SEQUENCE 1.0 STANDARD: PRT: 130 AA.

1D_TKN1_RAT 4 STANDARD: PRT: 130 AA.

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE PROTAHYKININ 1 PRECURSOR (PPT) [CONTAINS: SUBSTANCE P; NEUROKININ A

DE (NKA) (SUBSTANCE K) (NEUROMEDIN L); NEUROPEPTIDE K (NPK); NEUROPEPTIDE

DE GAMMA; C-TERMINAL FLANKING PEPTIDE].

GN TACT OR NKNA OR TAC2 OR NKA.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).

RC MEDLINE=9031040; PubMed=1695945;

RA Carter M.S., Krause J.E.;

RT "Structure, expression, and some regulatory mechanisms of the rat

preprotachykinin gene encoding substance P, neurokinin A,

neuropeptide K, and neuropeptide gamma.";

RL J. Neurosci. 10:2203-2214(1990).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).

RA Krause J.E., Chirgwin J.M., Carter M.S., Xu Z.S., Hershey A.D.;

RT "Three rat preprotachykinin mRNAs encode the neuropeptides substance

P and neurokinin A.";

RL Proc. Natl. Acad. Sci. U.S.A. 84:881-885(1987).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM GAMMA).

RX MEDLINE=87025808; PubMed=2429656;

RA Kawaguchi Y., Hoshimaru M., Nawa H., Nakanishi S.;

RT "Sequence analysis of cloned cDNA for rat substance P precursor:

existence of a third substance P precursor.";

RL Biochem. Biophys. Res. Commun. 139:1040-1046(1986).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM DELTA).

RC TISSUE=Dorsal root ganglion;

RX MEDLINE=91085565; PubMed=1702066;

RA Hartmar A.J., Hyde V., Chapman K.E.;

RT "Identification and cDNA sequence of delta-preprotachykinin, a fourth

spleting variant of the rat substance P precursor.";

RL FEBS Lett. 275:22-24(1990).

RN [5]

RP SEQUENCE OF 1-41 FROM N.A.

RX MEDLINE=93192337; PubMed=8448217;

RA Chapman K.E., Lyons V., Hartmar A.J.;

RT "The sequence of 5' flanking DNA from the rat preprotachykinin gene;

analysis of putative transcription factor binding sites.";

RL Biochim. Biophys. Acta 1172:361-363(1993).

CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,

EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND

SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH

MUSCLES.

CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: ALPHA, BETA (SHOWN HERE),

CC GAMMA AND DELTA, ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

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DR EMBL: M34162; AAA41926.1; -
 DR EMBL: M34159; AAA41926.1; JOINED.
 DR EMBL: M34160; AAA41926.1; JOINED.
 DR EMBL: M34161; AAA41926.1; JOINED.
 DR EMBL: M34184; AAA41925.1; -
 DR EMBL: M34183; AAA41929.1; -
 DR EMBL: M15191; AAA41928.1; -
 DR EMBL: M14312; AAA41927.1; -
 DR EMBL: M107328; AAA41924.1; -
 DR EMBL: X56306; CAA39752.1; -
 DR PIR: A26590; A26580.
 DR PIR: B26590; B26590.
 DR PIR: C26590; C26590.
 DR PIR: A37163; A37163.
 DR PIR: S12958; S12958.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR ProDom: PD005598; Protachykinin; 1.
 DR SMART: SM00203; TK; 2.
 DR PROSITE: PS00267; TACHYKININ; 2.
 DR Tachykinin; Neuropeptide; Cleavage on pair of basic residues; Amidation; Alternative splicing; Signal; Neurotransmitter.
 KW SIGNAL.
 FT PROPEP 1 19
 FT PEPTIDE 20 56
 FT PEPTIDE 58 68
 FT PEPTIDE 72 107
 FT PEPTIDE 72 73
 FT PEPTIDE 89 107
 FT PEPTIDE 98 107
 FT PEPTIDE 111 126
 FT MOD.RES 68 68
 FT MOD.RES 107 107
 FT VARSPIC 74 88
 FT VARSPIC 97 114
 FT VARSPIC 115 115
 FT SEQUENCE 130 AA; 15001 MW; B22FE860DCD75A CRC64;
 TKIN_RAT Length: 130 April 1, 2002 16:32 Type: P Check: 239 ..
 1 MKILVAVAF FLYSTQLFAE EIGANDLNL WSDWSDQI KEAMPEPEFH
 51 LQRIARRPR PQQFGFMK RDADSTIEQ VALLKALYGH GQISKRHHT
 101 DSIVGLMKR ALNSVAYERS AMONYERRRR
 11AA_SEQUENCE 1.0
 ID TKNA_CHICK J STANDARD; PRT; 11 AA.
 AC P19850;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine; PubMed=2452461;
 RX MEDLINE=88204263; PMID=2452461;
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
 RT "[Arg3]substance P and neurokinin A from chicken small intestine."; Regul. Pept. 20:171-180(1988).
 RL -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH MUSCLES.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.

DR PIR: JN0023; JN0023. Protachykinin.
 DR InterPro: IPR003580; Tachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 DR Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 KW MOD.RES 11 11
 FT SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C67 CRC64;
 TKNA_CHICK Length: 11 April 1, 2002 16:32 Type: P Check: 4995 ..
 1 RRPQQFFGL M
 11AA_SEQUENCE 1.0
 ID TKNA_HORSE J STANDARD; PRT; 11 AA.
 AC P01290;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Equus caballus (Horse), and Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NCBI_TaxID=9796, 10141;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Horse;
 RA Studer R.O., Trzeclak A., Lergler W.;
 RT "Isolation and amino-acid sequence of substance P from horse intestine.";
 RL Helv. Chim. Acta 56:860-866(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C. porcellus;
 RX MEDLINE=90044685; PubMed=2478925;
 RA Murphy R.;
 RT "Primary amino acid sequence of guinea-pig substance P."; Neuropeptides 14:105-110(1989).
 RL -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH MUSCLES.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 CC PIR: A01558; SPRO.
 DR PIR: A60554; A60554.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD.RES 11 11
 FT SEQUENCE 11 AA; 1349 MW; 3E757EE3C9D6C67 CRC64;
 TKNA_HORSE Length: 11 April 1, 2002 16:32 Type: P Check: 4974 ..
 1 RRPQQFFGL M
 11AA_SEQUENCE 1.0
 ID TKNA_ONCMY J STANDARD; PRT; 11 AA.
 AC P28499;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 NCBI_TaxID=8022;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 of the cod and trout.";
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -I- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: S23307; S23307.
 DR PIR: S23308; S23308.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KM Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

TKNA_ONCMY Length: 11 April 1, 2002 16:32 Type: P Check: 4943 ..

1 KRPQGQFGL M

11AA_SEQUENCE 1.0
 ID TKNA_SCYCA 6 STANDARD; PRT; 11 AA.
 AC P41333;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE SUBSTANCE P.
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphi; Galeoidae; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.
 OX NCBI_TaxId=7830;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=93292508; PubMed=7685693;
 RA Maugh D., Wang Y., Hazon N., Balmert R.J., Conlon J.M.;
 RT "Primary structures and biological activities of substance-P-related
 peptides from the brain of the dogfish, Scyliorhinus canicula.";
 RL Eur. J. Biochem. 214:469-474(1993).
 CC -I- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -I- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: S33300; S33300.
 DR InterPro: IPR003580; Protachykinin.
 DR InterPro: IPR002040; Tachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR SMART: SM00203; TK; 1.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KM Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

TKNA_SCYCA Length: 11 April 1, 2002 16:32 Type: P Check: 4938 ..

1 KRPQGQFGL M

11AA_SEQUENCE 1.0
 ID TRX_DROVI 1 STANDARD; PRT; 3828 AA.
 AC Q24742;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE TRITHORAX PROTEIN.

GN TRX.
 OS Drosophila virilis (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96100387; PubMed=8555104;
 RA Tillib S., Sedkov Y., Mizrokh L., Mazo A.;
 RT "Conservation of structure and expression of the trithorax gene
 between Drosophila virilis and Drosophila melanogaster.";
 RL Mech. Dev. 53:113-122(1995).
 CC -I- FUNCTION: FUNCTIONS IN SEGMENT DETERMINATION THROUGH INTERACTION
 WITH GENES OF TRITHORAX (BX-C) AND ANTENNAPEDIA (ANT-X) COMPLEXES.
 CC IT CAN BEHAVE AS AN ACTIVATOR OF BX-C.
 CC -I- SUBCELLULAR LOCATION: NUCLEAR.
 CC -I- SIMILARITY: BELONGS TO THE TRITHORAX FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -I- SIMILARITY: CONTAINS 1 'SET' DOMAIN.
 CC -I- SIMILARITY: CONTAINS 5 PHD-TYPE ZINC FINGERS.
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 CC EMBL: Z50038; CAA90349.1; -.
 DR HSSP: P04002; IWRP.
 DR FLYBASE: FBgn0014844; DvTr\trx.
 DR InterPro: IPR003889; Fyrich_C.
 DR InterPro: IPR003888; Fyrich_N.
 DR InterPro: IPR001965; PHD.
 DR InterPro: IPR003616; PostSET.
 DR InterPro: IPR001214; SET.
 DR InterPro: IPR001841; ZnF_ring.
 DR InterPro: IPR001628; Zf-C4.
 DR Pfam: PF00628; PHD; 2.
 DR Pfam: PF00856; SET; 1.
 DR SMART: SM00542; FYRIC; 1.
 DR SMART: SM00541; FYRNC; 1.
 DR SMART: SM00249; PHD; 4.
 DR SMART: SM00508; PostSET; 1.
 DR SMART: SM00184; RING; 2.
 DR SMART: SM00317; SET; 1.
 DR SMART: SM00399; ZNF_C4; 1.
 DR PROSITE: PS50280; SET; 1.
 KW Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
 KW Nuclear protein; Developmental protein; Activator.
 FT ZN_FING 1251 1334 PHD-TYPE 1.
 FT ZN_FING 1335 1380 PHD-TYPE 1.
 FT ZN_FING 1408 1469 PHD-TYPE 3.
 FT ZN_FING 1708 1767 PHD-TYPE 4 (ATYPICAL).
 FT ZN_FING 1768 1818 PHD-TYPE 5 (ATYPICAL).
 FT DOMAIN 3701 3810 SET.
 FT DOMAIN 28 41 POLY-ALA.
 FT DOMAIN 66 71 POLY-ASP.
 FT DOMAIN 160 164 POLY-ASP.
 FT DOMAIN 173 182 POLY-ALA.
 FT DOMAIN 221 228 POLY-GLN.
 FT DOMAIN 243 251 POLY-ALA.
 FT DOMAIN 253 258 POLY-THR.
 FT DOMAIN 292 296 POLY-ALA.
 FT DOMAIN 538 546 POLY-ASP.
 FT DOMAIN 1072 1075 POLY-GLU.
 FT DOMAIN 1072 1075 POLY-ASP.
 FT DOMAIN 2483 3271 GLN-RICH.
 FT DOMAIN 3333 3339 POLY-ASP.
 SQ SEQUENCE 3828 AA; 413721 MW; 32059CF30A3C504 CRC64;

TRX_DROVI Length: 3828 April 1, 2002 16:32 Type: P Check: 425 ..

1 MGRSKPEGNP SKSINKKRIS VLOLEDEAAS AAAAAAATA ATTEHQOSE
 51 QSAGSSASRE KGNMCDNDD DNAPSGATS GNRGASSGAS DAAPEGNRY
 101 GNGSSGSKT TNGGVNNGS HHKSATAPAE LKECKNOGQ IEPNNCIAAE
 151 PGTEDTNND DDDSSNDKK PTAAAAAANA AAEVPGPSAL ORARKGNKK
 201 FXNLNLARPE VMLPSTSKL QQQQQQLN CPASASASSL SAAAAAANA
 251 APTTTTTTAS ASATLTATAT STSTSLPDT PLVYIAGGG GAAALLIA
 301 NPASVETKV VEYNAATATA ATAAATAAG AGEDVGLKA SIEMANEGL
 351 EAVAVANKSS GSSPNHNHP NAVAGSTAA APGAPTATQ KTYVTKNL
 401 ETSDDKSVM RPYNDNRVP LVSLMKKDSL NRPLNYCRGS EPIVRPSILS
 451 KLINKNSNID KLSLKFERSV HASSNSIOES SSSPTNLFGS GLSRAGAPI
 501 DDDDAVSGV TERKQEPQHK TPEDNDDGS ASSDAIEDDE DDDDAEEN
 551 ELAASEKSAE TTSVDEKEA DDROLVMDKH FVLPKRSTRS SRIKPNKRL
 601 LEVGLICSKR SPSDANGKPK PKNYFGLATL PAKCTPRRR SAATALSOKL
 651 GKTFASFAT AKVNSFVL RPRLOFQDK SRSFVSAKPT LPTTYLPLAS
 701 S&AITSANVL SFGLALNNANS AVAAASTCAY CSAPVNNKA PLARKYGVIA
 751 CEVCRKENSR MTKISKLSRP MHSNPTSTA QSGQOLKCTD GGNCSILSEK
 801 SCLNFKKLY KERCKACWLK KCLATLOPA GHRSRLSAIL PASMREVP
 851 KDKCPPLLS PTASLFTAP TSSASSGTTI KWKSSAETAY NSIKSNPLAE
 901 NNVTFGGTPL LRPAILEKPL FLKIGSDNKK AKESKEALGL SPVSTSEAA
 951 VAPGKTARKA KODKEKAREL EAEKPLSPNA KKTTEANTPE TOKDEGPAST
 1001 TTIVSAASSS TSHTSSAATN SSOLETTTAA NASAVPDNLK RORIDLKGR
 1051 VKHVCRSASI VLGOPLATFG DEEBELAAE AGPAPTTTTT TSPEVIIRK
 1101 PKSPQPMQMI IDENDCASC ILTPEATAE AQPAVKSVLE SRSKSNTOGT
 1151 EAKKTPTSOG SSKGVYTRN ATATVTVAS SLVATKQRN IEVSSISSS
 1201 QAAATOSRRA LAKEVNRLKA LISIDFEMNY DPAEVCOTGF GLIVETVAQ
 1251 RALCFLOGST GIDPLIFCAG CCEPYHOVCY LDEVNKLHSS FEDTLMTSLL
 1301 ETSNNACAIIS AATNTALNOL TORLWMLCPR CTVCYTCNMS SSGKVCQKC
 1351 QKHVHSTCLG TSKRLIGADR PLICVNCUKC KSCATTKVSK FYGNLPMCTA
 1401 CFI LRKKNF CPTCQCYDD NDFDKMMEC GDCQOWHSHK CEBLSDEQIN
 1451 LLSLTPESE FTCKKCARRC DVSRRKADEW ROAVMEEFKS SLYSVLKLS
 1501 KSFQACALIK LSPRKNMRC SAGAOPAKAH SOGLQPKAL QFTYNGLGSD
 1551 GEFQNSDIY EFKEQHSNHR KPSPTVPCSG LQPLSQSPSF SLVDIQOKTA
 1601 SNPYVSLAEF NYDMOVIQO SNCELDIAY KELLSEOPW FONEKTACTD
 1651 ALEEDMFESC GYEELKESPT TYAEHHTASQ APRTGLDIP LDVDVLDGCG
 1701 AVKTRLDTRY CLFCRKSGBG LSGEARLLY CGHDCWYHIN CAMMSAEVE
 1751 EIDGSLQNVH SAVARGMRK CTVCNGRAT VGCNVKSGE HHYPCARTI

1801 DCAFLTDKSM YCPAHARNAL KANGSPSVTY ESNEVSRPV YVELERKKK
 1851 LIVPAKVQFH IGSVAVRQIG SIVPRFSDSF EALVPINFLC SRLYSSKEP
 1901 WKIVETVKT TIQNSYSTL TLDAGRNFV DHTNPMCSLV QGLAQIARM
 1951 HSSLARSDDL DTMAEFPPNS YVPADENTEE EPOONADLPE PEIKDAIFED
 2001 LPHELLDGIS MDIMFYEDL GDKTELFAMS EQSKDGTAT SQAGGASVLI
 2051 CDEDTNNSNS LNKHLVLSNC CTASNVPDDA MLCANSSSO EKECGDYLK
 2101 TDTAPTRSWP KLDGGSVAAF KRRRLSKNIA EGVLLSNOR SKENATVAG
 2151 ITRQSVCSG SELPAEGSAT MTKSFYWSA AKCLFENES REPAKLTIM
 2201 QMDGVDDSTI EYRTIGSDN LSTAOFTGOV KCERCOCOTR NYDSFORILG
 2251 SCEPMSTSES ESETATGTAQ LSAESLNEIQ KOALAATLIS NTGLNYLOT
 2301 SFPQVQNLAT LGQFGVQIGL GLQTLQLOPQ SLGNGFELSQ PMAAQATSNQ
 2351 NDVLOLYANS LONLANILGG GFTLTQPTMS TOAQPOLIAL STNPCTQOF
 2401 IOLPQNGAT TOLLQTAAPL RCNATYQTLQ ATNSDKKIYL LFLAGDPLQ
 2451 EYVTOAAQA TAAHQKQK SGHGVKPIQA KLGQOQOQOR HQHQHQHQH
 2501 QOQOQOQOQO QOQOQTPITY AQHGTTQL GQNLLOPOLL POSNAQPTQ
 2551 QULLPOTOAQ NIISFVTDG SQNOPLOYIS IPTTDFKPO QTTSTPTELT
 2601 APGAGATPLQ TDASGNLMLT TAPANSGLQW LTGOLQTOPO VIGTLIOPOT
 2651 LQLTGADGI QTATNOPLI LGGATGGTT GLEFATAPOV ILATQPMYTG
 2701 LETIVONTYA SSQOFVSTAM PGVLSONSSF SATTVQFQA SKIEPIVDLP
 2751 AGYVLNNAY DASGNTSMLO QSOTOATBDA TAOULLNAGF QOTPTPTST
 2801 QOTMSIDYAP PLVYTAKYVP VAQMKRNTNA NKSPISVLSK VOPQOQOSY
 2851 VNKVLPNTNY QOQOQOQOQO QOQOQOQOPK QOLAGNANLK LISOFOROQO
 2901 ANELKKNQAA GQGTGTCGA PPSIASKPLQ KKTNLIRPIH KYEVPKTIK
 2951 QAPKLATSA SMQHQQOOS PAALNQYAKV ALLQORLAPA PPOQOQEPB
 3001 EQOHLHQOQO QOQOQOQHMQ QHQOQOQOLS MPOLLRAQOP IISIVNTAEP
 3051 QAATQFVIRP ALQAQAQPIQ LQEQOSQOQO QQPAEQULNG KAARLORYAS
 3101 NSLPTNVNVP LQOQRCASAN NSSNSNTQO NSTITINSRP TNKVLPMQOR
 3151 QEPPTLSNDV VVQSPPTPKP IEEPVPAQAS TOKPIYKVA QLEOKSPGE
 3201 TELKTNTITLD NLEQTNISIT MQLQPOQGP IYEQJFEKQ SEAOQLEKP
 3251 KIHNDLMLLEA TSCQOQOQOQ QHMEMVYDNG FQLTNSESCL LEKHGFNVEA
 3301 VPMDETHYA SMKNSGGGA AEGIGQYVDA EDEDEDDDDF SLKMATSAON
 3351 DHEMSDEEP AVKEKISKIL DNLINDCSD SIATATTVEA SAGYOQWED
 3401 VLAATTAGSY STDETFAT AEAVEAASY INMAEABEL QLOLOAGYE
 3451 LDLKRPRLDV POQOPDTVP NVVPTAAAPQ QPPPMRPPK ISGPHLYEI
 3501 QSEDFYYS SSIATIEWY FEAVQVARRA HGLTLPLEGP LADMGSYQMI
 3551 GLKTNALKIY IEOLPGVEKC VKYTPKYHKR NGNVSTAAG GHARTAGSNP
 3601 AALAGAESL IDYGSDOEEL QENAYECARC EPYVSRSEYD MFSWLASHRR

3651 KQIQLVFPVQ SDNELVPRRG TGSNLPMAK YRTLKETYAD YVGVRSIIH
 3701 GRGLVCTMDI EAGMVIETEA GELIRSTLND KRERYDSNG IGCIMFKIDD
 3751 NLVVDATMRG NAAEFINHSC EPNCYSKAYD ILGKHIIIF ALRRIYOGEE
 3801 LTYDYKPFPE DEKIPSCSGS KRCKRYLN

11AA_SEQUENCE 1.0 STANDARD; PRT; 545 AA.
 ID_VNCS_DSDNV
 AC -071153;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NONCAPSID PROTEIN NS-1 (NONSTRUCTURAL PROTEIN NS1) (NCVP1).
 GN NS1.
 OS Diatraea saccharalis densovirus (DsdNV).
 OC Viruses; ssDNA viruses; Parvoviridae; Densovirinae; Densovirus.
 OX NCBI_Taxid=72003;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bobdlik Y., Kouassi K.N., Cavallaro C., Bergoin M.;
 RT "Complete nucleotide sequence and genome organization of an infectious
 clone of Diatraea saccharalis densovirus (DsdNV).";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE PARVOVIRUSES NONCAPSID PROTEIN FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF036333; AAC1999.1; -
 DR InterPro: IPR001257; Parvo_NS1.
 DR Pfam: PF01057; Parvo_NS1; 1.
 KW Nonstructural protein.
 SO SEQUENCE 545 AA; 63475 MW; 810ADE440432E2B1 CRC64;

VNCS_DSDNV Length: 545 April 1, 2002 16:32 Type: P Check: 3506 ..

1 MNNGDSNET DSTSRDQSN LRESPTRSPS SEQCSMVANT SRKREMAWG
 51 RGTMASTAKE SQENFOYMAE ELEKMGNOFF GYVTGOSVAP SSAYISDVII
 101 LRDILRDQC LDVLEYGERS RRMGLFGFSE EGDHIVHND CSYTRNSCRD
 151 IWLGVKPFPG TVOKTGKPVK YIMEFKRTDW YDVFIFYFVR KRGERAIYVR
 201 GESGKIPSD ECVWAREEFK EREMVSDDC TVYECEOE HKISRSNAG
 251 STNGRLYEKK TYSAKFAYI ROKTKALLRK YVSPISAIC DVEPRDDDL
 301 LCDPRNRDYI QAACDFGKD LNAMSUREIY NLTEDEYNT DDKELNPAQ
 351 FISSKKYDNL EGSUNIVNEL LKQCNDDED LIVEFTNLV NVLDRIRKL
 401 NAFLLISPPS GKNFFPDMI FGLLSYGOL GOANRHNLFA FOEAPNKRVL
 451 LMNEPNYESS LTDITKMMFG GDEYTVRVKN RMDAHVKRTP VILTNNTVP
 501 FMYELAFSDR ITYKKNAP FLKDYELKPH PMTFILLISK YNITF

11AA_SEQUENCE 1.0 STANDARD; PRT; 545 AA.
 ID_VNCS_JCDNV
 AC 090054;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NONCAPSID PROTEIN NS-1 (NONSTRUCTURAL PROTEIN NS1) (NCVP1).

GN NS1.
 OS Junonia coenia densovirus (JcdNV).
 OC Viruses; ssDNA viruses; Parvoviridae; Densovirinae; Densovirus.
 OX NCBI_Taxid=12524;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93033112; PubMed=1413502;
 RA Dumas B., Jourdan M., Pascud A.M., Bergoin M.;
 RT "Complete nucleotide sequence of the cloned infectious genome of
 Junonia coenia densovirus reveals an organization unique among
 parvoviruses.";
 RL Virology 191:202-222(1992).
 CC -1- SIMILARITY: BELONGS TO THE PARVOVIRUSES NONCAPSID PROTEIN FAMILY.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; S47266; AAB23699.1; -
 DR InterPro: IPR001257; Parvo_NS1.
 DR Pfam: PF01057; Parvo_NS1; 1.
 KW Nonstructural protein.
 SO SEQUENCE 545 AA; 63461 MW; 97CD825268ABC6AE CRC64;

VNCS_JCDNV Length: 545 April 1, 2002 16:32 Type: P Check: 1211 ..

1 MNNGDTNRET DSTRRPMDI IRESSGRTSP SEQCSMVANT SRKREWSHG
 51 RGTMASTAKE SQENFOYMAE ELEKMGSEFF GYVTGOSIKP SSAYISDVII
 101 LRDILRDQC LDVLEYGERS RRMGLFGFSE EGDHIVHND CSYTRNSCRD
 151 IWISQVKEPG SVOKTGKPVK FIMEFKRTDW YDVFIFYFVR KRGERAIYVR
 201 GESGKIPSD ECVWRTREFK EREMVSDDC TVYECEOE HKISRSNAG
 251 SSNGRLYEKK AYSAGKFAYI RKTTKALLRK YVSPISAIC DVEPRDDDL
 301 LCDPRNRDYI QAACDFGKD LNAMSUREIY NLTEDEYNT DEQELNPYAL
 351 FISSKKYDNL ENSLIIIEI LKQCNDDED LIVEFTNLV NVLDRIRKL
 401 NAFLLISPPS AGKNFFPDMI FGLLSYGOL GOANRHNLFA FOEAPNKRVL
 451 LMNEPNYESS LTDITKMMFG GDEYTVRVKN RMDAHVKRTP VILTNNTVP
 501 FMYELAFSDR ITYKKNAP FLKDYELKPH PMTFILLISK YNITF

11AA_SEQUENCE 1.0 STANDARD; PRT; 2124 AA.
 ID_Y192_HUMAN
 AC 093074;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).
 GN KIAA0192.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Bone marrow;
 RX MEDLINE=96281124; PubMed=8724849;
 RA Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;
 RT "Prediction of the coding sequences of unidentified human genes. V.
 RT The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced by
 RT DNA Res. 3:17-24(1996)."

CC -1 TISSUE SPECIFICITY: UBICUITOUS.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: D83783; BAI2112.1; -
 KW Hypothetical protein.
 FT NON_TER 1
 FT DOMAIN 599 602 POLY-SER.
 FT DOMAIN 1201 1207 POLY-GLY.
 FT DOMAIN 1998 2124 GLN-RICH.
 FT DOMAIN 1998 2023 POLY-GLN.
 FT DOMAIN 2028 2033 POLY-GLN.
 FT DOMAIN 2037 2070 POLY-GLN.
 FT DOMAIN 2090 2097 POLY-GLN.
 SQ SEQUENCE 2124 AA; 237207 MW; 255FB9419EC39F42 CRC64;
 Y192_HUMAN Length: 2124 April 1, 2002 16:32 Type: P Check: 6689 ..
 1 DHGSAKNVS FNPARISSNF SSIAEKLRG NTLPTGRRK POYNOKDNFW
 51 LVTARQSAL NTWFTDLACT KPLQLAKKV PIFSKEEVF GYLAKTVAV
 101 MFAAMLIKMT CAYIAAIST KVKKRHDPF MENTQITTKY LMEQLAKAE
 151 YRRPGASG GCGSTIGPLP HDVEVAIRQW DYTEKLAMFM FQDGMIDRHE
 201 FLTWVLECFE KIRPGEDELL KLLPLILRY SGEFVSAYL SRLAVFCIR
 251 RLALQDQVS SHSHVISAQ STSLPTTPA PGPPTSSTPS TPESDLAKCP
 301 QHRPLVEGLS CILQITILLCC PSALWHSYL TDSRIKTGSP LDHLPAPSN
 351 LPRPEGSNAF TQVRAKLRE IEQIKERQO AVEYRMSFDK COEATGFTI
 401 GRVLHLEVL DSHSPERSDF SNSLDSLCNR IFGLGSPKDG HEISSDDAV
 451 VSULCEMAVS CKRGRHRAM VVAKLLEKRO AEIEAERCGE SEAADEKGI
 501 ASSSLAPSA PLEQVYLQF LDFOAPMLTD PRSESEVEF FNVLVFCGL
 551 IRIDVSHNM YTCILSRGD LAFGAPGRP PSPDPDPAD PEKKEGESS
 601 SSKLEDPGLS ESMIDPSSS VLFEDMEKPD FSLFSPTPMC EKGSPSPER
 651 PDVEKEVKPP PREKIEGTG VLYDQPRHVQ YATHFPIPOE ESOCSHCNR
 701 LVVLFVGKQ RDDARHAIRK ITKDILKYN RKGTAEIDOL APIVPLNPED
 751 LTVLGEDGQ KRRNRPEAF PTADIFAKF QHLSHYDQO VTAOVSNNVL
 801 EQTSFALGM SYHLPLVGHV QEIFDLMEYS LSTISGLDFA IQLNELSVY
 851 EAILLLKSSD LVGYTTSILC LCYIAVLRHY HACLIINQOQ MAOVEGLCG
 901 VVHGNRRSD GSSARCIILA YLYDLYTSCS HLNRKEGELF SDPCSVKKNT
 951 IYCNVPPSES NMRWAPDFMI DLENPAAHT FTYTGIGKSL SENPARYSF
 1001 VCAALMHVCY GHDDPDVND IAILCAELTG YCKSLSEWL GYLKALCSS
 1051 NNCTGCFNDL LCNVDVSDLS FHDLSIAFVA ILIARQCLL EDLIRCAIP
 1101 SLTNAACSEQ DSEPARLTC RILHLFRT QLNPCQSDN KPYVGRSSC
 1151 DRLLLAASON RIVDCAVNAV LKAVFVLGDA ELKSGFTTV GGTIELPEEE
 1201 GGGSGSGRRQ GGRNISVETA SLDVAKYVL RSICQOEWG EBKLKSLCD

1251 SNDLQPVLS SAQAQRLMQL ICYPHRLDN EDGENPQOR IKRLQNLQD
 1301 WIMROSLLEI QUMIKOTENN EMNLLLENIA KATIEVPORS AETGSSGST
 1351 ASNMPPSSKT KPVLSLERS GWLVAPLIA KLPTSVQGVH LKAEELEK
 1401 GQHLGSSSRK EHRQKQKSM SLISQPFLS LVLTCLKGD EQREGLLNLSL
 1451 YGVQHIVNN WRDDOYLDDC KPKOLMHEAL KLRNLNVGM EDTVORSTQO
 1501 TTEWAMALLE IISGTVDMQ SNNELFTTVL DMLSVLINGT LAADSSISQ
 1551 GSMEENKRAY MNLAKKLOE LGEROSDLE KVRQLPLRK QTRDVITCEP
 1601 QGSLDITKGN KIAGFDSIFK KEGIQVSTQK KISPMPLFEG LKPSAPLSMG
 1651 WEGTVAVDRR VARGEEOQL LVYTHLRPR PRAVYLEPLP LPPEDEPPA
 1701 PLLLEPEKKA PEPPYTDKPG AAPSTEERK KSTKGKRS QPATKTEDYG
 1751 MGRGRSGPYG VIVPPDLNH PNEGSIHLN YRQSGIGLT QNOLPAGCP
 1801 RUDYRPRVRL PMOKLPTRP YPGVLPPTMT GVGLEPSSY KTSVYRQOP
 1851 AVPOGRLHQ QLOQSQMLG QSVHQMTPS SSYGLQTSQ YTPVYSHGL
 1901 QOHTGPRAGM VPPSSSQPY QSTHPSTNPT LVDPTHLQD RSGGVHQA
 1951 PYYHGLTST QFESHQTLQD TPMISTMTPM SAQVQAGVR STALLPEQOQ
 2001 QQQQQQQQQQ QQQQQQQQQQ QQQYHQQQ QQQILRQQQ QQQQQQQQQQ
 2051 QQQQQQQQQQ QQQQQQQQQQ AAPQOPQS QPQFQHQGLD QTQQQQQTTA
 2101 LVRLQQLQOLS NTQOPSTNI FGAY
 !!AA SEQUENCE 1.0
 ID Q9X8U0 } PRELIMINARY; PRT: 373 AA.
 AC Q9X8U0;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE HYPOTHEICAL 42.9 KDA PROTEIN.
 GN SCH24.26C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxId=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Oliver K., Harris D.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RX MEDLINE-97000351; PubMed-8843436;
 RA Redenbach M., Kleser H.M., Denaparte D., Elchner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL049826; CAB42732.1; -;
 DR InterPro: IPR003447; FemAB.
 DR Pfam: PF02388; FemAB; 1.

KW Hypothetical protein.
 SQ SEQUENCE 373 AA; 42910 MW; 7EFD1F982299DC6A CRC64;
 O9X800 Length: 373 April 1, 2002 16:32 Type: P Check: 1196 ..

1 MSLRLTISR EQLHAYIOSL PAASHQVPA MADVKAEMWS ENLGMFDDRT
 51 GELVAGAGLVL YRLPLIKRY LAYLPEGPVI NMFAPNLDQM MEPLAHLKQ
 101 OGAFSVKGGP PVIRRMDAT SIKKGIODDP VKRLADIEND HIEPRAFEVA
 151 DKLRRMGQQ GEDGAGFGD VQPRVYQVY IANRSLEEVH KNFNOLMRN
 201 IKKAERKAVE VVGQGYHDL EMQRLYEITA VADHFRPRPL SYFOEMMAL
 251 NNEDNRRRL YFARHNGVN SAATMLVVG HWYSTYGASD NIGREVRPSN
 301 AMQWMLRDS YALGATVYDL RGISDSLDES DHLFGLIOFK VGTGGQAAEY
 351 LGEMDFPLNK LHKALDIYM SRR

11AA SEQUENCE 1.0
 ID P96849.9 PRELIMINARY; PRT; 187 AA.
 AC P96849;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE HYPOTHEMETICAL 20.5 KDA PROTEIN.
 GN RV3567C OR MTCY06G11.14C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; Pubmed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sultson J.E.,
 RA Taylor K., Whitehead S., Barrell B.G.;
 RA "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 DR EMBL: Z92774; CAB07141.1; -;
 DR Tuberculist; RV3567C; -;
 DR InterPro: IPR002563; Flavin_Reduct.
 DR Pfam: PF01613; Flavin_Reduct; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 187 AA; 20539 MW; 4FF7CCE26F797BD1 CRC64;

P96849 Length: 187 April 1, 2002 16:32 Type: P Check: 8381 ..

1 MSAQIDPRTF RSVLGOEQTG ITVITYTHDD VPVGRACQSF AALSIEPLV
 51 LCPTRKVSRS WQAIASGRF CAVNLTEKOR DVSARFGSKE PDKFAGIDMR
 101 PSELSPITE GSLAYIDCTV ASVHDGDHF VVEGAVESLS EYPAVKPRPL
 151 LFYRGDYIGI EPEKTPAHW RDLLEAFLLT TTQDTWL

11AA SEQUENCE 1.0
 ID O928R8.9 PRELIMINARY; PRT; 286 AA.
 AC O928R8;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SVA SUPERFAMILY-RELATED PROTEIN.
 GN TWLC OR CPN0270 OR CP0489.

OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX MEDLINE=99206606; Pubmed=10192388;
 RA Kaiman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
 RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.,
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
 RL Nat. Genet. 21:385-389(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; Pubmed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; Pubmed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T.,
 RA Berry K., Bass S., Linher K., Weidman J., Khouli H., Craven B.,
 RA Bowman C., Dodson R., Gwin M., Nelson M., Deboy R., Kolonay J.,
 RA McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
 RT pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1397-1406(2000).
 DR EMBL: AE001612; AAD18419.1; -;
 DR EMBL: AP002546; BA98480.1; -;
 DR EMBL: AE002210; AAF38319.1; -;
 DR TIGR: CP0489; -;
 DR InterPro: IPR000666; Sna5_yc10_yrdC.
 DR Pfam: PF01300; Sna5_yc10_yrdC; 1.
 KW Complete proteome.
 SQ SEQUENCE 286 AA; 32082 MW; E8C1DBCD4A0223 CRC64;

O928R8 Length: 286 April 1, 2002 16:32 Type: P Check: 9351 ..

1 MDKKAQITF SLPEWMAIH QGKIVLPTD TYGGFVLSLY ASEAEERLYA
 51 LKDRPSKAF ALVYNSIEDI ENISGYPVLP TAKKLAQLFP GATLVYKHR
 101 NRPFRKETIA FRIYDHSYVR EIVDHGCTLI GTSANLSEPP SALTAQOEIFA
 151 DFADHDICF DGPCSHGLES TVVADPDIYI YREGLSRSV IENIAGTEAK
 201 IHRHSHAFS KHIIYTVKN QEOVLVSFLG SLDFKGVCE HPRKPNFYTR
 251 LREALKKTP SIVFIYDINT SDYPELEPFL SPYIIE

11AA SEQUENCE 1.0
 ID O91541.3 PRELIMINARY; PRT; 214 AA.
 AC O91541;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE NITRILE HYDRATASE ALPHA SUBUNIT.
 OS Bacillus sp. BR449.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=123759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR499;
 RA Kim S.-H., Ortel P.;
 RT "Cloning and Expression of the Nitrile Hydratase and Amidase Genes
 RT from Bacillus sp. BR449 into Escherichia coli.";
 RT Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF257489; AAF69002.1; -
 DR InterPro: IPR002114; PTS_Hpr_ser.
 DR PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.
 SO SEQUENCE 214 AA; 24572 MW; C31F78365CE54726 CRC64;

09J541 Length: 214 April 1, 2002 16:32 Type: P Check: 2826 ..

1 MTIDQKNTNI DPREPHNHR POSFEARAK ALESILIEKG HISSDAIERV
 51 IKHHEHLGR MNGAKYVAKA WTDPAFKORL LEDEPYLRE LGYGGQGEH
 101 TRVVENTDTV HNVVCTICS CYWPLDGLP PSWYKEPAYR ARVYKEPROV
 151 LKEFGDLDP SVEIRWDS S EIRFVLPQ RPECTEGMTE EELAKLVTRD
 201 SMIGVAKIEP LKLR

11AA_SEQUENCE 1.0

ID 09K760 J PRELIMINARY; PRT; 957 AA.

AC 09K760;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, last annotation update)

DE BH3513 PROTEIN.

GN BH3513.

OS Bacillus halodurans.

OC Bacteria: Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.

OX NCBI_TaxID=86665;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C-125 / JCM 9153;

RX MEDLINE=20512582; PubMed=11058132;

RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,

RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kubota S.,

RA Horikoshi K.;

RT "Complete genome sequence of the alkaliphilic bacterium Bacillus

RT halodurans and genomic sequence comparison with Bacillus subtilis.";

RL Nucleic Acids Res. 28:4317-4331(2000).

DR EMBL: AP001519; BAB07232.1; -

DR InterPro: IPR000209; Peptidase_S8.

DR PROSITE: PS00136; SUBSTITLASE_ASP; UNKNOWN_1.

DR Complete proteome.

KW SEQUENCE 957 AA; 108853 MW; DC6AANA50F6342B8 CRC64;

09K760 Length: 957 April 1, 2002 16:32 Type: P Check: 4652 ..

1 MKFTSWTLNE PSNAQFAEYA TEVSGEWR I LNPDAKMG GNOKNWLAIF
 51 MNHDKIYGV GLHDFGVNAD GTIYSYKAGE GYPVLNDET AIRMMNRDSL
 101 RFLVDHPNI KMSLQWCFD PSRVEPILDN VNGAQDFVR QLKIAELYL
 151 NRRFGRIKGI EMDFEKTSR PRSAQPEPKY RDLIRKXDE YCPRLGLEIR
 201 VNJHMTGEY NPSWYAMINV STIADADIE YQIMSYDFA GNTAPSPSTP
 251 VMNLLEVLIDH VRNVLPPEKT FTGNAAYGR WSLNRDLGT ALAYWQLLQW
 301 QNLFKHNAG QNRDQCEFTW FDQSFIPYCG FHDESGEY TFLHCYDRQ
 351 ARPARLLPYN NSQVYRGTY RNAEYITSY KHORAKFTGI ORVLTREATST
 401 SGHISDAHV WEPKDLPQY TFYGNLTLPQ QYLDATNS CVARASAIQ
 451 DGIWTSFSL STPGYRLIA TYFYPYLNCR IPIVNGVDY VIGEDIPDW
 501 PFLVNPSHR FDCGFSEFST SNTITVGTQ DSAQIMFVI CRDFEKGMSG
 551 GEVEYVNNLQ VPKKRSYLD GVTYKVDADM PDEVTLTAEI IRNHRPAIF
 601 WEDLFQFAD QEVENLTETN YTORATIGR APNGPYVDG ACRPLQNIC

651 YSNGWRPVA ASGDEAHVY CDARNSSAQL VLNREFSFNA HTEADRALD
 701 SNAIYGRFV AANPGTVNG YIAQLNRYNR TVRLVYESG SSQVLTATAM
 751 SETLANGLS RHTLTIRVHN GRILYGVAV EYINYSGLP GLSRQAMCV
 801 YANGTRIRCY RLHIATNDY EPMKVSAY DGREYALAE DRPYSDYLQ
 851 YLVYSGFND EGLDIDND YDNFPYINP SWGKNNIRI RLVDAGWMLR
 901 NRYVGGGEY STAMNSLEG FITTLGFIKN YGCKVGMNT IQEDPRVFT
 951 YLPPND

11AA_SEQUENCE 1.0

ID 059760 J PRELIMINARY; PRT; 236 AA.

AC 059760;

DT 01-AUG-1998 (Tremblrel. 07, Created)

DT 01-AUG-1998 (Tremblrel. 07, last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, last annotation update)

DE HYPOTHETICAL 26.5 KDA PROTEIN.

GN SPC1020.07.

OS Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972H-;

RA Oliver K., Harris D., Wood V., Lyne M., Rajandream M.A., Barrell B.G.;

RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL023518; CA18995.1; -

DR InterPro: IPR000531; TonB_box.

DR InterPro: IPR001454; Hydrolase.

DR Pfam: PF00702; Hydrolase_1.

DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.

DR Hypothetical protein.

KW SEQUENCE 236 AA; 26496 MW; 51EAC546F81A037B CRC64;

059760 Length: 236 April 1, 2002 16:32 Type: P Check: 5542 ..

1 MPEACLFDM DGLVDTESI YTKSTNIIK RYKNGFSME VAKKMGRTS
 51 KEASRIFLDM SGIDLTCSEY IALQRETOAE LMRHTRPLG VNMLSKLS
 101 LNIPIALATS SPTNFEKKS AHSILFDHF DGNIIIGDDP RLPGRGKPH
 151 PDIMFIALKM INDKRKAQOQ AEILPENCLV FEDSTIGVQS GRAAGKVVW
 201 VPDVNIIPFF SLSPEQADK HITKVLSEN FDTVTV
 11AA_SEQUENCE 1.0
 ID 09P3B8 J PRELIMINARY; PRT; 422 AA.
 AC 09P3B8;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE CONSERVED HYPOTHETICAL PROTEIN.
 GN B7N4.60.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hohelsel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL390218; CAB99237.1; .
 DR InterPro: IPR002965; P_rich_extensions.
 DR PRINTS: PR01217; PRICHECKTENS.
 SQ SEQUENCE 422 AA; 47111 MW; DEDB1307CE33E1AD CRC64;

09P388 Length: 422 April 1, 2002 16:32 Type: P Check: 9296 ..

1 MDNLNRMGAR GGEGLLPGLH DRLFLPEFMD TAMEARVRRRA IMAAEFTPG
 51 RYTGSDSLE RLREERARQ RQANQDRVRE RRAEVOGR LRGGSDDA
 101 DAERGSMER RSSSRVEIQS TSQASPGIO RVTTVRSOS RSRSRRRR
 151 RSDNPQTS SSODRKPDL HVFTSGTKH PKRRSSAVL SCKRPVATK
 201 CHTKEDYSC LPPHPITPS CHSRPRKTP VYAKCPRP KPAITYPLP
 251 PCHPISFSP PYAPAOQTC PRASSQOVCH SSKPRKATY RPRPRPQC
 301 GPVKSREPI YREVPYHEI PVREIREVEY EYVREVEY EYVREVEY
 351 PVRVNPARY PVHVPVHPV PÖPVPYHGG GGGGGYGGG GYGGHGRYG
 401 ARADEGPWYP FKAVTWQSGP PF

11AA-SEQUENCE 1.0

ID 013512 PRELIMINARY: PRT: 551 AA.

AC 013512; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE PROTEIN B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PIBROSARCOMA;
 RX MEDLINE=96303695; PubMed=8723724;
 RA Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E., Spanos S.,
 RA Mailey T., Gibbs R.A.;
 RA "A gene-rich cluster between the CD4 and triosephosphate isomerase
 RT genes at human chromosome 12p13.";
 RT Genome Res. 6:314-326(1996).
 DR EMBL: U47926; AAC50464.1; .
 DR InterPro: IPR000886; ER_target.
 DR PROSITE: PS00014; ER_TARGET; UNKNOWN_1.
 SQ SEQUENCE 551 AA; 62264 MW; F16E4048C0664F58 CRC64;

013512 Length: 551 April 1, 2002 16:32 Type: P Check: 4657 ..

1 MHLQMEDMA KYRMSGVPR QSFRLDLETPR HMAAYDTGLE LIGROEAGIA
 51 LPLLEBALOG SLAQWESCRD DCEGPEBOG AEEEDGAAS OGGLYEALAG
 101 HMIQVLOCRQ KCVGEAATRP GRSPVPDFL PNQLRLHEA HAOVNLISA
 151 IENVLSVLLF YPEDEAARKA LNOYQAOGE PRPGLPREL IORFLISLG
 201 EKROLTYAME HLGTSFKDPD PWTPALILPE ALREKLREDD EKRPMDHEPV
 251 KKRPPLYMKD VILLEGVILT QDSROLNGSE RAVLDGLTPR ACCGYLDIA
 301 KDAAGAGANS GYGRRSRPH PHERFEGITV LKAQOLARAG TVSGOGAKLL
 351 LEYSEHVRTL TOAYFSPER LHLSTHLVC RSAIEGBOQ RMDLSHPVA
 401 DNGVLDPDG ECGREPRAT YRDSGLLYL NDDPOGDLF FTEPNALTYT
 451 ARVPRPGRL VAFSSGVENP HGVAWVTRGR RCALALMHTW ADEHROEMI
 501 EAKELLQESQ EEEEEEEEM PSKDPSPERP SRHRQVQDK TGRAPVREE

551 L

11AA-SEQUENCE 1.0
 ID 015410 PRELIMINARY: PRT: 652 AA.

AC 015410; 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE CAGH45.
 GN CAGH45.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RX MEDLINE=97369492; PubMed=9225980;
 RA Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai A.S.,
 RA Breschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;
 RT "CDNs with long CAG trinucleotide repeats from human brain.";
 RL Hum. Genet. 100:114-122(1997).
 DR EMBL: U80742; AAB91440.1; .
 SQ SEQUENCE 652 AA; 73626 MW; 7A72D515989C546B CRC64;

015410 Length: 652 April 1, 2002 16:32 Type: P Check: 7370 ..

1 MHEALKRLN LVGMEDTVQ RSTQQTTEWA MLLEIITISG TVDMQNNEL
 51 FTTVLDMLSV LINGTLADM SSISQSGMEE NKRAVNNLAK KLOKEIGERO
 101 SDSLKVRQL LPLPKQTRDV ITCPOGSLI DTKGNKIAG DSIFKKEGIQ
 151 VSTQKISPW DFEGLKPSA PLSWGFVY RVDRAVARG EQRLLLYHT
 201 HLPRPRARY LEPLRPEDD EEPAPITLLE PEKKAPEPP TDKPAAPS
 251 TERKKKSTK GKRSQAPTK TEDYGMGPR SGYGYTVPR DLLHPNPS
 301 ITHLNRQGS IGLYQNOPL PAGSPRPDPY RPYRLPMQKL PRRPYPGVL
 351 PTTMGVMGL EPPSYKTSYV RQQPAPVPOG QRLRQQLQAK IQSGMLGGS
 401 SYQMTPPSS YGLQTSQYT PYSHVGLQ HTGPAGTWPR PYSQPIYS
 451 THPSTNPLV DPTRLQORP SGVYHQAPY YGHGLTSTOR FSHQTLQOTP
 501 MSTWTPMSA QGVQGVNST ALPEQOQOQ QOQOQOQOQO QOQOQOQOQO
 551 QYHIRQOQOQ QILRQOQOQO QOQOQOQOQO QOQOQOQOQO HOOQOQOQAA
 601 PPOPOPOPO OFOROLOQOT QOQOQOQOQO QOQOQOQOQO QOQOQOQOQO
 651 RV
 11AA-SEQUENCE 1.0
 ID 075557 PRELIMINARY: PRT: 2023 AA.
 AC 075557; 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE OPA-CONTAINING PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Philibert R.A., King B.H., Cook E.H., Lee Y.-H., Stubbsfield B.,
 RA Damschroder-Williams P., Dea C., Palotie A., Tengstrom C.,
 RA Martin B.M., Gins E.I.;
 RT "The association of a dodecamer insertional variant with mental

RT retardation.";
 RL MOL. PSYCH. 0:0-0(1998).
 DR EMBL: AF071309; AAC83163.1; -
 DR InterPro: IPR001241; DNA_TopoISOM.
 DR PROSITE: PS00177; TOPOISOMERASE-II; UNKNOWN_1.
 SO SEQUENCE 2023 AA; 225881 MW; 1263335676047484 CRC64;
 075557 Length: 2023 April 1, 2002 16:32 Type: P Check: 6311

1 MRAAMLIKMT CAYVAISET KYKKAHNDP MENTOITTKY LMEQLOKMAE
 51 YTRPGASG GCGSTIGPLP HDVEVAIRW DYTEKLMFM FODGMLDRHE
 101 FJTWLECFE KIRGEDELL KLLPLLLRY SGFEVGSAYL SRIAYFCTR
 151 RLALQDGVG SHSHVYSNQ STSLPTTPA PPTTSSTPS TTPSDLMKP
 201 QHRPLVFGLS CILQTLILCC PSALWMHYSL TDSRIKTGSP LDHLPIAPSN
 251 LPMPEGNSAF TOQVRAKLRE IEOQIKERQ AVEVMSFDK COEATAGFTI
 301 GIVLHLEVL DSHSPERSDF SNSLDSLCNR IFGLGSPKDG HEISSDDAV
 351 VSLCEMAVS CKRSGRRHAM VVAKLEKRQ AEIEAERCGE SEADEKSGSI
 401 ASGSLAPSA PIFQVYLQF LDTQAPMLTD PRSESEVEF FNLVLLFCEL
 451 IHHVYSHNM YTCILSRGD LAFGAPGRP PSPDPDAD PEKKEGSGS
 501 SKLEDPGLS ESMIDPSSS VLFEDMEKPD FSLESPTMPC EKGSPSPER
 551 PVEKEVKRP PREKIEGTG VLYDQPRHQ YATHFPIPO ESCSHECNR
 601 LVVLFVGKQ RDDARHAIK ITKDLAKLN RKGAEIDQL APVPLNPED
 651 LTFVGEGDQ KRRNRPEAF PTAEIDFAK QHLSHRDQH VTAQVSRNVL
 701 EQITSFALGM SYHPLVQHV QFIEDLMEYS LSISGLIDFA IQLNELSVY
 751 EAELLKSSD LVGSYTSLC LCIVAVLHY HACILNQDQ MAQVEGSLCG
 801 VVKGHNRSD GSSAERCILA YLYDLYTSCS HLKNGKELF SPFCSKVNT
 851 IYCNVERSES NMRWAPEFMI DTLENPAHT FTYTGKLSL SENPARYSF
 901 VCAALMHVCV GHHDPRVND IAILCAELTG YCKSLSEML GYLKALCCS
 951 NNSTCGFNDL LCNVDVSDIS FHDLSIAFVA ILIARQCLL EDLIRCAIP
 1001 SLZNAACSEQ DSEPGARLTC RILLHLEKTP QLNPCQSDGN KPTVGIRSSC
 1051 DRHLLAASQ RIVDAVFAV LKAVFVLGA ELKSGFTTV GGEELPEBE
 1101 GGGSGGGRQ GGRNISVETA SLDVYAKYVL RSICQDEWVG ERLCSLCEB
 1151 SNLQDPVLS SAQAOLMQL ICYPHRLDN EDGENPQROR IKRIQNLDO
 1201 WTRQSSLEL QLMIKOTPNM EMNSILENIA KATIEVQOS AETGSSSGST
 1251 ASIMPSSSKT KPYLSLERS GVMVLAPLIA KLPTSVQGVH LKAAGELEK
 1301 GQHLGSSSRK ERDROKQSM SLSSQPFSL LVLTCLKGD EOREGLTSL
 1351 YSVQHOIVNN WRDDOYLDC KPKOLMHAL KLRLNLVGM FDTVQSTQD
 1401 TTEMAMILLE IISGTVMQ SNNEFTTVL DMLSVLLNGT LAADMSSISQ
 1451 GSKENKRAY MNLAKLQKE LGERQSDLE KVRQLPLPK QTRDVIYTCBP
 1501 QGSLIDTKG KTAGFDSIFK KEGLOVSTKQ KISPMULFEG LKPSAPLSMG
 1551 WFGTVRVDR VARGEQORL LLYHTHLRPR PRAYVLEPLP LPPEDEEPPA

1601 PTLLEPEKKA PEPPKTDKPG AAPSTEERK KRSTGKKRS QPATKEDYG
 1651 MGPRSGRPG VTPVPDLLHN PNGSITHLN YROGSLGLYT QNOPLPAGP
 1701 RUDYPRVRL PMOKLPTPT YPGVLPPTMT GVGLEPSSY KTSVYRQOP
 1751 AVPGQRLRQ QLOSGMLGQ SSVHQMTSS SYGLQTSOGY TPVYSHVGLQ
 1801 QHTGPRAGTAV PPSYSSQRYQ STHPSTNPTL VDPTRHLQOR PSGYHQAAP
 1851 TYGHGLTSTQ RESHOTLOOT PMISTMTMS AQGVQAGVNS TAILPEQOQ
 1901 QOQOQOQOQOQ QOQOQOQOQOQ QQYHIRQOQO QQILRQOQOQ QOQOQOQOQOQ
 1951 QOQOQOQOQOQ QHQQOQOQOQOQ APPQOPQSQ PQFRQGLQOQ TQOQOQTAL
 2001 VROLQOQLSN TQOPSTNIF GRV

11AA-SEQUENCE 1.0
 ID 09Y6V5 PRELIMINARY; PRT: 128 AA.
 AC 09Y6V5;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE WUGSC:H_DJ0841B21.1 PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96303695; PubMed=8723724;
 RA Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E., Spanos S.,
 RA Mailey T., Gibbs R.A.;
 RT "A gene-rich cluster between the CD4 and triosephosphate isomerase
 genes at human chromosome 12p13.";

09Y6V5 Length: 128 April 1, 2002 16:32 Type: P Check: 8014

1 MKILVALAVF FLYSTOLFPE EIGANDDLNY WSDWYSDQI KEELPEPEEH
 51 LQRIARPRK PQQFGLMGK RDAASIEKQ VALLKALYGH KTDSPVGLMG
 101 KRALNSGMYE IMTENROYIK SITSFSKT

11AA-SEQUENCE 1.0
 ID 015740 PRELIMINARY; PRT: 551 AA.
 AC 015740;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE B PROTEIN.
 GN B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96303695; PubMed=8723724;
 RA Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E., Spanos S.,
 RA Mailey T., Gibbs R.A.;
 RT "A gene-rich cluster between the CD4 and triosephosphate isomerase
 genes at human chromosome 12p13.";

RL Genome Res. 6:314-326(1996).
 DR EMBL; U47924; AAB51312.1; -;
 DR InterPro; IPR000886; ER_target.
 DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
 SO SEQUENCE 551 AA; 62294 MW; ICAAA83E15659886 CRC64;

015740 Length: 551 April 1, 2002 16:32 Type: P Check: 4695

1 MHLQNRDMA KYRMSCGVR QSFRLDETPP HMAAVDTGLE LLRQEGAGLA
 51 LPRLEALQGS SLAOMESCRA DCEGPEEQG AEEEDGAAS QGGLYEALAG
 101 HMIOVLQCRQ RCVGETATRP GRSPVPDEL PMQLRLRHEA HAQVGNLSQA
 151 IENVLSVLE YPEDEAKRA LNQYQALGE PRPGIGPRHD IQRLILSLGS
 201 EKROLTYAME HLGTSFKDPD PWTPLALPE ALREKLREDO EKRWDHEPV
 251 KRPRLTYWKD VLLLEGVLT ODSROLNGSE RAVLDGLLTP AECGVLLQLA
 301 KDAAGAGARS GYRGRRSPHT PHERFEGLYV LKAQLARAG TVGSQAKLL
 351 LEVSERVTL TQAVFSPEPP LHLSTHLYC NSAIQGEBOQ RMDLSHPVHA
 401 DNCVLDPDPTG ECWREPPAYT YRDYSGLLYL NDDFOGDLF FTEPNALTVT
 451 ARVPRGRL VAPSSGVENP HGWMATYRGR RCALALMHTW APREHDEMI
 501 EAKELLQESQ EEEEEEEEM PSKDPSEPP SRHQRVODK TGRAPVREE
 551 L

11AA-SEQUENCE 1.0
 ID_075339 PRELIMINARY; PRT; 1184 AA.

AC_075339
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CARTILAGE INTERMEDIATE LAYER PROTEIN.
 GN CLIP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-ARTICULAR CARTILAGE;
 RA MEDLINE=98389785; PubMed=9722584;
 RX Lorenzo P., Neame P., Sommarin Y., Heinegard D.;
 RT "Cloning and deduced amino acid sequence of a novel cartilage protein
 (CLIP) identifies a proform including a nucleotide
 RT pyrophosphohydrolase.";
 RL J. Biol. Chem. 273:23469-23475(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Nakamura I., Okawa A., Ikegawa S., Takaoka K., Nakamura Y.;
 RT "Genomic organization, mapping, and polymorphisms of the gene encoding
 RT human cartilage intermediate layer protein (CLIP).";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lorenzo P., Aman P., Sommarin Y., Heinegard D.;
 RT "Pro-CLIP: Gene structure and chromosomal localization";
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL; AF035408; AAC33838.1; -;
 DR EMBL; AB022430; BAA76692.1; -;
 DR EMBL; AF035455; AAF14689.1; -;
 DR EMBL; AF035448; AAF14689.1; JOINED.
 DR EMBL; AF035449; AAF14689.1; JOINED.
 DR EMBL; AF035451; AAF14689.1; JOINED.
 DR EMBL; AF035453; AAF14689.1; JOINED.

DR InterPro; IPR002086; Aldehyde_dehydr.
 DR InterPro; IPR001451; Hexapep_transf.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR00884; TSP1.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00090; TSP_1; 1.
 DR SMART; SM00408; IgC2; 1.
 DR SMART; SM00209; TSP1; 1.
 DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; UNKNOWN_1.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; UNKNOWN_1.
 DR PROSITE; PS50092; TSP1; 1.
 SO SEQUENCE 1184 AA; 132538 MW; 4449F05537CC99C3 CRC64;

075339 Length: 1184 April 1, 2002 16:32 Type: P Check: 4681

1 MYGTAWFVS FLVLEVTSVL GRQTMLTQSV RRVQPKKNP SIFAKPADTL
 51 ESPGEWTLLE NIDYPGKGD YERLDAIRFY YGDRVCARPL RLEARTTDMT
 101 PAGSTGQVYH GSPREGFWCL NREQRGQNC SMYTVRFCLP PGSLRROTFR
 151 IWSFWSFWSK CSAAGQGTQV QTRTRICLAE MYSLCSEASE EGQHCWGQDC
 201 TACDLTCEPMG QVNADCDACM CODFMLHGAV SLPGAPASG AAIYLLTKTP
 251 KLTLQTDSDG RFRIPGLCPD GKSLIKITKY KRAPIVLTPP KTSLKAAITK
 301 AEFVRAETPY MYMNPETKAR RAGQSVSLCC KATGRPRDK YFWYHNDTLL
 351 DPLXKHESK LVLRKLOHQ AGEYFCKAOS DAGAVSKVA QLIYASDET
 401 PCNPYPESTL IRLPHDCEQN ATNSFYTDVG RCPVATCAQ QDNGTRCDA
 451 VONCGGISKT EEREIOCSGY TLPTVAKEC SCQRCETRS IVRGVSAAD
 501 NEEPFRFGHV YMGNSRVSMT GYKGTFLHV PDTERLVLT FVDRLOKRVN
 551 TTKVLPFNKK GSAVFHEIKM LRKEPTTLE AMETNIPIIG EYVGDDPAE
 601 LEIPSRSEFYR QNGEPTYIGV KASVTELDPR NISTATAQT DLNFINDEGD
 651 TPFLRTYGMF SVDRDEYTS EPLNAGKVY HLDSTQVKMP EHISTVKLMS
 701 LNPDTGIMEE EGDFKFNOR RNRKREDTFL VGNLEIRERK LENLDVPSR
 751 RCFVVRAYR SERELPSEOI QGVVIVINL EERTGFLSNP RAMGRFDSVI
 801 TGPNGACVPA FCDQSPDAY SAYVLASLAG EELQAVESSP KFNPAIGVP
 851 QYLNKLINR RTDHEDDPRV KTAFOISMAL PRPNSAEESN GPITYAFENLR
 901 ACEEAPPSAA HRFYQIEGD RYDNTVPFN EDDPMSTED YLAWMPKEME
 951 PRACYIKVXI VGPLEVNVRS RNMGTGTHRT VGKLYGIRDV RSTRDRQPN
 1001 VSAACLEFEC SGMLYDQDRV DRILYKITYP GSCRRASVNP MIHELYVHNL
 1051 PLAVNNDTSE YTMCLAPLDPL GHNYGIYTVT DDDPRTAKEL ALGRCFDSTS
 1101 DSSSRIMKSN VGVALTFNCY EROVGROSAL QYLOSTPAOS PAAGTVQGRV
 1151 PSRRORASR GGOROSSVVA SLRFPRAAQ PLIN
 11AA-SEQUENCE 1.0
 ID_090ND7 PRELIMINARY; PRT; 2023 AA.
 AC_090ND7
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE OPA-CONTAINING PROTEIN.
 GN HOPA.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Philibert R.A., Winfield S., Damschoeder-Williams P., Martin B.M.,
 RA Glins E.;
 RT "The genomic structure and developmental expression patterns of the
 RT Human CPA containing gene (HCPA)";
 RT Submitted (Feb-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF132033; AAD4162.1;
 DR InterPro; IPR001241; DNA_topoisomII;
 DR PROSITE; PS00177; TOPOISOMERASE_II; UNKNOWN_1.
 SQ SEQUENCE 2023 AA; 225874 MW; C5746B9ACA25DBC2 CRC64;

090ND7 Length: 2023 April 1, 2002 16:32 Type: P Check: 7074

1 MRAAMLIKMT CAYYAISET KVKRRHVPF MENTQITIKY LMEOLQKMAE
 51 YVRPGPAGSG GCGSTIGPLP HDVEVALROW DYTEKLAMFW FODGMLDRHE
 101 FLTWVECTE KIRGEDELL KLLPLLRV SGFVQSAVL SRLAVFCIR
 151 RLALQDGVV SHSHVISAQ STSTLPTTPA POPPTSTPS TFSDLMLCP
 201 QHRPLVFGLS CILQITILCC PSALVMHYSL TDSRIKTGSP LDHLPIAPSN
 251 LPRPBNNSAF TQOVRAKURE IEQOIKERQO AVEVRKSPFK COEATAGFTI
 301 GRVLTLEVL DSHSFERSDF SNSLSDICNR IFGLGFSKDG HEISSDDDAV
 351 VSLCEMAVS CKRSGRHRAM VVAKLEKRO AEIEARCGE SEAADEKGI
 401 ASSSLAPSA PIFQOVLLQF LDTPAPMLTD PRESERIVER FVLVLLFCFL
 451 IRHDFESHNM YTCILISRGD LAFGAPGPRP PSFDDPADD PEHKAEGSS
 501 SSXLDEPGLS BSMIDPSSS VLFEDMEKRP FSLFPTMPC EKGSGSPSEK
 551 PDVEKEVPRP PREKIEGTGL VLYDQPRHVQ YATHFPIPOE EECSHCNOR
 601 LVYLFVGVQ RDDARHAIRK ITKIDILKVLN RKCTAETDOL ADIVPLNPGD
 651 LPLFGEDGQ KRRNRPEAF PTAEDIFAKF QHLSHYDHO VTAQVSRNVL
 701 EOTSPALDM SYHLPLVQHV QFIDLMWYS LSLSGILDR IOLMLBSLV
 751 EAPLLIKSSD LVGSTTSLC LCIVAVLRHY HACLLINODQ MAOVEGILCG
 801 VVRHGNRSD GSSAERCILA YLYDLYTSCS HLKNGEGELF SDFCSKVNT
 851 IYCNVEXPS NMRAPFEMI DTLENPAANT FTYTGIGKSL SENPNRNSF
 901 VCHALMHVCV GHHPDRVND IAILCABLGT YCKSLSAEWL GYLKALCCSS
 951 NNGTCGFNDL LCNVDVSDLS FHDSLATEVA ILIARQCLLL EDLIRCAIIP
 1001 SLINACSRQ DSVPGARLTC RILLHFKTP QLNPCOSDGN KTYVGISSC
 1051 DRHLLAASQ RIVDGAFAV LKAVFLGDA ELKSGFTYV GSTEELPEEE
 1101 GGGGSGGRQ GGRNISVETA SLDVYAKYVL RSICQEWVG ECKLSLCEB
 1151 SMDLPVLS SAQORLMQL ICTYHRLDN EDENPOROR IRIILONLDO
 1201 WTVROSSLEL QLMIKOTPNN EMNSLENIA KATIEVFOOS AETGSSGSE
 1251 ASNPSSSKT KPVLSLERS GVLVAPLIA KLPTVOGHV LKAAGEELEK
 1301 GQHGSSSKK ERDROKQSM SLISQOPPLS LVITCLKGD EOREGLITSL
 1351 YSVOHIVANN WRDDOYLDDC KPKOLMHEAL KIRLNLVGVG PDTVORSTQO

1401 TEMAMALLE IISGTVDMQ SNNELFTTVL DMLSVLNGT LAADSSISO
 1451 GSEMEKRAY MNLAKKLOKE LGERQSDLE KYRQLLPLRK QTRDVITEP
 1501 QCSLIDTKGN KIAGDSIFK KEGLOVSTKO KISPMWLFEG LKPSAPLSWG
 1551 WFTVAVDRR VARGEQOQL LLYHTHLRPR PRAVYLEEPY LPPEDEEPPA
 1601 PLLPEEKA PEPRTDKAP AAPPSTEERK KSTKCKKS QPATTEDEYG
 1651 MGRKSGPYG VTPPDLHH PNCOSTHNL YKQSIGLYT ONQPLPAGP
 1701 RVDPRPVRL PMOKLPTRP YPGLPTTMT GWGLPESSY KTSYVRQOOP
 1751 AVPOGRLNQ QLOSGMIGQ SSVHQMPSS SYGLQTSQY TPVSHVGLQ
 1801 QHTGPAGTAV PPSYSSQPYQ STHESTNPTL VDETRHLOR PSGYHQOAP
 1851 TYGHGLTSTQ RFSHOTLOOT PMISTWTPMS AGCVQAGVRS TAILPEQOQO
 1901 QQQQQQQQQQ QQQQQQQQQQ QYHIRQQQ QQLIRQQQQQ QQQQQQQQQQ
 1951 QQQQQQQQQQ QQQQQQQQQA APPQOPQSQ POFQROGLQO TQOQOQTAL
 2001 VRLOQQLSN TOPQSTNIF GRY

11AA: SEQUENCE 1.0

ID 090HV6 PRELIMINARY: PRT: 2212 AA.

AC 090HV6: 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE THYROID HORMONE RECEPTOR-ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP230.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99214851; PubMed=10198638;
 RA Ito M., Yuan C.X., Malik S., Gu W., Fondell J.D., Yamamura S.,
 RA Fu Z.Y., Zhang X., Qin J., Roeder R.G.;
 RT "Identity between TRAP and SMCC complexes indicates novel pathways for
 RT the function of nuclear TRAP and SMCC complexes and diverse mammalian activators";
 RL Mol. Cell 3:361-370(1999).
 DR EMBL; AF117755; AAD2033.1;
 DR InterPro; IPR001241; DNA_topoisomII;
 DR PROSITE; PS00177; TOPOISOMERASE_II; UNKNOWN_1.
 KW Receptor.
 SQ SEQUENCE 2212 AA; 247332 MW; E959525836147630 CRC64;

090HV6 Length: 2212 April 1, 2002 16:32 Type: P Check: 8071

1 MKQSMPSLHT KILFCYFHL TNSWCLRRYG LGMMAFGIL SYEHRPLKRP
 51 RPLGPPDYV PODPKOKEDE LIALNVKQGF NNQPAVSGDE HGSANVSEFN
 101 PAKISSNFS IIAEKLRCNT LPTDGRKKPQ VNOKDFMVL TARSSAINT
 151 WFTDLAGTRP LTQAKKVPY ESKKEVEFGY LAKYTVVNR AAMLKMTCA
 201 YVAAISETKV KKRHVDPFME WTQITIKYLM EQLQKAEYV RGPAGSGGC
 251 GSTIGPLPD VVALRQWDY TEKLAMPFQ DGMLDHNEFL TWVLECFEKI
 301 RGEDELLKL LPLLLRYSG EFVQSAVLS RLAVFCTRR ALQLDGVSSH
 351 SHVISAQST STLPTTAPQ PTSSSTSTP FSDLLMCPQ RPLVGLSCI
 401 LOTILLCCPS ALVWHYSLTD SRIKTSPLD HLPIDASNLP MEGSATSQ
 451 QVRAKLEIRE QOIKERQOAV EVRWSFDKQ EATAGFTIGR VLHTEVLDS

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501 HSPERSPSN SLDSLNCRIE GLGPKSKGHE ISSDDDAVVS LCEMAVWSC
551 RSGRHRAWV AKLEKROAE IEAERGGESE AADEKSIAS GSLSPASAPI
601 FQDVLQFLD TQAPMLTDR SESERVEFN LVLLFCELR HDVFSHMYT
651 CTLLSRGDLA FGAPGRPPS PRDDPADPE HKEAEGSSSS KLEDPGLSES
701 MDIDSSSVL FEDMEKPDFS LFSPTMPCBG KGSPSEKPD VEKEVKPPK
751 EKIGTIGLV YDQPRHVOA THFPIPOES CSHECNOPLV VLGVCQORD
801 DARHAIKIT KDILKVLNR GAETDQALP TVPLNPGDLT FLGEDQOKR
851 RRRPEAFPT AEDIFAKQH LSHYDQHYT AOVSRNVLEQ ITSFALMSY
901 HLPVQHVQF IPDLMEYSL ISGLIDFAIQ LLNELSYEA ELLIKSSDLV
951 GSYTSLCLC IVAVLRHYHA CLLNODOMA QVFEGLCGV KHGNRSRDS
1001 SAERCLAYL YDLYTSCSHL KKFGLFSD FCSKYKNITY CNVEPSNM
1051 RMAEFMIDT LEMPAHTFT YTGGLKSLSE NPANRYFVC NALMHVCVGH
1101 HDPDRVNDIA ILCAEELGYC KSLSAEWLGV LKALCCSSNN GTGCFNDILC
1151 NVDVSDLSFH DSLATFVAIL IARQCLLED LIRCAIPSL LNAACSRDS
1201 EPGARLCRI LHLFTPOL NPCQSDGKP TVGIRSSCDR HLAAQONRI
1251 VDGAVFAYLK AVELGDDEL KSGFVTGSG TEELPEEBEG GSGGRRQGG
1301 RNISVETASL DVAKYVLRS IQQEWVGER CLKSCEDSN DLDQPVLSA
1351 QAQMLQOLC YPHRLDNEB GENPORQRIK RILONLDMT MROSSLLOL
1401 MIKOTPNEM NSLENIARA TIEVORSAL TGSSSGSTAS NMPSSSKTKP
1451 VLSLERSGV WLVAPLIAKL PTVQGHVYK AAGELEKQ HLGSSSKER
1501 DRQOKSMXL LSQOPLSLV LTLKAGQDBQ REGLLTSLYS QVHGVNNWR
1551 DDQYLDCKP KOLMEALKL RLNLVGMED TVORSTOQT EMAMLLLEII
1601 ISGTVMQSN NEFTTYLDM LSVLNGTLA ADMSSISQGS MEKKRAYMN
1651 LAKLOKELG EROSDLEKY ROLPLPKOT RDVITCEPQG SLIDTKENKI
1701 AGFDSIERKE GLQVSTRQKI SPWDLFEGLK PSAPLSMGWF GYAVDRRA
1751 RGEQORLLL YTHLRPRPR AYLEPLPLR PEDEPPAPT LLEPKKAPE
1801 PPKTDKGA A PRSTEEKKK STRGKKRSOP ATKEDYMG PGKSGPGVT
1851 VPPDLHHRN PGSITHLNR QGSIGLYTON QPLPAGPRV DYAVRRLPM
1901 OKLPTPTYP GVLPTMTYG MGLEPSSYKT SVYRQQQPAV PQGRLRQOL
1951 QOSGMGLGS SVHOMTPSSS YGLQTSQGYT PYVSHVIGLO HTGPAQWVP
2001 PYSAPQYQS THPSTNPTLV DPTRLQORP SGYVHQAPT YGHGLSTOR
2051 FSHQTLQOTR MISTMTPMSA QGVQAGVST AILPEQQQQQ QQQQQQQQQQ
2101 QQQQQQQQQQ QYHTRQQQQ QILRQQQQQQ QQQQQQQQQQ QQQQQQQQQQ
2151 HQQQQQQQQA PPOPOPOSOP QFQROGLQOT QQQQOQTAALV ROLQOOLST
2201 QOPSTNIFG RY

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11AA SEQUENCE 1.0
PRELIMINARY: PRT: 72 AA.

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DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE GAMMA PREPROTACHYKININ (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE= BLOOD, AND BRAIN;
RA Lai J.P., Douglas S.D., Rappaport E., Wu J.M., Ho W.Z.;
RT "Identification of a Delta isoform of preprotachykinin mRNA in Human
RT Mononuclear Phagocytes and Lymphocytes."
RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF050657; AAC15703.1;
DR InterPro; IPR002040; Tachykinin.
DR InterPro; IPR003580; Protachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; UNKNOWN_2.
DR SMART; SM00203; TK; 2.
FT NON_TER 1
FT NON_TER 72
FT NON_TER 72
SQ SEQUENCE 72 AA; 8274 MW; 2C02B2BA41EAD16 CRC64;

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09Y494 Length: 72 April 1, 2002 16:32 Type: P Check: 3943 ..

1 DSDQIKELP EPPHLLQRI ARRPKQOFF GLMKRQDGH GQISHKHKHT
51 DSVGLMGKR ALNSVAYERS AM

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11AA SEQUENCE 1.0
ID_09H6A8 PRELIMINARY: PRT: 566 AA.
AC 09H6A8
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CDNA: FLJ22428 FIS, CLONE HRC09055.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Oktani R., Ota T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project."
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK026081; BAB15354.1;
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 3.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00320; WD40; 3.
DR PROSITE; PS50181; FBOX; 1.
DR PROSITE; PS50082; WD_REPEATS_2; 2.
DR PROSITE; PS50294; WD_REPEATS_REGION; 2.
KW Repeat; WD repeat.
SQ SEQUENCE 566 AA; 63864 MW; C2C50AB6F6CD5CB2 CRC64;

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09H6A8 Length: 566 April 1, 2002 16:32 Type: P Check: 4809 ..

1 MDEGTPLLP DSLVYQIFLS LCPADVLVAG LYCRQMOAVS RDEFLMRQF
51 YRYQVARDV PRHPAAMSWY EEFQRLYDVT PCVEVQTLRE HTDQVHLHSF
101 SHSGYQFASC SKDQTVKWS NDLFTSLHS ADMRPYNSY TQSQFNKDD
151 SLLASGVFL GPHNSSGEI AVISLDSFAL LSRVNRKPYD VFGCWLTETS
201 LISGLNHRIG DITSCSVLWL NNAFDQVESE NVNVVKRLFK IONLMASTVR

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251 TVWVADCSR FDSPLLLEAG DPATSPCRIF DLGSDNEEV AGPAPAHKE
301 GLHFHLDVL EGRNQPLSE RMLETVAEL LAQHTKPRPE RSATGASKY
351 LIFTTGCLTY SPOIGIKOI LPHQMTTACG VLGEGRGSDA FFDALDHVID
401 IGHITIGML SPDNRVLVYN SRAMPNGAVY ADPMOPPIA EEIDLVEFDL
451 KTMREVRAL RAHRYTPND ECFEFLDVS RDFVSGAEG RHGXTMRHY
501 NICARLHE DVNSVVFSP QEOELLTAS DDATKAMS PRIMVLOAP
551 RPRPTEFSW LASQRR

IIA_SEQUENCE 1.0
ID_09HB06 0 PRELIMINARY; PRT: 159 AA.
AC_09HB06;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE HYPOTHEICAL 18.5 KDA PROTEIN (SIMILAR TO F-BOX AND WD-40 DOMAIN
DE PROTEIN 5).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.O., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RT "Novel Human cDNA clones with function of inhibiting cancer cell
RT growth.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=CERVIX CARCINOMA;
RA Strauberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF217998; AAG17240.1; -
DR EMBL; BC000850; AAH00850.1; -
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40. 2.
DR SMART; SM00320; WD40. 2.
DR PROSITE; PS50082; WD_REPEATS.2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION. 1.
DR Hypothetical protein; Repeat; WD repeat.
KW SEQUENCE 159 AA; 18545 MW; 2DDBFB544D00E68 CRC64;
SQ
Q9HB06 Length: 159 April 1, 2002 16:32 Type: P Check: 4523
1 MGLSPDNLYL YVNSRAMPNG AVYADPMOPR PIAEIDLIV FDLTMRVR
51 RALRAHRAVT PNDECFIFL DVSRDFVAG AEDRHGYIWD RHYNICIARL
101 RHEGVNVSIV ESPQOELL TASDATIKA WSPRTMRVL QAPRPRTF
151 FSWLASQRR

IIA_SEQUENCE 1.0
ID_09BY45 0 PRELIMINARY; PRT: 175 AA.
AC_09BY45;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE HTPAP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;

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RA Li Y., Wu T., Xu S., Ren S., Chen Z., Han Z.;
RT "A novel gene expressed in human liver non-tumor tissue.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF212238; AAK14924.1; -
SQ SEQUENCE 175 AA; 19766 MW; 0133956D40539F83 CRC64;
Q9BY45 Length: 175 April 1, 2002 16:32 Type: P Check: 3438
1 MWLYNPYVE AEYPTKPMF VIAFLSPSL IFLAKFLKA DTRSRQACL
51 AASLALALNG VFTNTIKLIV GRPRDPFYR CEPDGLASD LMTGDKDV
101 NEGRKSPFGS HSPFAFAGLA FASFYLAGKL HCFTPGNCK SWRECAPLSP
151 LIFAVALS RTCDYKHHNQ GPPEK

IIA_SEQUENCE 1.0
ID_09BT44 0 PRELIMINARY; PRT: 649 AA.
AC_09BT44;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE TRINUCLEOTIDE REPEAT CONTAINING 11 (THR-ASSOCIATED PROTEIN, 230 KDA
DE SUBUNIT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RETINOLASTOMA;
RA Strauberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004354; AAH04354.1; -
SQ SEQUENCE 649 AA; 73313 MW; CD4030E5A095B08A CRC64;
Q9BT44 Length: 649 April 1, 2002 16:32 Type: P Check: 1992
1 MHEALKLYN LVGMPFDYQ RSTQOTTENA MLLELIISG TVDMQNNEL
51 PTVVDMLSV LINGTLADM SSISQSMEE NKRAYMNLAK KLOKELGERQ
101 SDSLEKRVOL LPLPKOTRDV ITCEPOGSLI DTKGNKIAGF DSIFKKEGLQ
151 VSTKOKISPM DLFEGLKPSA PLSMGMPGV RYDRVARGE EQQRLILYHT
201 HLRPRRAYV LEPLRLPED EEPRAPTLE PEKKAPEPK TDKGGAAPS
251 TEERKKSTK GKRSOPATK TEDYGMGRG SGRYGVYPR DLLNPNFS
301 ITHNLVROGS IGLYTONPL RAGGRVDRY RYVRLPMOKL PTRRTYRVL
351 PTTMTGWLGL EPSSYKTSVY RQOQRAVPOG QRLRQOLOOS QGMIGQSSVH
401 QMTSSSYGL QTSQGYTPVY SHVGLQNHG PAGTWPRSY SSOPYQSTNP
451 STNPLVDPRT RHLQDRPGV VHQDAPTYGH GLTSQGRSH QTLQGTPLIS
501 TWTPMSAGV OAGVSTAIL PEQOQOQOQO QOQOQOQOQO QOQOQOQOYH
551 IROOQOQOIL ROOQOQOQOQ QOQOQOQOQO QOQOQOQOQO QOQOQOAPRQ
601 PQPOQPOPOQ RQGLQOQOQO QQTALVRLQ QOQLSNTQPO PSTNIFGRY

IIA_SEQUENCE 1.0
ID_09BS08 0 PRELIMINARY; PRT: 433 AA.
AC_09BS08;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, last annotation update)
DE UNKNOWN (PROTEIN FOR IMAGE:3951723) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY ADENOCARCINOMA;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC004541; AA04541.1; -
 FT ON TERN 1
 SO SEQUENCE 433 AA; 48413 MW; 952DFC6E113C39F CRC64;

09BS08 Length: 433 April 1, 2002 16:32 Type: P Check: 5292 ..

1 ARGNNSTYQF SQFNKDDSL LASGFLGPH NSSSGEIAVI SLDSFALLSR
 51 VNRKRYDVG CWLFTSLIS GNLHIGDIT SCSVLMLNNA FQDSESVN
 101 VVKRLFKION LMASTVRVM VADCSRRDSP DILLEAGDPA TSPCRIFDLG
 151 SDNEEVAVGP APAHAKGLR HFLDRVLEGR AQPOLSERNL ETKVAELLAQ
 201 GHTKPEPSA TGAASKYLIF TTGCLTYSPH QIGIKQILPH QMTAGPYLG
 251 EGRGSDAFED ALDHVIDING HIIGMGLSPD NRYLYNSRA WPNQAVVADP
 301 MOPPIAEI DLVLEDLKTM REYRRLRAH RAYTPNDECF FILDVSRDF
 351 VASGAEDEHG YIMDRHYNIC LARLRHEDV NSVFSPOEQ ELLLTASDA
 401 TIKAWRSPT MRVLQAPRP PRTFSSWLAS ORR

11AA_SEQUENCE 1.0 PRELIMINARY; PRT; 173 AA.
 ID 044981
 AC 044981

DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE C54G6.3 PROTEIN.
 GN C54G6.3
 OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans."
 RL Nature 368:32-38(1994).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Tin-Wollam A., Graves T., Ozersky P.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF03698; AAB97561.1; -
 SO SEQUENCE 173 AA; 20156 MW; 053E67461C2D59F3 CRC64;

044981 Length: 173 April 1, 2002 16:32 Type: P Check: 8718 ..
 1 MALVKVRDEC TKLVGYOELN SHICICISLI QLLVCCMAVA QHVSYNMTHS
 51 KILKDFLEEG SLPLEAVDAV IPIRIEFHYL WGIKGCVAEY LDGEGGRLLM
 101 CVSHCLTFVE SIPYTFISHP KPCLEFWPLLF QVSWLKRFKQ KLELNFERRA
 151 QMDPRRLPLT TAMFESAMVL EKF

11AA_SEQUENCE 1.0 PRELIMINARY; PRT; 206 AA.
 ID 061761
 AC 061761

DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE F56C3.9 PROTEIN.
 GN F56C3.9
 OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodermidae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans."
 RL Nature 368:32-38(1994).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Stoneking T.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF067214; AAC17009.1; -
 SO SEQUENCE 206 AA; 24599 MW; 3F530D03A57CD7A9 CRC64;

061761 Length: 206 April 1, 2002 16:32 Type: P Check: 3281 ..

1 MTQOKMHMS TETALRKFOI NTQSDTIYVN LNYLAESEY FHILRTGFYS
 51 EMTEAEVNIN DVPAEDLVF LSYVCPDGE FORTIQNHNI TPLVFSRDL
 101 VEPWAKREVN KYLNSAFON EIYDTELLV LCYLHSQNT SEIDVFKKI
 151 ALIDNPLVVD RLVQETDSD VQSFETKIL QYRPYTERKR PQMFDMOHT
 201 PYSAYV

11AA_SEQUENCE 1.0 PRELIMINARY; PRT; 1264 AA.
 ID P91767
 AC P91767

DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE NEUROGLIAN.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditylaria;
 OC Sphingioidea; Sphingidae; Sphinginae; Manduca.
 OX NCBI_TaxId=7130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LARVAL NERVE CORDS;
 RX MEDLINE=97167642; PubMed=9015260;
 RA Chen C. N., Lampe D. J., Robertson H. M., Nardi J. B.;
 RT "Neuroglial is expressed on cells destined to form the prothoracic
 glands of Manduca embryos as they segregate from surrounding cells and
 rearrange during morphogenesis.";
 RT Dev. Biol. 181:1-13(1997).
 RL -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: U50719; AAC47451.1; -.
 DR HSSP: P20241; ICFB.
 DR InterPro: IPR003962; FN1I_repeat.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003529; Hematopo_receptor_L_F2.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003600; Ig_MHC.
 DR InterPro: IPR001005; MyD_DNA_bind.
 DR InterPro: IPR000130; Zn_MTPeptide.
 DR Pfam: PF00041; fn3; 5.
 DR Pfam: PF00047; Ig; 6.
 DR PRINTS: PRO0014; ENTPEPIL.
 DR SMART: SM00408; ICG2; 4.
 DR SMART: SM00410; IG_Like; 2.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
 DR Repeat.
 KM SEQUENCE 1264 AA; 139733 MW; 02CE935D000F429C CRC64;
 P91767 Length: 1264 April 1, 2002 16:32 Type: P Check: 6396 ..

1 MCTTFCFTA IAAQAALLT SPKMKQPT QEELFCVAQ AGEVDPFII
 51 ECGEAGEGE GPKYRMING KPEYTSIDN RIIOQSRCGT LVASPRDED
 101 LGYOGEFAYN EMGTAASNSV FVRAELNSF KETDGOQVVK AEEGRFKLT
 151 CEPPDHPKP KYWMLQGDQ GOLKTINNSR MTLDPGCLM FSNVTPNDAS
 201 VDAVYICTAN SIFRNEYKFG NKIYLDYQT GISPILNRHA PERQITTTI
 251 EKALGKRYE LVCYGGTFL PQIYWKDGH NIIPSASITQ DNYGKTLVVK
 301 YPAYEDSGTY TCEVSNVGT ALYSIQLNI EAAPFTVER DVQNLAEGET
 351 AVIRCEAGGT PYRKITWIHN GKPLEQAEPN PRQVYANSTI VTLDVKKRT
 401 GNYGNATSS IGYVYKDYI NVQSIPEIK EGPENLTQV GSEAVLKCV
 451 FGAPKEIVW MRDVIDITGG KYNTISEGLD VIRDAVSTVD GYQCYAKNK
 501 FGKSAFGSL AVKRTVITD KPEDIYVAAG SSATFRCNAN ADDSLKTLIV
 551 WLHDGOLIDE ENQPRFRMTN DYSLISDTT ELDSGOYTCI AKTAIDEARA
 601 QATLVQDQRP NPALDVEEC GAATATLRMR SMGDNRAVY RQIHNTSF
 651 TPISSMAAAD HVPALDTSWT VQLSPWANYT FRIVAVNKIG PSPSPSHSY
 701 CTTQDPVPYK NPDNVKGGES DPTNMVTSWS KMPQIEHNGP GYIYLVSWR
 751 NIGDEWNRK QVRDQOTEY IVTNTPTFOP YKIKYAVNF KQTSNVTPE
 801 VIGWSEDRP LQAPANFTLY QVTGTGALL SMAVAPESV RGHFGYKIQ
 851 TWTGSEDRL KEIYKADST SALVTKTRPF KKNNAIILY NGRFNGPPSD

901 ILSFTEPEK PGTVRTFGVY PIGSSAMLLK WEKPVDENGV LTGYKIYYOK
 951 VTGTSIGPLQ ERKKEIDPKF DRAKLAGLER NTKYRIIIRA KTKAEGDEX
 1001 VYEQTTSKAV TAKPEIPLFE TRTLSAREGT AHILVRNIPS LDGAGSHFV
 1051 AWKLGKMPD WLKNTDITDD DYVILTGLEP GQYVEVKVTA HDGEYFSTSE
 1101 IKVDTTITG PLYKDEKMA AAGWFIGVYL ALAFLLLVLY LVCYVRRNRG
 1151 GKVDVHREL AHGRDYAEG GFHEYTHPLD NKSRSMSG TKPGESDTD
 1201 SMAVEGEGET GFRTEDGSFI GQYVGARVL PPAPGARAPL SPSPAPAP
 1251 APAAPAPAP PTVY

11AA SEQUENCE 10
 ID 017532 PRELIMINARY; PRT; 912 AA.
 AC 017532;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE B0564.7 PROTEIN.
 GN B0564.7.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Paloderinae; Caenorhabditis.
 OX NCBI_TaxId=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Riffen L., Roopra A., Saunders D., Showkseen R.,
 RA Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Spoat J., Woldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RT Nature 368:32-38(1994).
 RL Nature 368:32-38(1994).
 CC -1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
 CC EMBL: Z73422; CAA97769.1; -.
 DR InterPro: IPR000822; Znf_C2H2.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
 DR PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.
 KM Zinc-finger.
 SO SEQUENCE 912 AA; 103309 MW; 69A0ADEFA9D7DD8 CRC64;
 Q17532 Length: 912 April 1, 2002 16:32 Type: P Check: 558 ..

1 MMSRGLPTIC RTIPCRQFSV AAGGAGPAE IDOLFHSIAA APTQKLVNKR
 51 TVLESTTEFF KWLBNPIKS IDQITTAQM AITVAKSTEON KAFSKIIDIA
 101 KVLKPFYEN EGPKEVDAL REVVLQNSKG KYSTDIONLF LEKKISQSDL
 151 QVVPFDLVM IIRYSSSID QNVIESIATS LISRIEKELA NPADLLAIIA
 201 GDCYEKSKWF HNEAFLEKAE RLVAVNGMAE KCALLKHMAY NKQRNOLLG
 251 AINNAISSS QVLIVSQIVS VTGSCSALTY YPPKIARKIS NDLEKNSVNL

11AA-SEQUENCE 1.0
ID: 09V010.0 PRELIMINARY; PRT: 823 AA.
AC 09V010.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CG5481 PROTEIN.
GN ROBO2 OR CG5481 OR CG5574 OR CG14347 OR CG14348.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dopp L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.D., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabori A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Plittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Zheng H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AE003586; AAF51373.1; .
DR DR HSSP: P56276; 1TLK.
DR DR Flybase: FBgn0024195; robo2.
DR DR InterPro: IPR003962; FNIII_repeat.
DR DR InterPro: IPR003961; FN_III.
DR DR InterPro: IPR003598; Ig_c2.
DR DR InterPro: IPR003600; Ig_1like.
DR DR InterPro: IPR003006; Ig_1like.
DR DR InterPro: IPR001412; tRNA-synt_1.
DR DR Pfam: PF00041; fn3; 1.
DR DR Pfam: PF00047; igf; 5.
DR DR PRINTS: PR00014; FNTPETII.
DR DR SMART: SM00060; FN3; 2.
DR DR SMART: SM00408; IGc2; 4.
DR DR SMART: SM00410; IG_1like; 1.
DR DR PROSITE: PS00178; AA_TRNA_LIGASE_L; UNKNOWN_1.
KW Repeat.
SQ SEQUENCE 823 AA; 89715 MW; 36FC0B91F36F2F19 CRC64;
09V010 Length: 823 April 1, 2002 16:32 Type: P Check: 4431 ..
1 MPTTVKKNP FTENQCAEGN PPTIQWFKD GRLEKDTGS HIMLPAGSL
51 FFLKTVHSR ESDACTYCE AKNEGVARS RNATLOVAFI RDEFRLEPAN
101 TRYAGEVAL MECGAPRSG EPQISWRKG QTLNLVGNKR IRIVDGNILA
151 IDEARQSDG RYQCVKKNV GTRESATAFL KVHVRFILIR GQNGTAVVG
201 SSVVFOCRIG GDPDPVLMR RTASGGMNPR RVHVLDRSL KIDVYLEDM
251 GEYTCADNA VGGITATGIL TVHAPKFEVI RPKNQLVEIG DEVLFEQCAN
301 GHPRLFLYMS VEGNSLLLP GYRGRMEVT LPEBGSVLS IARFARBDG
351 KVVTCNALNA VGSVSSRTIV SVDTQFELP PIIEGPRVNO TLVPSIYVL
401 PCRTLGTPV QVSWYLDGIP IDVOEHERRN LSDAGALTIS DIORREDEGL
451 YTCVASNRNG KSSMSGYLR LDTPTNPINKF FRAPELSTIV GPPGRPOME
501 KGENSVTLNW TRSNKVGSS LVGVYIEMFG KNETDGVAV GTRYONTFT
551 QTCGLPGVNY FELIRAENSH GLSLPSPSE PIVGTYSSE NNSFTLMFPS
601 LIHYPSLPH PORYNSGLD LSEKASLIS GDVVELSMAS VVDSISMKLT
651 WOVNENLTDG STADPSTIAH RHLIRASFL MQIINKRYE GPVYAROLP
701 NPVNNPAPV TSNTNPLDGS TSTSASASAS ASALISTKPN IAAGRROGE
751 TNOSGGCAPT PLNTRYRMIL ILNCGGASSC TTIGLVQYTL YEFFIVPYK
801 SVEGKPSNSR IARTLEDEL SNF
11AA-SEQUENCE 1.0
ID: 09VKA3.0 PRELIMINARY; PRT: 1677 AA.
AC 09VKA3.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CG17215 PROTEIN.

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
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 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003435; AAF46077.2; -
 DR FLYbase: FBgn0029801; CG15771.
 DR InterPro: IPR001454; Hydrolase.
 DR Pfam: PF00702; Hydrolase; 1.
 DR PRINTS: PR00413; HADHALOGNASE.
 SQ SEQUENCE 355 AA; 40368 MW; 7592A145923F0031 CRC64;

Q9W481 Length: 355 April 1, 2002 16:32 Type: P Check: 4133 ..
 1 MAASFFHCGK QLTATSHFD ATCAKIRAFY EDLDTLTIPT RAGDSKAIRK
 51 LADPLETOYQ FSKDAMQAT QNLFKAFRRC PDSQTSILDS WRTHLMRESL
 101 PARHHHLAQ IYRKWKIRY RYLAAPADV QLLLRMRQNG YALALITNGP
 151 SNAQMEKYAE LNVRGYFDCV LVSSDLPEWK PHPEIFYAAC NFLNVKPOEC
 201 VMIGDKLETD IKGGHLAQIG LTFWTPLSNS SAAQSLIEDV EYKPHVKLGS
 251 LLEWKKYPR LNSVALPEMP SVSRRRGSHM SPISSGSSGS SSSSALICPG
 301 AGHGYNHHNH QQHQQQQQH HHHHHQRL YRKGVSLEPM DCSNSEANS
 351 CDSFL

11AA-SEQUENCE 1.0
 CTD Q9W481 PRELIMINARY: PRT: 412 AA.
 Q9W481 Q9W481 Q9W481
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CG12746 PROTEIN.
 GN CG12746
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; *Drosophila*.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -! ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 DR EMBL: AE003602; AAF52007.1; -
 DR EMBL: AE003602; AAF52008.1; -
 DR FLYbase: FBgn0037341; CG12746.
 DR InterPro: IPR000326; PA_PPFase.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidppc; 1.
 DR Alternative splicing; Hypothetical protein.
 KW VARSPLIC 1 49 MISSING (IN SHORT ISOFORM).
 FT SEQUENCE 412 AA; 46736 MW; 0966CA340A4444C1 CRC64;

Q9W481 Length: 412 April 1, 2002 16:32 Type: P Check: 2785 ..
 1 MPDSCTADLR SRRRENPIDR NGNIGTGKE QATSTPKLTL TTYTQRTNEM
 51 TASKQGESR RTLSDSAED VRNTGSRTRT NDEEMRNEL AMNTDSSVQ
 101 PEKREERSHR TGNNAKLSD ADVVLAVLL VITFFKLETM TAFKREIHE
 151 ELMLYKNPRR PDYVNGGELL FWYLVAPPLV TIAFYVTRD RQDFRAASNA
 201 WTLALCMNGI PTSLYKLTGV RPRPDYFRC FPDGVAVLNT TSNQVDTSL
 251 DFNCTGLPDD INEGRKSPS GHSSEFAFSE GLFAYIYGAK LHAQPSRGNG
 301 HWRCLIAVI PLFIALVAV SRTCDYNNHM ODVTIGGLIG LFAGIYSTIQ
 351 YVPSIFCPDA GIPLVWPSR EGSQYORLGS KDNNGSRGPH HLDGGDAVRR

401 PLADKESK WY

11AA SEQUENCE 1.0
ID 09GPP7 PRELIMINARY: PRT: 1406 AA.

AC 09GPP7
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ROUNDABOUT 2.
GN ROBO2 OR CG5481 OR CG5574 OR CG14347 OR CG14348.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyroidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Pubmed-11163265;
RA Rajagopalan S., Vivanos V., Vivanos V., Berger J., Dickson B.J.;
RT "Crossing the midline: Roles and regulation of Robo Receptors.";
RL Neuron 28:767-777(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Pubmed-11163179;
RA Simpson J.H., Bland K.S., Fetter R.D., Goodman C.S.;
RT "Short-range and long-range guidance by slit and its Robo receptors: A
RT Combinatorial Code of Robo Receptors Controls Lateral Position.";
RL Cell 103:1019-1032(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Pubmed-11163180;
RA Rajagopalan S., Vivanos V., Vivanos V., Dickson B.J.;
RT "Selecting a Longitudinal Pathway: Robo Receptors Specify the Lateral
RT Position of Axons in the Drosophila CNS.";
RL Cell 103:1033-1045(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Simpson J.H., Kidd T., Bland K.S., Goodman C.S.;
RT "Short-range and long-range guidance by slit and its Robo receptors:
RT Robo and Robo2 play distinct roles in midline guidance.";
RL Neuron 28:753-766(2000).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF312579: AAG41425.1: -
DR Flybase: FBgn0024195: robo2.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003598; Ig.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00047; Ig; 5.
DR PRINTS: PR00014; FNYPEIII.
DR SMART: SM00060; FN3; 3.
DR SMART: SM00409; IG; 5.
DR SMART: SM00408; ICG2; 5.
DR SMART: SM00410; IG_Like; 3.
KW Repeat.
FT VARIANT 805 806 SE -> F*.
FT VARIANT 1070 1070 G -> S.
FT VARIANT 1077 1077 T -> A.
SQ SEQUENCE 1406 AA: 153139 MW: 3EF8302A64EC28DD CRC64:

09GPP7 Length: 1406 April 1, 2002 16:32 Type: P Check: 6657

1 MPYDRRAV FLLLLAGL NGLYGVGLK GENPRRIEH MOTYPKNP
51 FTFNCAEEN PPTIOWERD GRELKTDTGS HRIMLPAGL FLKYIHSR
101 ESFAGTWCE AKNEGVARS RNATLOVAFL RDEFLEPAN TRVAGEVAL

151 MEGAPRGSP EPOISMRKG QTLNLYGNKR IRIVDGNLA IOEARQSDG
201 RUCQVKNV GRESATAFL KVHVRPLLIR GPONQTAAYG SSVVQCRIG
251 GDELDPVLMR RTASGNMPL RRHVLEDRS LKLDVLTLED MGEYCEADN
301 AVGGIATGCI LTVHAPPKVF IRPNQOLVEI GDEVLPECCA NGHPRLTYW
351 SVGNSSLLL PGYRGHREV TLTPEGRSVL SIAFRAREDS GAVYCNMLN
401 AVGSVSRIV VSDTQFELP PLIEGGPNV QTLVKSIVV LPCRILGPV
451 PGVSWILDCI PIDVQEHRR NLSAGALTI SDRQHEDEG LYTCVASNEN
501 GKSSMSGYLIR LDTPTNPNIK FFRAPELSTY PGPPGRPOWY EKGESVTLN
551 WTRSNKVGGS SLVGYIEMF GKNETDQWVA VGTIVONTTF TOTGLPGVN
601 YFELLIRAEVS HGLSLPSPMS EPITVGTIRYF NSGLDLSSEAR ASLSGDVVE
651 LSMASVVDST SMKLWQILIN GKVEGCVYV ARQLPPIYV NPAPYTSNTN
701 PLIGSTSTSA SASASASALI STKPNIAAG KRDETNQSG GGAPTPLNTK
751 YRMILTLNGG GASCTITGL VQYTLVEFFI VPFRKSVGEG PENSRIARTL
801 EDVPSAPRG MEALLNNSA VELKWKAPEL KDRHGVILAN HVIYGLDIA
851 HNEFRILTNV TIDAASPTLV LANLVEGMY TVGVAAGNNA GVGYCVPAT
901 LRLDPITKRL DFINQRYPI NODHVNDVLT QPWFILLGA ILAVMLSEFG
951 AMWFVARKHM MKKOSALNTM RGNHTSVLK MPBLSARNGN GWNDSSTGC
1001 MWRRPSPGD SLEWQKHIA DYAPVCGAPG SPAGGTSNG GSGAGSGAS
1051 GGDIDHGHG SERNOQRYVY EYSNIPDYA EVSFGKAPS EYGRHGNASP
1101 APYATSTILS PQOQOQOQOQ RYQGRVPYGY GLDRPHNPH QOQOQOQOQA
1151 QOTHQOQAL QOHQQLPPSN IYQOMSTTSE IYPTNTGPSR SVYSQOYYYP
1201 KDKORIHIT ENKLNSCHTY EAAPGAKOSS PISSOPASVR RQOLPNCST
1251 GRESARFXYL NTDQGNQON LLDLDGSSMC YNLADSGCG GSPSTMAMLM
1301 SHEDHALYH TADGDLDMF RLYVKVDEQO PQOQOQQLIP LYPQHPABGH
1351 LOSWRNQSTR SSRKNGQECI KEPSELIYAP GSVAERSILL SNSGSGTSSQ
1401 PAGHNV

11AA SEQUENCE 1.0
ID 028733 PRELIMINARY: PRT: 6875 AA.

AC 028733
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE TITIN (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CE12;
RL Submitted (Feb-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-6805 FROM N.A.
RC STRAIN=CE12;
RX MEDLINE=92258380; Pubmed=1582406;

RA Labelt S., Gautei M., Lakey A., Trinick J.;
RT "Towards a molecular understanding of titin.";
RL EMBL J. 11:1711-1716(1992).
RN [3]
RP SEQUENCE OF 4305-5320 FROM N.A.
RC TISSUE=PSOAS MUSCLE;
RX MEDLINE=90238553; PubMed=2129545;
RA Labelt S., Barlow D.P., Gautei M., Gibson T., Holt J., Hsieh C.L.,
RA Francke U., Leonard K., Mardale J., Whiting A., Trinick J.;
RT "A regular pattern of two types of 100-residue motif in the sequence
of titin.";
RL Nature 345:273-276(1990).
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL: X64696; CAA45937.1; -;
DR EMBL: X17329; CAA35207.1; -;
DR HSSP: P56276; 1TLK.
DR InterPro: IPR000282; CytoK_receptor_2.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 15.
DR Pfam: PF00047; Ig; 50.
DR PRINTS: PR00014; FNIIIPEP11.
DR SMART: SM00060; FN3; 48.
DR SMART: SM00408; IGC2; 3.
DR SMART: SM00410; Ig_Like; 15.
KW Muscle protein; Myosin; Repeat.
FT NON_TER 1
FT 6875
SQ SEQUENCE 6875 AA; 759127 MW; 50C45B84F3668C55 CRC64;

028733 Length: 6875 April 1, 2002 16:32 Type: P Check: 9453

1 EYFRCYCAEN KVGVGPIET KPIILAINPI DRPEPENLH IADKGTVEY
51 LKMRPDIYD GSPNLSYHE RRLKSTDE RHKKSIXET HVLVCKEYEN
101 QIYERFVQTK NEGGEDEWK TEEVYKEDL QKPVLDLKLK GVLTVKAGET
151 IRLKAGVRGK PEPEYVWTKD KDATDFTRSP RAKIDTSADS SKFSLTKAKR
201 SDGKGYVYTA TMTAGSFWAY ATVAVNDLKPQ PVANLKIPIVY SSDRCTIRND
251 PEDDGGCEI QNYILEKCES KRWVSTYSA TVLTPTTVY RLIEGNEYIF
301 RVRAENKIGT GPTESEKPIV AKTKYDRGR PDEPEYTKVS KEEMTVVMS
351 PEYDGGKSTT GYLEKKEKH SVRWVPYKNS AIPERLKYQ NLIPGHEYOF
401 RVKAENEIGV GEPSLPSRPV VAKDPIEPG PPINKLVDT TKSSITLSWG
451 KPYDGGAPI IGYVEVVRPK IADASDEGW KRCNAAQLY RTEFTVSLD
501 ENQYEFRCV AQNOVGIGRP AELKEAIKPK EILEPEIDL DASMKLVVY
551 RAGCPIRLFA IVRGRPAKV TWKRVGIDNV VRKQVLDVY TMAFLVIPS
601 TDDSGKYSL TLVNPAGEKA VEVAVRVIDT PCGVSDLKVS DVTKTSCHVS
651 WAPPENDGS QVTHIVKRR DAEKTKSTV NPEVKTSCQ VTNLVPGNEY
701 YRVVTAIVNEV GGVPAADVPK PVLASDGLSE PDPKRLEVT EMTKNSATLA
751 WPLPLRDGA KIDGYIISYR EEDQPADRMT EYSVVKDSL VITGLKEGKK
801 YKFRVAARNA VGVSLPREAE GYFAKQOLI PKIILMPEOI TIKAGKKLRI
851 EAHVYKPOP ICKWKKGEDD VTSSHLAVH KAESSILIT KDVTKRDGCV
901 YSLTANSSG TDTQIKIVY MDRPGPOP FDISIDADA CSLSMHIPLE

951 DGSNTNTNY VEKODVSRGD WYALASVTK TSCRICKLIP GGEYFRVRA
1001 ENRFGISEPL QSPKMLAOP EGVSEPKNA RYTKVKNDCI EVAMDRPDS
1051 GSPITGYLI ERKGRNSLW VKANDTAVRS TEXPAGLVE GLEVSFRYA
1101 LKAGSSPPS KPEVTVART PVDPGKPEV IDVTKTSLV IMARKKHOG
1151 SKIIGYFVA CKLPEDKVR CNTPHOIPH EETVYGLEB NAQYFRAIA
1201 KTAVINISQS ELRPEVTIHA ENVPRIOLS VAKSSELYK AGTVNCLDAT
1251 VFGKPMPTVS WKKESTVLRK AEGIKMAMOR NCTLELFVS NKKDGGDTI
1301 TAENSSGSKS ATKIKLVDR PGPPASVKIN KMSDRAMS WEPLEDGGS
1351 EITNYIVDR ETSSRNMAQV SANVPITCS VEKLIGHEV QPRICAENKY
1401 GVGDVFTER AIARNPYDP GRCDPVISN VTKDHMTVSW KPPADGGSP
1451 ITGYLLEKRE THAVNMTKN RKPVIERTIK ATGLQEGTEY ERYVAINKA
1501 GFGKPSDASK AVYAODPLYP PGPPAPPKVY DTRSSVSIS WCKPAYDGS
1551 PIIGLYVEVK RADTDMWVRC NLPOKLQKTR FEVTGLMENT EQQFRVAVN
1601 KVGYSDDSDV PDKHCPOIL IPPEGLDAD LRKTLILRAG VTMRLVYVK
1651 GRPPKITS KPNVNLREI GLDIKSTDF TFLRCENVK YDAGYIITL
1701 ENSCGKKGYT IVVKVLDTPG PPVAVTYKEI SRSAVITWD PIVDGGSP
1751 INVVEKDA ERKSWTVYT ECKSTSPRS NLEBKSYFF RYANENGI
1801 GDPGETRDV KASETPGPV DKLVLVTKS SCNIGMKPR SDGSGRTGY
1851 VVDFLTEBK WQVVKSLSL QYSTKDLNEG KYTFPRSAE NNGGTPSE
1901 ITVAKADVY APDLDLKLDP DLYLAKENS NFKLKPQHOG KAPSVYTKK
1951 GEDPLATDR VSSESAVNT TLVYVDCOKS DAKGYITTLK NYAGTKEGTL
2001 SIYVGCKPGI PTGPIKPEV TAAITLTKG PRKDDGSEI TWILEKRS
2051 VNNKWTCAS AVOKTFRYT RLHEGMEYF RVSAENKYG GGLKSEPIV
2101 AKHPFVPPDA PPPNIIVDR HDSVSLWTD PRKTGSGPIT GYHIEKERN
2151 SLMKRANKT PIRMKDFKYT GLTEGLEVEF RVAINLAGV GRPSLPSEY
2201 VALDPIPPG KPEVINTRN SVLLIWTEPK YDGGHKLTY IYKRDLPK
2251 TWKKAHINW PDCAFTVTD VEGGYEFRI RAKNTAGALS APSESTGTII
2301 CKDEYAPPI VDPITIKDL TIKAGDTIVL NAKSIIGKPL PKSSMSKAK
2351 DIRPSDITOI TSTPTSSMLT VKIASRKDAG EYTTATNPF GKKEHVRVT
2401 VLDVPGPPG IEISNVSAEK ATLWTPELE DGGSPIKSYV LEKRETSRL
2451 WYVVAEDIOS CRHVYTKLIQ GNEYLFRSA VNHYGKEPV QSEPKVMVR
2501 FGPPGPPGP EVSNVTKNTA TVSKKRPTD GGSEITGYV ERREKGLRW
2551 VRATKTPVD LCKVTLGLOE GNTYEFRSA ENRAGIGPPS DASNYIMKD
2601 VAAAPGPSN ARVDTTKS ASLAMKPHY DGLLEITGY VEHOKVGDGT
2651 WVKDTGPAL RITEFVVDL HTKEKYNFRI SAINDAGVE PAVIDVEIV
2701 ERMADPEL DAELRRLVY RAGSIRIVY PIRGRAPAVY TWTKDINK

2751 TRANIENTES FTLLIIPBCN RYDTGKFWMT IENDPAGKSG FVNVRLDTP
 2801 GPVLNLRPTD ITRDSVTLHM DLPLIDGSGR ITNVIYEKRE ATRKSYSTVT
 2851 TKHCKCTYKV TGLSECEYF FRVAENENYG IGESETEKER VAKASERSPR
 2901 D3JNIMDTIK STVSLAMPKP KHDGSKITG YVIEAQRKGS DOWTHITTVK
 2951 GJECVARNLT EGEYTFQVM AVNSAGRSAP RESRPVIKVE QJMLPELDLR
 3001 GIVQKLVIAK AGDNIKVEIP VLGRRKPIVT WKKGDQVLKQ TORVNNENTA
 3051 T3TILLINSEC VRSDGPPPL TAKNIVGEG DVITIQVHDI PGPPGPPIKF
 3101 DEVSDFEVT SWEPENDGG VPISNVIEM RQDSTTWVE LATTVIRITY
 3151 KATRLTTGVE YQFRVKAQNR YGVGCGITSA SIYANYPEKV PGPPGPPOYT
 3201 AVTKDSMTIS WHEPLSDGGS PILGYHVERK ERNGIIMQTV SKALVGNIF
 3251 KSSGLTJGIA YEFVIAENM AGSKSPSKPS EPVLALDPID PGKPIPLNI
 3301 THHTVILKMA KPEYTGGEFKI TSYIYEKRD. PNGRMILKANF SNLENEFTV
 3351 SGLTEDAAYE FRVIAKNAAG AISPPSEPSD AITCRDQVEA PRILVDPRK
 3401 DVIILKAGEA FPLEADVSGR PPTPMWMTKD GKELEGTGKL ERIADESTY
 3451 LNKDSSRRD SGAYILTATD PGGFAKHIFN VKVILDRGPP EGPLAVSEYT
 3501 SEKCVLSWLP PLDDGAKIE HYIVQKRETS RLANTNVASE VOYTKLKVTK
 3551 LKGNEXIYFR VMAVNKYGVG EPLESEPVLA VNPYGRPPDP KNEVTTITIK
 3601 DEMVVCWGHF DSDGSEITN YIVERRDKAG QRWVKCNKKT VDDLREKVS
 3651 LLEGHEYEFR IMAENAGIS APSRTSPYK ACDAVEKPGP PGNPRVLDTIS
 3701 RSSISIAMNK PIYDGGSEIT GYWEIALPE EDEWKIVTPP AGLKATSYTI
 3751 TNLVENEYK IRIYAMNSEG LGEPALVPGT PKAEDRLPPE EIELDLK
 3801 LVVIRACCTL RLFVPIKGRP DPEVAKWTREH GESIDKASIE STISSYLLIV
 3851 GNVNREDSGR YILTVENSNG SKSAFVNVVR LDTPEGPQDL KYKEVTKTSV
 3901 TLTWDPPLLD GSKIKINYIV EKRESTRKAY STVATNCHKT SMKVDLOJEG
 3951 SSYFRVLAE NEYGIGLPAE TAESYKASER PLPPKITLV DVTRNSVLS
 4001 WEKREHDGGS RILGYIVEMQ SKGSDKMATC ATVAVTEATI TGLIQEEYS
 4051 FRUSAQNEKG ISDPRQLSVP VIADVLVPR AFKLEFNTFT VLAGEDLKID
 4101 VPJIGREPTP VTWHKDDVPL KQTRRVNAES TENSSILLISIK EACREDVGHY
 4151 VVKLSNSAGE ATEFLNAIIL DKPGPTGPV KMDEVTAESI TISMEPKYD
 4201 GGSISINNIYV EKRDSTTTW QIVSATVART TIKASRLKTG CEYOFILIAE
 4251 NRJGKSTYLN SEPVAQYPF KVPGPPTGPF VTLSSRDSME VQMEPVPNDG
 4301 GSHVIGYHLE RKEENSILMV KLNKTIPIOT KFKTTGLEEG IEVEFRVSAB
 4351 NIVGICKPSK VSECYVARDP CDPPGRPERI IVTRNSVTLO WKKPTIDGGS
 4401 KITGYVEEKK ELPDGRWMAKA SFTNIMDTQF EVTGLVEDHR YEFRVIARNA
 4451 AGVSESESES TGAITARDEI DPPRISMDPK YKDTIVVHAG ESERIDADIY
 4501 GKPIPTQWI KGDQELSNIA RLEIKSTQFA TSLSVKDAFR VDSGNVLKA
 4551 QNVAGERSVT VNVKVLDRPG PPEGPIVSG VTAEKTLIAM KPPLDQDGD

4601 IINYIVERRE TSRLVWTVD ANVOQLSCKV TKLLEGNEXI FRVMAVNKYG
 4651 VGEPLESEPV IAKNPFVVPD APKAPECTTV TKDSMIYWE RASOGGSEI
 4701 LGIVLEKRDK EGIRWTRCHK RLIGELRLRV TGLIENHNE FRVSAENAG
 4751 LSEPPSPSAY OKACDPIYK GPNNPKVMD ITRSSVFLSW SKPIYDGE
 4801 IQGYIVEKCD VSVGEWMTCT PPTGINKTNI EVEKLEKHE YNFRICAVNK
 4851 AGVDHADVP GYVIEEKL EAPDIDLDEL RKIINIRBAG SLRLPPIYG
 4901 RPTPEVKWCK VDEIRDAAI IDSTSFTSL VLDNVNRYDS GRYTTLENS
 4951 SGTSAFVTV RVLDTSPSPV NLKVTETIKD SVSITMEPPL LDGSKIKNY
 5001 IYERKDSIRK STAAVYTNCH KSMKIDOLQ EGSYIYFRVT AENENGICLP
 5051 ARTADPIKVA EYPOPPKIT VDDVTRNSVS LSMTKPEHDG GSKIIQYIVE
 5101 MQAKHSEKMS ECARVKSLEA VITNLQGE YLFRVAVNE KGRSDPRSLA
 5151 VPIVADLVI EPDVKPAESS YSVQGDQDL IEVPISGRPK PIITWTKDGL
 5201 PLKQTRINAV ADSLDLTLS IKETHKDDSG HGYITVANYV GOKTASIEII
 5251 TLDPKPPPKG PVKPFDEVSAB SITLSMNPPL YTGCGQITNY IYHKRDTTIT
 5301 VMDVSAITVA RTLLKVTKIK TGTEYOFRIF PENRYGOSFA LDSEPIVAOY
 5351 PYKEPGRPGT PEVTATSKDS MVVOMHEPIN NGSPILGYH LERKENSTIL
 5401 WTKVDSIIH DTQFKALNE EGIEYFRVY AENIVYGKA SNSECVYAR
 5451 DPCDDPGTPE AIIVKRNELT LQWTKPYVDG GSNITGYIVE KNDLPEGRMM
 5501 KASFTNVIET QFTVSGLTED QRYEFRVIAK NAAATWSKPS DSTGPTIAND
 5551 EVELPRISMD PKFRDTIVN AGEFTRLEAD VHOKPLPTIE WLRGQEVBE
 5601 SARCEIRKND FKALLIVKDA IRIDGQYIL RASNVAGSKS FRYNVKVLDR
 5651 PGPEGPVQV TGVTCCKCTL TWSPPLDDGG SDIPHYVEK RETSRLAMTV
 5701 VASEVVTNSL KITKLEGNE YIFRIMAVNK YGVGEPLESA PYLMKPEVY
 5751 PGPPKSLEVT NIAKDSMTYC WNRPDGSGGS EITGYIYEK DSGIRIMIC
 5801 NKRRTVDLRF RYTGLTEDHE YEFRVSAENA AGVEESPAT VYKACDPVF
 5851 KPGPTINAHV VDTKNSITL AMGKPIYDGG SEVLGYIIEI CADEEMQOI
 5901 VTPQGTGLKAN REISKLIEH QEYKIRYCAL NKVGLGEAAS VGTYKAPDEK
 5951 LEAPELDLDS ELRKGIYVRA GGSARIHIF KGRTPDITW SREGEFTDK
 6001 VOYEKGVNT QLSIDNCORN DAKYIVKLE NSSGTKAFAV TVKVLDTPEP
 6051 PQLNAVKEK KDSAVLWEP PILDGAKVR NYVIDKREST RAIYANVSK
 6101 CNKTTKVEN LTGAIYYFR VMAENEGVG VPVEYDAVK AAEPPSPGK
 6151 VTLTIVSQT SASMKEKPEH DGGSRLGVY VEMQPKTEK MSVAVESKYC
 6201 NAVVTGLSSG HEYOFRVAKY NEKGSDBRV LGVPIVAKDL TIQPSKLPF
 6251 KRYSVAGED LKIEIPVIGR PRPEIFWYKD GEPLRQTRV NYEETATSTI
 6301 LHIKSSKOD FGKYTTTATN SAGTATENLS VIVLEKGRPP VGVVREDEIS
 6351 ADFVVLWSEP PAYTGCGQIS NYIYEKDDT TTMHVIYSAT VARTTIKVTK

6401 LKTSGEYOPR IYAENRYGKS TSLDSKEPIV QYPFKEGPP GTPEVTSYR
 6451 DGMVOMHEP VNDGSKVLG YHLEQKEKS ILWVYKNKL IQDTFKXTG
 6501 LDEGLEYEK VSAENYIG KPSKVSCEV ARDPCCPPR PEALYITNN
 6551 VTLKKRPAY DGSKITGYI VERKDLDPGR WMKASFTNL ETEFTVGLV
 6601 EOGREFRVI ARNAAGNLSE PSSESGAITA RDEIDAPNAS LDPKKVDIV
 6651 VVAGETFEVL ADIRKPIPD VVMLDKGEL EETTAMEIK STIOKTLIV
 6701 KDCIRTDGO YVLKLSNVG TKSPLITVKY LDRPGPEEP LKVSQTAEK
 6751 CYLWNPPLQ DGASISHYI IEKRETSRLS WTVQSVTEVA LNYKTKLLP
 6801 GMEYIFRWVA VNKYIGIEPL ESEPIVACNP YKPPGPPSP EASAITKDSM
 6851 VVTWAPVDD GGAEIEGYIL EKRDK

11AA-SEQUENCE 1.0

ID: 097947 PRELIMINARY: PRT: 114 AA.

AC 097947
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
 DE GAMMA PREPROTACHYKININ I.
 OS Tupia belangeri (northern tree shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.
 OX NCBI_TaxID=37347;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Helldand A., Maegert H.J., Kruboeffer M., Forssmann W.G.;
 RT "Tachykinin precursors are highly conserved among different mammals.";
 RL Submitted (Aug-1995) to the EMBL/Genbank/DBJ databases.
 DR EMBL; 250785; CAA90648.1;
 DR InterPro: IPR002040; Tachykinin.
 DR InterPro: IPR003580; Protachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR ProDom: PD005598; Protachykinin; 1.
 DR PROSITE: PS00267; TACHYKININ; UNKNOWN_2.
 DR SMART; SM00203; TK; 2.
 FT CHAIN 58 68 SUBSTANCE P.
 FT CHAIN 83 92 NEUROKININ A.
 FT CHAIN 92 92 NEUROKININ A.
 SQ SEQUENCE 114 AA; 13281 MW; B439C3D27FDA7CAB CRC64;

097947 Length: 114 April 1, 2002 16:32 Type: P Check: 870 ..

1 MKILVALAV FLYSQLFAE EIGANDLNY WSDMSDDQI KEELPEPEH
 51 LQRIARRPK PQOFGLMGK RDAGHQISH KRHKTSFVG LMGRALNSV
 101 AYERNAMQDY ERRR

11AA-SEQUENCE 1.0

ID: 097948 PRELIMINARY: PRT: 129 AA.

AC 097948
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
 DE BETA PREPROTACHYKININ I.
 OS Tupia belangeri (northern tree shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupia.
 OX NCBI_TaxID=37347;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Helldand A., Maegert H.J., Kruboeffer M., Forssmann W.G.;
 RT "Tachykinin precursors are highly conserved among different mammals.";

RL Submitted (Aug-1995) to the EMBL/Genbank/DBJ databases.
 DR EMBL; 250786; CAA90649.1;
 DR InterPro: IPR002040; Tachykinin.
 DR InterPro: IPR003580; Protachykinin.
 DR Pfam: PF02202; Tachykinin; 1.
 DR ProDom: PD005598; Protachykinin; 1.
 DR PROSITE: PS00267; TACHYKININ; UNKNOWN_2.
 DR SMART; SM00203; TK; 2.
 FT CHAIN 58 68 SUBSTANCE P.
 FT CHAIN 72 107 NEUROPEPTIDE K.
 FT CHAIN 98 107 NEUROKININ A.
 SQ SEQUENCE 129 AA; 14941 MW; 5855E7ADC2D8674E CRC64;

097948 Length: 129 April 1, 2002 16:32 Type: P Check: 8952 ..

1 MKILVALAV FLYSQLFAE EIGANDLNY WSDMSDDQI KEELPEPEH
 51 LQRIARRPK PQOFGLMGK RDADSTIEQ VALLKALYGH GOISHRRHKT
 101 DSFVGLMGKR ALNSVAYERN AMQDYERRR

11AA-SEQUENCE 1.0

ID: 09M081 PRELIMINARY: PRT: 355 AA.

AC 09M081
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, last annotation update)
 DE MITOCHONDRIAL DNA, COMPLETE GENOME.
 OS Physarum polycephalum (Slime mold).
 OC Mitochondrion.
 OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
 OC Physarum.
 OX NCBI_TaxID=5791;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Takano H., Abe T., Sakurai R., Moriyama Y., Miyazawa Y., Nozaki H.,
 RA Kawano S., Sasaki N., Kuroiwa T.;
 RT "The complete DNA sequence of the mitochondrial genome of Physarum
 polycephalum.";
 RL Mol. Gen. Genet. 0:0-0(2000).
 DR EMBL; AB027295; BAB08081.1;
 KW Mitochondrion.
 SQ SEQUENCE 355 AA; 43335 MW; 5CE0AABD08D6E88F CRC64;

09M081 Length: 355 April 1, 2002 16:32 Type: P Check: 5275 ..

1 MITYLLNSF LLIKLILFIL IRIPLINIF SKYIIIFPS IIYICQKYP
 51 RINILIKEDL PEVALKTTKE KMINICITTL YITFYIGIF YIRYINITRK
 101 VDLKIYYIML KNLFEFTKE EILNVVILI TFIIVIFILI YKFTQYFKLO
 151 VIKRHLYLIG IPLNNWYST VHKRYLWPLA NSFLKISIKH KIELLYKXY
 201 FDKRPHKPRP DNFSLSSEA KILFEKNPPT LPELLFHKKK KNSITIDNLL
 251 TKGHYFLIL SILYDVINND FILTFIOL PWIFVELFL RISKFDVDM
 301 IPYDQALNHL IYSKRLKYN EETLMIDDEP HDMSFYODIN EHYIRGFVK
 351 DPNNI

11AA-SEQUENCE 1.0

ID: 09ZU49 PRELIMINARY: PRT: 302 AA.

AC 09ZU49
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
 DE PUTATIVE PHOSPHATIDIC ACID PHOSPHATASE.

GN F10A8.6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
 RA Barnstead M.E., Mason T.M., Bowman C.L., Rongling C.M., Benito M.,
 RA Carretero A.O., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
 RA Fraser C.M., Venter J.C.;
 RT "Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC006200; AAD14518.1; -
 DR InterPro: IPR000326; PA_PTPase.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidppc; 1.
 SQ SEQUENCE 302 AA; 33739 MW; 9E1C6D7DAFD569D6 CRC64;
 09ZU49 Length: 302 April 1, 2002 16:32 Type: P Check: 2420 ..
 1 MOEIDLSVHT IKSHGGRVNS KHKHDWILV ILAIEIGLN LISPFYRYVG
 51 KDMWTDLKYP FKDNTPYIWS VPYVAVLLPI IVFVCFYLKR TCVYDLHHSI
 101 LGLLFAVLIT GYTDSIKVA TGRPRPNFYW RCFPDGKELY DALGVCVCHG
 151 KAAEVEKGHK SFPSCGHTSWS FAGLFLSLY LSGKIFANN EGHVAKLCIV
 201 IFPLLAACLIV GISRVDDYWH HMVDVFAGL IGTLVAFYCY RQFYRPNYHE
 251 EGAGPFAVEK AAGERGVPYT SSQNGDALARA MSLQMDSTSL ENNESTSTRA
 301 PR
 11AA-SEQUENCE 1.0
 ID 09ZSD3 PRELIMINARY; PRT; 182 AA.
 AC 09ZSD3;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE GAMESTOPPYTIC ANTHERIDIOGEN-INDUCED PROTEIN.
 GN ANI1.
 OS Ceratopteris richardii.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Filicophyta; Filicopsida; Filicales; Pteridaceae; Ceratopteris.
 OX NCBI_TaxID=49495;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. HNN;
 RA Men C.K., Smith R.H., Banks J.A.;
 RT "ANI1: A sex pheromone-induced gene in Ceratopteris gametophytes and
 RT its possible role in sex determination."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF113324; AAD13287.1; -
 SQ SEQUENCE 182 AA; 22213 MW; 9061F4AD8B4033DB CRC64;
 09ZSD3 Length: 182 April 1, 2002 16:32 Type: P Check: 6830 ..
 1 MAIQRRFSYI LCAVATCSLL LIMPNSAYY EDEKETPEN YSKPSTTYV
 51 GKIEKDFEDV YKPSITYVEE EKEPEFYRYK KPYVYGDKHR PRVYVYKKEK
 101 EKYHHRKPRT VVYKPRPYA YKPKPVVIT KPVVVIYKRP KPVVVIYKRP
 151 AVYKHEEK YNYHYSYDKK PDFSPYEPK GY
 11AA-SEQUENCE 1.0
 ID 09X160 PRELIMINARY; PRT; 290 AA.
 AC 09X160;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE F9L1.2 PROTEIN.
 GN F9L1.2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Ienz C., Liu S.,
 RA Lee J., Liu A., Li J., Kremenetskaia I., Luros J., Gonzalez A.,
 RA Altati H., Arujo R., Brooks S., Buehler E., Chao Q., Conn L.,
 RA Conway A.B., Dunn P., Hansen N., Huizar L., Khan S., Kim C., Palm C.,
 RA Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R.,
 RA Federpsiel N.A., Theologis A.;
 RT "Arabidopsis thaliana chromosome 1 BAC F9L1 sequence."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC007591; AAD39637.1; -
 DR InterPro: IPR000326; PA_PTPase.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidppc; 1.
 SQ SEQUENCE 290 AA; 32702 MW; BF14A9A0C23B4429 CRC64;
 09X160 Length: 290 April 1, 2002 16:32 Type: P Check: 4011 ..
 1 MEPIHGANT IRSHGVYVAR FHHMDWILV LLIIVEIVLN VIEPFRVVG
 51 EDMLTDLRYP LODNTIPFMA VPLIAYVLPF AVICVYFYFR NDVYDLHNAI
 101 LGLLFSVLIT GYTDAIKDA VGRPRPDFW RCFPDGIGIF HNVTKNVLCI
 151 GAKDVYKEGH KSPSCGHTSW SFAGLFLSL YLSGKIRVD QRGHAKLCI
 201 VILPLVLAAL VGSVRDDYWH HMVDVFGA IIGLVVATPC YLQFPPPYD
 251 PDGCPHAYE QMLADSRNDV QDSAGMNLHS VROTELESVR
 11AA-SEQUENCE 1.0
 ID 09SV85 PRELIMINARY; PRT; 705 AA.
 AC 09SV85;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE HYPOTHEICAL 81.4 KDA PROTEIN (FRAGMENT).
 GN F24G24.170.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
 RA Mayer K.F.X., Scheller C.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL049488; CAB39790.1; -
 DR InterPro: IPR001064; Crystallin.
 DR InterPro: IPR001876; ZnF-RanBP.
 DR InterPro: IPR001965; PHD.
 DR InterPro: IPR002219; DAG_PE-bind.
 DR InterPro: IPR003006; IG_MHC.
 DR PROSITE: PS00225; CRYSTALLIN BETAGAMMA; UNKNOWN_1.
 DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 DR SMART: SM00249; PHD; 4.
 DR SMART: SM00547; ZnF_RBZ; 1.

KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 705 AA; 81384 MW; 13751CA016F99B19 CRC64;

Q9SV85 Length: 705 April 1, 2002 16:32 Type: P Check: 9930

1 GEEKRNKTK IQIPVYVAMS SVGVFHKVEM DENLYFYVKL TQTDYPTSSG
51 EVLWADSTGD DQPLDQPLFL CPDARIKFHK LKIQREDGDI FDYDFKPHFY
101 ISSPHFPSKR SGDOGESL DCEDEGICLK PVVPLFWCN KESDSREQC
151 GCGRDSMLSA SYVACLOCEK KFKKECVESD LEIKHPTLFL HSLRLYYHRA
201 PEFCICCKTE VEMIFYHCLT CNLSMHPVCA MKVPEFIDH PKSPHPPLTF
251 PPTQASLVCH FCALIKKLPD TYICTKCVFY HKKGLGFPH VIRLSRHTNR
301 ISFTSSLPFG KLSGVCVHQ VDNDYGAISC KKDAYEVVHS KCALQRHWD
351 GKDLSEVPEE DMIDIDGEPF KRIADGILH PPHSHNLHQ TTRAYDENTY
401 CCGCALPIYE GQFYSCIESD FILHEHCANA PMKRNHPLHP HPLILVYATR
451 GPGNEEGTFQ CDACHRKGTG FFEYHHTDOE NIFMDIHCA SIFPEFYOG
501 HEHPLFLPSE PNKWRGCOMC TFEYVNLNLN CLECDYILCF HCATLPHYVR
551 YKHDSHFLKI CNGKEANDOS YWCEICEGKI EGTETAFYV TPKKDTSYRK
601 CNACTTLHQ RCLLGIDITYM KPGETVKDYL SSIKYASEGQ SKESITVDQI
651 LNSSPTRPPI CTRCLRCRPF PIFFKGHNTI PCSWDCVEDS AMRSYQRLLY
701 SFLMG

11AA_SEQUENCE 1.0
ID Q9SV87 PRELIMINARY; PRT; 85 AA.
AC Q9SV87;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AT2G15340 PROTEIN.
GN AT2G15340.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.C., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Talon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome II of Arabidopsis thaliana.";
RL Nature 402:761-768(1999).
DR EMBL: AC006920; AAD22290.1;
SQ SEQUENCE 85 AA; 8733 MW; 7FDCP6B8EDD2C9F8 CRC64;

Q9SV87 Length: 85 April 1, 2002 16:32 Type: P Check: 8684
1 MALSSQKKR RGAGVLTAT AGGDMLALA PLPAQVQL VIGTLAVQTL
51 EYRILVTLAP LGDLGGVGD PTALGARPH MLXF
11AA_SEQUENCE 1.0
ID Q9SV87 PRELIMINARY; PRT; 667 AA.

AC Q9MAG7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE F12M16.24.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim C., Brooks S., Buehler E., Chao Q., Dunn P., Khan S., Shin P.,
RA Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F.,
RA Huizar L., Kremetska I., Lenz C., Li J., Liu S., Luros S.,
RA Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W.,
RA Federis J.N.A., Theologis A., Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F12M16 from chromosome
I.";
RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AC008007; AAF69544.1; -
DR InterPro: IPR001965; PHD.
DR InterPro: IPR001876; Znf-RanBP.
DR SMART: SM00249; PHD; 4.
DR SMART: SM00547; Znf_RBZ; 1.
SQ SEQUENCE 667 AA; 76885 MW; E54B20F8325B2844 CRC64;

Q9MAG7 Length: 667 April 1, 2002 16:32 Type: P Check: 2190

1 MNSNSVGEFR EGEIDGNPL IYTLISQTEP PSSREAAVDS DGGTVDDLSTV
51 EPLILCPTLR LKVNKLKPYT SDSDRSPFL VVSSHPTTIO SGHOQPEYML
101 QSYCKLPL PLFWCDKNP NIDFICRAC TTIBGTSYV VCVTCGDOFH
151 KECVGALEF KHPYPSLSL QLYSPSGRY LSCCQKPIY GMNYCYPTSN
201 FTLHFCARF PTPVIDHPK RHPHPLTFP KQSLPCVHC SLIKKIPTY
251 ICIRAFVYH QDCIFYPRVI KIRHHHRIS YSSLSGKM SCGYCROEVD
301 NDYGAYSCNK CDDYFVHSRC ALRRDIMGI ELEGVEELE IIVEPITIS
351 DGIHFSHG HHLKLDTSKA YDENKICQAC TLPYEGGY SGVBCDPTL
401 HEACANAPCK KYHALNPYPL TLKVTNEYH DNKGRFCDA CORESCPTVY
451 VDFRGCVAD TKDYKFKIDI RCASVSEPP YLGHEHPLYL ALNPEEESA
501 ICHIQESKD ESFCKKLNC IECDFVICK CATLPHYKARY QHDKHFLKFY
551 EAKEANDHSE WCDVCERRIA DLRRKGFYSC DDCCTTLHID CLGEGDMYK
601 PCHTLMYNT GSRKHOKKL HHSNMTLSR PCSCEGGERC ROKIVFEYKE
651 KIIFCAVSCQ KLVIDYS

11AA_SEQUENCE 1.0
ID Q9M882 PRELIMINARY; PRT; 314 AA.
AC Q9M882;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE PHOSPHATIDATE PHOSPHOHYDROLASE.
GN F16B3.23.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;

RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
 RA Rongning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Niernan W.C., Fraser C.M.:
 RT "Arabidopsis thaliana chromosome III BAC F16b3 genomic sequence."
 DR Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AC021640; AAF32467.1; -
 DR InterPro: IPR000326; PA_PTPase.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidppc; 1.
 KM Hydrolase.
 SQ SEQUENCE 314 AA; 35184 MW; 5F1B8546058C497 CRC64;

Q9M82 Length: 314 April 1, 2002 16:32 Type: P Check: 6307

1 MFEAQLGHT LRSHGWTVAR THMDWILV LVLILECVLL IHPEFRFVG
 51 KIMMTDLSYR LKSNVYPTNS VPVYAMLLPL VIFFIIFRR RDYVDLHNAV
 101 LGLLYSLVLT AVLTDARKNA VGRPRDFEW RCEPDGKALY DSLGDIYCHG
 151 DKSVIREGKH SFPSSGHTSNS FSGIGLFLSY LSGKIQAFDG KGHVAKLCIV
 201 ILPLFLALY GISRDYDWH HMODYFAGGL LGLAISTICY LGFFPPPHYR
 251 EGMGPYAFQ VLEARVQGA ANGAVQPPR QVNNGEEDG GFMGLHLVDN
 301 PTMRREDE TGRG

11AA-SEQUENCE 1.0
 ID Q9M82 PRELIMINARY; PRT; 676 AA.

AC Q9M82; 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE HYPOTHEICAL 78.2 KDA PROTEIN.
 GN ATAG10370.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;

RA [1]
 RP SEQUENCE FROM N.A.
 RA Murphy J., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL161517; CAB78160.1; -
 DR InterPro: IPR001064; Crystallin.
 DR InterPro: IPR000345; CytC_heme_bind.
 DR InterPro: IPR002219; DAG_Pe-bind.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR001965; PHD.
 DR InterPro: IPR001876; ZnF-RanBP.
 DR SMART: SM00547; ZnF_RBZ; 1.
 DR SMART: SM00547; ZnF_RBZ; 1.
 DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_2.
 DR PROSITE: PS00881; DAG_Pe_BIND_DOM_2; 1.
 DR PROSITE: PS00290; Ig_MHC; UNKNOWN_1.
 KM Hypothetical protein.
 SQ SEQUENCE 676 AA; 78165 MW; 25D1F73FB1585E0 CRC64;

Q9M05 Length: 676 April 1, 2002 16:32 Type: P Check: 7623

1 MDNLVFFVYK LTQTDYPTSS GEVLAMDSTG DDQPLDPLF LCPDARIKPH
 51 KLTIQREDGD IFDYDEKPHR YISSPHPSK RSGDQGESL LDDDEGICK
 101 LPVPLFLWCN NKESDSREFQ CGGCRDSMLS ASYIACIQCE KPFHKECVES

151 PLEIKHPTHL FSHRLYYHP APEFCICCKT EYEMIFVHCL TGNLSMHPVC
 201 AMKRVFFID HKSHRPHLT FFFQASLYVC HFCALKKLD PVIYTKCVF
 251 VHKGCIGEP HVIKSRHWH RISTSSLPK GLKSCGVCHO QVNDYGAVS
 301 CKKCDAYFVH SKCALQRHWH DKGDLVEPDE EDMIDGEP FKRIADGIIL
 351 HPHSHNLHL QTRAYDENT YCRGALPIY EGOFYSCIES DILHEHCAN
 401 APRMKRPHLH PHLPLVAVT RCPGNERGTE QCDACHRKGT GFYEHHTDQ
 451 ENIFMDIHC ASIFEPFOYQ GHEHPLFLPS EPNKMGRCQM CYEYVNLNL
 501 NCLECYIILC FHCATLPYKV RYKHDSHPLK ICKGKEANDQ SYWCEICEBK
 551 IEEGTERRAF NTPKRDTSFY KGNACCTTLH QRLCLGIDTY MKRGETWKDY
 601 LSSIKYASEG QSKESITDQ ILLNSPTRP ICTRCICRCP PFIFPKHNT
 651 IFCSMQVED SAMRSYQRL YSFLMG

11AA-SEQUENCE 1.0
 ID Q9M05 PRELIMINARY; PRT; 681 AA.

AC Q9M05; 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE CHP-RICH ZINC FINGER PROTEIN-LIKE.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
 RT clones."
 RL DNA Res. 7:131-135(2000).
 DR EMBL: AB028611; BAB01837.1; -
 DR InterPro: IPR000345; CytC_heme_bind.
 DR InterPro: IPR001965; PHD.
 DR InterPro: IPR001841; ZnF_Ring.
 DR SMART: SM00249; PHD; 2.
 DR SMART: SM00184; RING; 2.
 DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
 SQ SEQUENCE 681 AA; 78805 MW; ABCB58E239519FC9 CRC64;

Q9LRV1 Length: 681 April 1, 2002 16:32 Type: P Check: 6135

1 MSSVGFVDV ENDEKSYLVY TLITQKHPTS SAVESGDDI PLQPLFSCPY
 51 ARIIRSHKPV EKNYDGVNF NHPFNSYPH FPRTRSYOQ GSLLDYDHH
 101 NICKFVYVPL FWCNNKTPDS NEFCGCEE SKTSRSYVAC LECGNKPFHQ
 151 CVESPLEIHN PSHPHSLRL YSHPTHWCI CGRLYSNMF YHCYTCDSLMS
 201 DPICAMEPIR FVVDHPRKSH HPITFFPTQA TLACNICGLV KMLDPTYICI
 251 QCVFVIHKOC MGYPHVIRIS RHQHRISFAS SLFYGNLSCG VCHQAVDNNY
 301 GAYSCGKDA YFVHSCAFH RNWDGKELE GVSEEDDIID DEEPERISD

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351 GYLPHYHSH HLRLEISKVY DENKCYRCS EPIYEGFYS CKECPILHE
401 SCANAPRMKR HPLHPHPLTL NVATKELGN EGVYHONVCG RDGTGFYEH
451 HIGERFRID LRCASTREPF EYCHKHPLC IASELEKVA COICGKSS
501 KLNCECDYI ICFRCATPEY KVRKXDSHF LRIRGKKAS DEPDCEVC
551 GRIEYKERE SPWKRERMR FYKNCDCCTT LHVECLLGR MYMKPGNSVK
601 DISKSLGI EGTOWTDVVR FLNLSLRPI CTCGMRCLE PLVFGYNTI
651 PCSWECIGYG DTVEHPTSN PFSSIVLEL M

11AA-SEQUENCE 1.0
<ID 09LN20: } PRELIMINARY: PRT: 734 AA.
AC 09LN20:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE P9C16.28.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kilecawa J., Kim C., Altati H., Bel Q., Chin C., Chlou J., Choi E.,
RA Com L., Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thayeri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,
RA Theologis A., Ecker J.R.;
RT Genomic sequence for Arabidopsis thaliana BAC P9C16 from chromosome
RT I."
RN [2]
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altati H., Bel B., Chin C., Chlou J., Choi E.,
RA Com L., Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thayeri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC022314; AAF79671.1; -.
DR InterPro: IPR000345; Cyrc.heme_bind.
DR InterPro: IPR002219; DAG.pe_bind.
DR InterPro: IPR001965; PHD.
DR SMART: SM00249; PHD; 3.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE: PS0081; DAG.pe_bind_DOM_2; 1.
SEQUENCE 734 AA; 84111 MW; DABFEFOCA3FABI CRC64;

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09LN20 Length: 734 April 1, 2002 16:32 Type: P Check: 5875

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1 MNSVGFERKE EIDGKSFYV TLTOTDPTS SGEALMDSG GDDLPLPIPLF
51 FCPAARINFA KLRKMHND DDDDAEDDN GDKKESDD NKGDSDDDN
101 EDDNEDDND DDDDDDDDD DDDDDDDDDG DDDNEDGDCD DDDGILLPF

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151 DSTPHFPSTR SGDOGESL DCNHPDYCKL PVPLEWCNN KERSTVGEFC
201 GACKMTLCE SYFACLOCG KFKKEVESP PEIKHPSHPF HSLRLCSFOT
251 RLTSGCCRI TFGMYOCTT CNLSMRYCA MRVPLVVDH PSHHPHLSF
301 PFTQASTVCH ICARKHLDP TYICIQCFV IHKCGMFPH TIRISHPHR
351 ISFTSLSPR TLSGCVCHQ VDNNGAYSC NNCDGFEVHS KCAHPKWD
401 GKELEVPPE DDLIDGEPF ERISDGIHH PHSHLRHE MSITDESKY
451 COGALPIYE GQFYSCEBD FILHSCANA PRMKRRLPX HPITLKFAV
501 RNNSFTSQFR CAVCDRHNG FFEYHGEDK MFLDLRCL ILEPLVGGH
551 MHPFLMDD TESLISCOMC KKSYYQLF CLECEYSLC KCVTPPYKVR
601 YKHDSHFLT CDVKEASDEL DMCDCGSKI EEEKEREYMW DDRERELRY
651 KCNDCTALH VDCILGVDMY MKPTDYISV ITLTSKTR KDLMTPLNNS
701 LRPICTTCL SRCPPIFFK GHTKIFCSLY CSED

11AA-SEQUENCE 1.0
<ID 09LIS2: } PRELIMINARY: PRT: 90 AA.
AC 09LIS2:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE SELF-INCOMPATIBILITY ASSOCIATED RIBONUCLEASE (FRAGMENT).
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Prunus.
OX NCBI_TaxID=3755;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BOA CASTA;
RA Ma R., Oliveira M.M.;
RT "Molecular Characterization of Almond Cultivars Using S-RNase Gene
RT Sequences as Markers."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157010; AAF82614.1; -.
DR InterPro: IPR001568; RNase_T2.
DR Pfam: PF00445; ribonuclease_T2; 1.
DR PROSITE: PS00530; RNase_T2_1; 1.
FT NON_TER 1 90
FT 1
SEQUENCE 90 AA; 10654 MW; D862FE388684C2076 CRC64;

09LIS2 Length: 90 April 1, 2002 16:32 Type: P Check: 2503

1 QFVQWPTN CWRIRKPCS KRPLOYFTI HGLMPSNYSN PRIPNCTGS
51 QFKKQNLVRY LQSVLKKSMP DVESGNDTKF WEGEMNKHGT

11AA-SEQUENCE 1.0
<ID 09LLO7: } PRELIMINARY: PRT: 374 AA.
AC 09LLO7:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE PHOSPHATIDIC ACID PHOSPHATASE ALPHA (EC 3.1.3.4).
OS Vigna unguiculata (Cowpea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Vigna.
OX NCBI_TaxID=3917;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV. EPACE-1; TISSUE=LEAF;
RA Franca M.G.C., Matos A.R., d'Arcy-Lameta A., Zully-Fodil Y.,

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RA Pham-Thi A.T.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF165891; AAF89579.1; -.
 DR InterPro: IPR000326; PA_PTase.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidppc; 1.
 KW Hydrolase.
 SQ SEQUENCE 374 AA; 42336 MW; B50DAD5707D0A0BC CRC64;

091LQ7 Length: 374 April 1, 2002 16:32 Type: P Check: 92 ..

1 MASWMDLRRL FGFOSITRPF ODLSSRRIGI SAVSGAHSS INFPLIDKN
 51 EIDPFREYQ LGSHTVSSHG YAVARTHKD WLILLLVV ALGLYVHPF
 101 HRFYKDMMT DLRYPLKNT VPWMSIPIYA VLLPIVLELV VYIRRDYVD
 151 LHHAVGLLF SLITNAVTE AIKNGVGRPR PDEFWRCPD GKDVYDKLD
 201 VICHGKGVV KEGYKSPSG HTSWFSGLG FLSTYLSGI KAFDRGHYA
 251 KICLVFPL PL FASVIGISRV DDYMHMDV FAGLLGLTV STFCYIQFP
 301 PFHSEGWGP VAYFRMLEES RQMTQVNPV NSGHAQLETV QAEGERGQC
 351 HCGMGLSLR DRNATLNDIE SGRG

11AA SEQUENCE 1.0
 ID 091LQ8 PRELIMINARY; PRT; 307 AA.

AC 091LQ8;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PHOSPHATIDIC ACID PHOSPHATASE-LIKE PROTEIN.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA Nakamura Y.;
 RX PubMed=10907853;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
 RT TAC and BAC clones."
 RL DNA Res. 7:217-221(2000).
 DR EMBL: AP000414; BAB01172.1; -.
 DR InterPro: IPR000326; PA_PTase.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidppc; 1.
 SQ SEQUENCE 307 AA; 34951 MW; 06E394DD1C79DB3B CRC64;

091LQ8 Length: 307 April 1, 2002 16:32 Type: P Check: 3777 ..

1 MAXIMIGSHS VSHGWKVAR EHLCDWLIVL VLGILDIVL VIEPFRYIG
 51 PDMITDLTFP FYEDTIPMA VPICILVPI CIFIYVYYYR RDYVDLHNAI
 101 LGIGFSLVLT GVTDSIKDA VGRPRNPFY RCFPNKRPV PDKRVVCHG
 151 VKIIEGYK SPSGHTSMS FAGLTFLLWY LSGRIKVEDR RGHVAKLCV
 201 FLPLISILI GISRDYWH HMTDVFAGAI IGIFVASFSY LHFPPPYDE
 251 NGNAPHAYFR MLEIRSTGRA TTMRTGSGRG MLDNDVEPGN SASSPDRHR

301 ESTDSDF

11AA SEQUENCE 1.0
 ID 091LS4 PRELIMINARY; PRT; 221 AA.

AC 091LS4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE SELF-INCOMPATIBILITY ASSOCIATED RIBONUCLEASE.
 OS Prunus dulcis (Almond) (Prunus amygdalus).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Rosales; Rosaceae; Prunus.
 OX NCBI_Taxid=3755;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CODIFICADA;
 RA Ma R., Oliveira M.M.;
 RT "Molecular Characterization of Almond Cultivars Using S-RNase Gene
 RT Sequences as Markers."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF157008; AAF82612.2; -.
 DR InterPro: IPR001568; RNase_T2.
 DR Pfam: PF00445; ribonuclease_T2; 1.
 DR PROSITE: PS00530; RNASE_T2_1; 1.
 SQ SEQUENCE 221 AA; 25844 MW; 073C2F245BD8FF2C CRC64;

091LS4 Length: 221 April 1, 2002 16:32 Type: P Check: 4935 ..

1 MGILKSLAE IVLGFAFFEC YWSSGSYDY FQFVQMPPT NCRVTRKSK
 51 PRDLYFTTIH GLMPNSNP TPSNCSKFE DERNVSQRLR NKLKRSMPDY
 101 ESNDRKFE GEMNKHGICS EQLNQFOYF ERSQDMKSH NTELLKANS
 151 IYPSATQNMW YSDIVSPIK ATKRPILRC KQDKTQLLH EVFCETVNA
 201 LKQIDCNRTS GCMNSVINISF P

11AA SEQUENCE 1.0
 ID 09FVLI PRELIMINARY; PRT; 322 AA.

AC 09FVLI;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE PHOSPHATIDIC ACID PHOSPHATASE BETA (EC 3.1.3.4).
 OS Vigna unguiculata (Cowpea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Vigna.
 OX NCBI_Taxid=3917;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. EPAGE-L; TISSUE-LEAF;
 RA Franca M.G.C., Matos A.R., d'Arcy-Lameta A., Zully-Fodil Y.,
 RA Pham-Thi A.T.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF171230; AAF89745.3; -.
 DR InterPro: IPR000326; PA_PTase.
 DR Pfam: PF01569; PAP2; 1.
 DR SMART: SM00014; acidppc; 1.
 KW Hydrolase.
 SQ SEQUENCE 322 AA; 36224 MW; 67B7B572DCAAF8E CRC64;

09FVLI Length: 322 April 1, 2002 16:32 Type: P Check: 8335 ..

1 MPEIQGMHT IRSHGTVAR IHMDWLILL LVYIADVAV IIEPFRFVG
 51 EGMNTDLRNP LKNTIPFMA VPVAILLPL AVFLVYFYR KQYDFHNAI
 101 LGILFSLVLT AVYTDALDQ VGRPRDPFW RCFPDKGVF DVTSDVRCST
 151 GQGVIEKGT KVSFSGHTSW SFAGLVYLSW KLSGKIRVED RGHVAKLCL

201 VEPILVAM IAGSRVDDYW HHMDVPAG LIGTTASFC YLQFYPPYD
251 LQGMGHAF OMLAESRNG QPSTVNNH HVOSELQAV SYITPQMDA
301 DFRVNSWDS PMLGASQNR TH

11AA SEQUENCE 1.0
ID 09FVJ1 PRELIMINARY: PRT: 162 AA.

AC 09FVJ1: 0
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE SE-RNASE (FRAGMENT).
GN SE-RNASE.
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Prunus.
OX NCBI_TaxID=3755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CODIFICADA; TISSUE=PISTILS;
RA Ma R.-C., Oliveira M.M.;
RT "Detection of S-RNase related sequences in almond.";
RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF177923; AAG09286.1; -
DR InterPro: IPR001568; RNase_T2.
DR Pfam: PF00445; rbonuclease_T2; 1.
DR PROSITE: PS00530; RNase_T2_1; 1.
FT NON_TER 1 162
FT NON_TER 162 162
SQ SEQUENCE 162 AA: 19094 MW: 440078B97171736C CRC64;

09FVJ1 Length: 162 April 1, 2002 16:32 Type: P Check: 7946

1 QFVQWPTN CWRTRCKSKP RPLQYFTING LMPNSYNSPT PSNCGSKFD
51 DRVSPQLRN KLRKSPDVE SGNDTKFMEG EMNKHGICSE QTLNQFYRE
101 RSODMKSHN ITELKNAI VPSATQWRY SDIVSPIKRA TKRTPLRCK
151 ODKTQLLHE VV

11AA SEQUENCE 1.0
ID 09FVJ0 PRELIMINARY: PRT: 172 AA.

AC 09FVJ0: 0
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE SG-RNASE (FRAGMENT).
GN SG-RNASE.
OS Prunus dulcis (Almond) (Prunus amygdalus).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Prunus.
OX NCBI_TaxID=3755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BOA CASTA; TISSUE=PISTILS;
RA Ma R.-C., Oliveira M.M.;
RT "Detection of S-RNase related sequences in almond.";
RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF177924; AAG09287.1; -
DR InterPro: IPR001568; RNase_T2.
DR Pfam: PF00445; rbonuclease_T2; 1.
DR PROSITE: PS00530; RNase_T2_1; 1.
FT NON_TER 1 172
FT NON_TER 172 172
SQ SEQUENCE 172 AA: 20104 MW: 76BDA0A077FFD9AB CRC64;

09FVJ0 Length: 172 April 1, 2002 16:32 Type: P Check: 5836

1 QFVQWPTN CWRTRCKSKP RPLQYFTI HGLMPNSYNS PRIPSNCTGS
51 QFRKQNLVRY LQSVLAKSWP DVDSGNDTKF WEGEMNKHGT CSERLNIHQ
101 YFORSYAMWK SHNITELLQV ASIVPHPTQT WKYSIESPI KTATKRTPLV
151 RCKPDPQNK SQPKTQLLHE VV

11AA SEQUENCE 1.0
ID 09FM61 PRELIMINARY: PRT: 685 AA.

AC 09FM61: 0
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE SIMILARTY TO CHP-RICH ZINC FINGER PROTEIN-LIKE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98290546; PubMed=9628582;
RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
RT Sequence features of the regions of 1,456,315 bp covered by nineteen
RT physically assigned P1 and YAC clones.";
RL DNA Res. 5:41-54(1998).
DR EMBL: AB009050; BAB09245.1; -
DR InterPro: IPR002219; DAG_PE-blind.
DR InterPro: IPR001965; PHD.
DR SMART: SM00109; C1; 3.
DR SMART: SM00249; PHD; 3.
SQ SEQUENCE 685 AA: 79297 MW: 427694EFD52BC4F0 CRC64;

09FM61 Length: 685 April 1, 2002 16:32 Type: P Check: 7091

1 MSEVGVFRKE EIDGKFLAY TLTOTETPTS SGDAALAAAK AMFYGVDDL
51 LQPLFCPSV RIKFLSKPK NHDDHHNGG FMEHPLNSTP HPCCTRSHDQ
101 QGESLLDCDK DYCKLVYIP LFWCNKKEFR YGFEDCRACN GNIPTSYFT
151 CLQCGKFKK ECVESPLEIK HPSHPFSLR LSSGSSNQKC SCCKYTPPM
201 YHCTTCELS MNPVCAMRPV PLVVDHFKSH PHLSEFPDQ ASTVCNICAM
251 IKKLDPYIC IQCVVINKG CMGPHIIRI SRHPHISFT SSLPGNFSK
301 GVCROQVNN YGANSCEICD DYVHSKCSL LPRIMDGEL EGVPEDDKI
351 DGEPEKRIA DGIILPHFS HHMLREIDKA YDGNKYCRGC ALPIYEGOFY
401 SCWECDFILH ESCANAPRMK RYPLYPHPT LKOTTRHNE QKGKVCSCBC
451 RRDNGFFYE YRKEKEIFOL DLRCASITP EDYQGHQHL PLPDTKKKT
501 RCMCKYESK ESKLCECD YSICFCATF PYKARYKHS HFLTIDCKE
551 ESDPEWCEV CEGKIEVKE TGYMWKGTK ELKYYCNCQ CVALHVDCLF
601 GRMVIKPEE TEKEVLSFD FFSBEDYWK MVRALLNS LSRPLNGCK
651 CRCPPIFYK GDLIFCSMY CLKIHPPTP SRVSW

11AA SEQUENCE 1.0
ID 09CAP2 PRELIMINARY: PRT: 421 AA.

AC 09CAP2: 0
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE HYPOTHETICAL 47.7 KDA PROTEIN.
GN T5M16.25.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE#21016719; PubMed-11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White D., Alonso J., Altati H., Araujo R., Bowmen C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chen Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Mafti R., Marshall A.I.,
RA Miltner J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vayenberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venier J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana."
RL Nature 408:816-820(2000).
DR EMBL; AC010704; AAG51667.1; -
DR InterPro; IPR003409; MORF.
DR Pfam; PF02493; MORF; 7.
KW Hypothetical protein.
SQ
SEQUENCE 421 AA; 47731 MW; 08361C916235663 CRC64;
O9CAP2 length: 421 April 1, 2002 16:32 Type: P Check: 8387 ..

1 MSQKILTRQ SSLRSPPT RSSIQSLSSI TECDDFNETS HHRQEDLEA
51 GEHEEQRORR KPVKSGSMN RIKGLAFTL ACISFLSLSS FLFFVDELF
101 TSNLLGLI EYALAFRAS RNMAVINGTV IAIKQIRVRS RIKHKRPVQ
151 WYIGDSKPER IKEETRLVY KEGVQFSGS DYEGERNRG KNGSGVYY
201 YVNGRREGDW INGRYDGYI ECMSKSGYK GQYKQGLRHG FGYYEFTYGD
251 SYSGEWFNGO SHGFGVQTC DSSSFVGEFK FGYNHGLGSY HERNDDKYAG
301 EYFGDKINGF GYVHPANGHY YEGAMHGRK OGGYTYRFT GDIKSGEMDD
351 GNLVNLPLPD SDPVRAVOS ARERAKNGVN QRRIDEVIR AYAANKAAT
401 AARVAAYKAV QNMMDKICD N

11AA_SEQUENCE 1.0
ID_09AWT8 PRELIMINARY; PRT: 362 AA.
AC_09AWT8:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE PUTATIVE PHOSPHATIDIC ACID PHOSPHATASE ALPHA.
GN P0480E02.6.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxId=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa nipponbare(ga3) genomic DNA, chromosome 1, PAC
clone:P0480E02."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002913; BAB21200.1; -
SQ SEQUENCE 362 AA; 40682 MW; 8C4F1141F8BF5176 CRC64;
O9AWT8 length: 362 April 1, 2002 16:32 Type: P Check: 2435 ..

1 MDGRREVQGS PHTIOTNGVR LARNHLDHW VILLAAVVI ALHFAPEPSR
51 FPGKDMATVP SYPKQSTVP AMGVPIISIV CPVITPLSVY IARRVYDLH
101 HATGLVLSV LITAVVTVV KNAYGRPRPD FFWRCPPDCK QLYDQVTDV
151 ICHGEKSFVK DGRKSPSGH TSMSEAGLGF LSLYLSGKIK VEDROGHYAK
201 LCIIMPLPLI ASLVGSRID DYRNHWDFV AGGLLGFIMA MLCYHAFPP
251 PYNHGFSAP LSKFVHGMV GDRMHTSICL RSFKWPTPTM QKASSQCVGI
301 MSLYDYTLA GHQEMWKLK VCNIPMLKT EBAACTVAVS NGVPLTLVS
351 LKQERNLARI TA

11AA_SEQUENCE 1.0
ID_088542 PRELIMINARY; PRT: 2074 AA.
AC_088542:
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE OPA-CONTAINING PROTEIN 1.
GN TNRC11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Philibert R.A., King B.H., Cook E.H., Lee Y.-H., Stubblefield B.,
RA Damschroder-Williams P., Dea C., Palotie A., Tengstrom C.,
RA Martin B.M., Gims E.I.;
RT "The association of a dodecamer insertion variant with mental
retardation."
RL Mol. Psych. 0:0-0(1998).
DR EMBL; AF071310; AAC83164.1; -
DR MGI; MGI:192612; Tnrc11.
DR InterPro; IPR001241; DNA_topoisom_II; UNKNOWN_1.
DR ProSITE; PS00177; TOPOISOMERASE_II;
SQ SEQUENCE 2074 AA; 231808 MW; 293224D9BF46208 CRC64;
O88542 length: 2074 April 1, 2002 16:32 Type: P Check: 415 ..

1 MNQKDNFVLV TARQSALNT WFTDLAGTKP LTHLAKVVI FSKKEVGY
51 LAKYTPVNR AAMLKMTCA YVAMSETKV KKNTRADPT EWTQITRYL
101 WEOLOKMAEY YRPGPAGSG CGSTIGPLPH DYEMAIRQMD YNEKLALMF
151 QDGMIDRHEF LTVVLECFEK IRGEDELLK LLLPLLRIS GFQVSATLS
201 RLIAVFCSTR LALDLDVSS HSHVIAAOS TSSLPTTPAP QPPTSTPST
251 PPSDLLMCPQ HRLVFGSLC ILQITLLCP SALVMHYSLT DSRITGSPL
301 DILPIAPSNL PMPEGNSAFT QOYRAKLREI EOIKERGCA VEVRKSPFKC
351 QEATAGFTIG RVLHTLEVLD SHSPERSDFS NSLSDLCNRI FGLGSPKDGH
401 EISSDDDAV SLCEMAVSC KRSGRHRAW VAKLLEKQA EIEARCGES
451 EAADEKGSVA SGLSAPSPAP IFQDVLLQFL DTQAPMLTLP RSESRVFF
501 NLVLFCELI RHDVFSHMY TCTLISRGDL AFGAPGRPP SPFDDPTDDP

551 ERKEAGSSSS SKLEDPGLISE SMDIDPSSTV LFEDEKPDF SLFSTMPCE
 601 GKSGSPKEP DVEKEKPEPA KEKIEGLIGI LYDQPRHVOY ATHPIPIQEE
 651 SCSEHCNORL VVLFVGKOR DDARHAIKTI TKDILKVLNR KQTAETDOLA
 701 PIVPLNPGDL TFLGEDGQK RRRNRPEAPF TAEDIFAKFO HLSHYDQHOV
 751 TQVARNVLE QITSPALGMS YHLPIVOHQV FIFDLMEYVL SISGLIDAI
 801 QLLNELSYVE AELLIKSSDL VGSYTSLSL CIYAVLRHYH ACLILNDOM
 851 AQVFGELGV VKHGMNRSBG SSAERCLAY LYDLTSCSH LKSKFGLFS
 901 DCSGVKNNTI YCNVPSRSN MRNAPFEMID TLENPAHNF TYTGKGLS
 951 ENPANRYSFV CNALHVCVG HHDPDRVNDI AILCAELTGY CKSLSAEWLG
 1001 VLKALCSSN NGTCGFNDLL CNVDVDSLSE HDLAFVVAI LIAROLLLE
 1051 DLRCAAPIS LINAACSEOD SEGGARLTCK ILHLFKTQO LNPOSDGNK
 1101 PTVGIRSSCD RHLLAASOR IVDGAVFAVL KAVFVLGDAE LKSGFTVPG
 1151 GTEELPEEBG GGGSSGRROG GRNIVETAS LDVYAKYVLR SICQEWVGE
 1201 RCLKSLCEBS NDLODPVLS AQAOQLMQLI CYPHLLDNE DGENQORRI
 1251 KRILKNLDM TMRÖSSELO LMIKQTPNTE MNSLENIAR ATIEVQOSA
 1301 EFGSSSGSTA SNMPSSTKT PYLSLERSG VMLVAPLIAK LPTSVOGHVL
 1351 KAGEBLEKG QHLGSSSRKE RDRQOKOSMS LLSQDPFSL VLTCLKGDE
 1401 QREGLAŠH SQVHOIYINM RENQYLDCK PROLMHEALK LRLNLVGME
 1451 DTVORSTOOT TEMAQLLEI IISGTVMOS NNELFTTVLD MSLVINGTL
 1501 AADMSISOG SMEENKRAYM NLVKKLOKL GERÖSDSLK VHOLLPLKO
 1551 NRQVITCEPO GSLIDTKGN IAGFDSIFKK EGIÖVSTKÖK ISPMELFEGJ
 1601 KPSTAPLSMA WEGTVRVDRR VARGEEOQL LYHTHLRDR PRAYYLEPLP
 1651 LPPEDEEPPA PALLEPEKKA PEPPKTDKPG AAPPSTEERK KKSITGKKRS
 1701 QPATRNEDYG MGPRSGPYG VTPPPDLLH ANPGSISHLS YROSSMGLYT
 1751 QNOPLPAGP RVDPYRPVRL PMOKLPTRP YPGVLPTMS TYMGLEPSSY
 1801 KTSVTRQOOP TVPOGÖRLÖ QLOOSQGMG QSSVHOMTPS SSYGLÖTSOL
 1851 SSPSLÖGYTS YVSHVGLÖH TGPADPTRLH QORPSGVHÖ QAPTYGHGLT
 1901 STÖRESHÖTL QÖTPMGGTMT PLSAQVOAG VRSSTILPEO QÖQÖQÖQÖQÖQ
 1951 QÖQÖQÖQÖQÖQ QÖQÖQÖQÖQÖQ QÖYHIKQÖQ QÖQMLRQÖQ QÖQÖQÖQÖQÖQ
 2001 QÖQÖQÖQÖQÖQ QÖQPRHÖQÖQ AAPPOPOQS QPOFORÖGLÖ QTOÖQÖQÖTA
 2051 LVROIQÖQLS NTÖPOPSTNI FGRY

11A-SEQUENCE 1.0

AC 09D788; PRELIMINARY; PRT: 158 AA.

DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, last annotation update)
 DE 2310022A04RIK PROTEIN.
 GN 2310022A04RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TONGUE;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Felschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
 RA Wyszew-Boris A., Yoshida K., Hasegawa T., Kawai H., Kontsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 DR EMBL: AK009455; BAB26299.1;
 DR MGD: MGI:1919160; 2310022A04RIK.
 SQ SEQUENCE 158 AA: 17517 MW; B05FA8090DA3C14 CRC64;

09D788 Length: 158 April 1, 2002 16:32 Type: P Check: 7438 ..

1 MGTALGAEL GVRVLLPFAF LVTELLPFPQ RHIOPEELM YRNPVEAEY
 51 PPTGRMFVIA FLTPLSLIFL AKFLRKADAT DSKQACLAAS LALALNGVFT
 101 NIILIVGRP RPDEFYRCFP DGLAHSDLTG TGDEDEVNKG RKSPPSGHSS
 151 CMSFMGTT


```

1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35:  THERS      RPKPQOFF      GLX

AAR21932  ck: 3913  len: 43  1 Aar21932 Substance P (1-9) fragment. 6/1992
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      G

AAR21934  ck: 1501  len: 45  1 Aar21934 Substance P [Tyr7] and fragment (7
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      GLM

AAR21935  ck: 1109  len: 45  1 Aar21935 Substance P [Pro 9] or [D-Pro 9].
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      PLM

AAR21936  ck: 1217  len: 45  1 Aar21936 Substance P or (7-11) [Ethionine 1
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      GLX

AAR21937  ck: 677   len: 45  1 Aar21937 Substance P or (7-11) [Norleucine
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      GLL

AAR21938  ck: 722   len: 45  1 Aar21938 Substance P [Me-Leu 10]. 6/1992
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      GLM

AAR21940  ck: 898   len: 45  1 Aar21940 Substance P [Pro 10]. 6/1992
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      GPM

AAR21942  ck: 722   len: 45  1 Aar21942 Substance P [Metet 11]. 6/1992
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      GLM

AAR21944  ck: 857   len: 45  1 Aar21944 Substance P [Pro 11]. 6/1992
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      GLP

AAR21946  ck: 722   len: 45  1 Aar21946 Substance P [Me-Phe 8]. 6/1992
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)

1      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
35:  THERS      RPKPQOFF      GLM

AAR21951  ck: 254   len: 45  1 Aar21951 Substance P [Glu 3]. 6/1992
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      GLM

AAR21954  ck: 722   len: 45  1 Aar21954 Substance P [Me-Gly 9]. 6/1992
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      GLM

AAR21958  ck: 464   len: 45  1 Aar21958 Substance P [Ala 9] or [D-Ala 9
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      ALM

AAR21962  ck: 722   len: 45  1 Aar21962 Substance P [Me Gly 6, Met (O2)
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      GLM

AAR21963  ck: 722   len: 45  1 Aar21963 Substance P [p-Chloro-Phe 7,8].
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      GLM

AAR28442  ck: 722   len: 45  1 Aar28442 Substance P. 3/1993
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      GLM

AAR28443  ck: 980   len: 45  1 Aar28443 Neurokinin 1 ligand #1. 3/1993
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      MLM

AAR28445  ck: 1520  len: 45  1 Aar28445 Neurokinin 1 ligand #3. 3/1993
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      GLM

AAR28680  ck: 344   len: 58  1 Aar28680 Galanin(1-12)-Pro-Spanide amid
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      WLL

AAR28392  ck: 1785  len: 45  1 Aar28392 Bradykinin receptor antagonist
35:  THERS      (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)
      (R)P(K)P-P-P(F)(F)
      RPKPQOFF      WLX

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1	<u>AAAR55229</u>	ck: 2172 len: 526	1	Aar45229 APP-REP 751 amyloid precursor prot
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLMGS
1	396: DKYLE			
1	<u>AAAR32798</u>	ck: 4680 len: 46	1	Aar32798 Tyr-1 substance P used for binding
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	36: HERSY			
1	<u>AAAR42646</u>	ck: 722 len: 45	1	Aar42646 Neurokinin 1 receptor affinity-con
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	35: THERS			
1	<u>AAAR42647</u>	ck: 1453 len: 45	1	Aar42647 Neurokinin 1 receptor affinity-con
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	35: THERS			
1	<u>AAAR42649</u>	ck: 1520 len: 45	1	Aar42649 Neurokinin 1 receptor affinity-con
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	35: THERS			
1	<u>AAAR5243</u>	ck: 722 len: 45	1	Aar5243 Substance P peptide. 8/1997
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	35: THERS			
1	<u>AAAR5244</u>	ck: 3804 len: 46	1	Aar5244 Substance P analogue peptide Cys-6
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLMC
1	35: THERS			
1	<u>AAAR9003</u>	ck: 677 len: 45	1	Aar9003 Substance P analogue, acts as subs
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLL
1	35: THERS			
1	<u>AAAR9004</u>	ck: 2602 len: 45	1	Aar9004 Spantide analogue, acts as substan
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		WLX
1	35: THERS			
1	<u>AAAR7310</u>	ck: 722 len: 45	1	Aar7310 Substance P. 3/1996
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	35: THERS			
1	<u>AAAR7982</u>	ck: 1342 len: 45	1	Aar7982 [D-Arg1, D-Phe5, D-Trp7,9, Leu11]
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	35: THERS			
1	<u>AAAR2620</u>	ck: 4569 len: 254	1	Aar2620 Bacillus smithii nitrile hydrat
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(H)P(K)P-P-P(F)(F)		
		HPRPQSFH		EARAK
1	56: RPPHH			
1	<u>AAAR33181</u>	ck: 477 len: 45	1	Aar33181 Mono-DTPA-Lys1 Substance P. 1/1
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(K)P(K)P-P-P(F)(F)		
		KRPKPQOFF		GLM
1	35: THERS			
1	<u>AAAR33180</u>	ck: 722 len: 45	1	Aar33180 Mono-DTPA-Arg1 Substance P. 1/1
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	35: THERS			
1	<u>AAAR26509</u>	ck: 2172 len: 526	1	Aar26509 Amyloid precursor protein subst
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLMGS
1	396: DKYLE			
1	<u>AAAR26510</u>	ck: 8039 len: 521	1	Aar26510 Amyloid precursor protein subst
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLMGS
1	396: DKYLE			
1	<u>AAAR26393</u>	ck: 2172 len: 526	1	Aar26393 Amyloid precursor protein subst
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLMGS
1	396: DKYLE			
1	<u>AAAR26394</u>	ck: 8039 len: 521	1	Aar26394 Amyloid precursor protein subst
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLMGS
1	396: DKYLE			
1	<u>AAAR16339</u>	ck: 9887 len: 435	1	Aar16339 DAB389-SP-Gly fusion toxin. 9/1
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLMG
1	424: HKTHA			
1	<u>AAAR4616</u>	ck: 722 len: 45	1	Aar4616 Substance P peptide for mass sp
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	35: THERS			
1	<u>AAAR7975</u>	ck: 242 len: 45	1	Aar7975 Substance P. 1/1999
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W)		
		(R)P(K)P-P-P(F)(F)		
		RPKPQOFF		GLM
1	35: THERS			

1	AAW50978	ck: 765	len: 45	1	Aaw50978 Substance P analogue [D-Arg1,D-Pro	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
1	35: THERS						RPKPQOFF	
1	AAW50966	ck: 2062	len: 45	1	Aaw50966 Substance P analogue, spantide I.	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F)	GLM
1	35: THERS						RPKPQOFF	
1	AAW50968	ck: 1410	len: 45	1	Aaw50968 Substance P analogue, [D-Pro2,D-P	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLM
1	35: THERS						RPKPQOFF	
1	AAW50969	ck: 2107	len: 45	1	Aaw50969 Substance P analogue, [D-Pro2,D-T	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F)	WLM
1	35: THERS						RPKPQOFF	
1	AAW50972	ck: 1633	len: 45	1	Aaw50972 Substance P analogue, [D-Arg1,D-P	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F)	WLL
1	35: THERS						RPKPQOFF	
1	AAW50958	ck: 2062	len: 45	1	Aaw50958 Substance P analogue, [D-Arg1,D-P	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F)	WLL
1	35: THERS						RPKPQOFF	
1	AAW50942	ck: 1633	len: 45	1	Aaw50942 Substance P antagonist (SP1). 7/19	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F)	GLM
1	35: THERS						RPKPQOFF	
1	AAW44744	ck: 2172	len: 526	1	Aaw44744 APP-REP 751 protein from PCLL602.	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
1	396: DKYLE						RPKPQOFF	
1	AAW44745	ck: 8039	len: 521	1	Aaw44745 APP-REP 751 protein from PCLL621.	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
1	396: DKYLE						RPKPQOFF	
1	AAW42978	ck: 2172	len: 526	1	Aaw42978 Amyloid precursor protein mutant A	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
1	396: DKYLE						RPKPQOFF	
1	AAW42979	ck: 8039	len: 521	1	Aaw42979 Amyloid precursor protein mutant A	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
1	396: DKYLE						RPKPQOFF	
1	AAW42973	ck: 722	len: 45	1	Aaw42973 Substrate P reporter epitope. 5	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLM
1	35: THERS						RPKPQOFF	
1	AAW30985	ck: 722	len: 45	1	Aay30985 Non-crosslinked protein particl	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLM
1	35: THERS						RPKPQOFF	
1	AAW34864	ck: 8364	len: 252	1	Aay34864 Chlamydia pneumoniae transmembr	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLM
1	207: GYVCE						HPKPKNFY	TRLRE
1	AAW13564	ck: 940	len: 1,415	1	Aay13564 Drosophila Robo 2 polypeptide. 7	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(K)P-P-P(Y)(W)	SVEGN
1	357: COANG						HPRPTLYW	
1	AAW08402	ck: 7245	len: 1,414	1	Aay08402 Drosophila sp. ROBO2 extracellu	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(K)P-P-P(Y)(W)	SVEGN
1	357: COANG						HPRPTLYW	
1	AAW03156	ck: 722	len: 45	1	Aay03156 Substance P. 6/1999	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLM
1	35: THERS						RPKPQOFF	
1	AAW03157	ck: 3988	len: 46	1	Aay03157 Substance P-Glycine. 6/1999	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
1	35: THERS						RPKPQOFF	
1	AAW03158	ck: 7513	len: 47	1	Aay03158 Substance P-Glycine-Lysine. 6/1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
1	35: THERS						RPKPQOFF	
1	AAW03159	ck: 1449	len: 48	1	Aay03159 Substance P-Glycine-Lysine-Arg1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	GLMG
1	35: THERS						RPKPQOFF	
1	AAW03162	ck: 3913	len: 43	1	Aay03162 Substance P fragment P/1-9#. 6/	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	G
1	35: THERS						RPKPQOFF	

1	AAW99689	ck: 677	len: 45	1	Aaw99689 Substance P analogue #6. 6/1999	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPRKQOFF	GLM
1	35: THERS			1		1		
1	AAW99690	ck: 2602	len: 45	1	Aaw99690 Substance P analogue #7. 6/1999	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F) RPRKQOFF	WLX
1	35: THERS			1		1		
1	AAW99691	ck: 2602	len: 45	1	Aaw99691 Substance P analogue #8. 6/1999	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F) RPRKQOFF	WLX
1	35: THERS			1		1		
1	AAW74445	ck: 9834	len: 1,218	1	Aaw74445 Human nucleotide pyrophosphohydroly	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(Y)(F) KPRDKYF	WYHND
1	369: CKATG			1		1		
1	AAW92709	ck: 1217	len: 45	1	Aaw92709 Human tachykinin agonist beta-amy1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPRKQOFF	GLX
1	35: THERS			1		1		
1	AAW92711	ck: 860	len: 42	1	Aaw92711 Human tachykinin agonist beta-amy1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPRKQOFF	GLM
1	35: THERS			1		1		
1	AAW92715	ck: 722	len: 45	1	Aaw92715 Human tachykinin agonist beta-amy1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPRKQOFF	GLM
1	35: THERS			1		1		
1	AAW92716	ck: 898	len: 45	1	Aaw92716 Human tachykinin agonist beta-amy1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPRKQOFF	GLM
1	35: THERS			1		1		
1	AAW92717	ck: 1217	len: 45	1	Aaw92717 Human tachykinin agonist beta-amy1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPRKQOFF	GLX
1	35: THERS			1		1		
1	AAW92718	ck: 857	len: 45	1	Aaw92718 Human tachykinin agonist beta-amy1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPRKQOFF	GLP
1	35: THERS			1		1		
1	AAW92719	ck: 722	len: 45	1	Aaw92719 Human tachykinin agonist beta-amy1	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPRKQOFF	GLM
1	35: THERS			1		1		
1	AAW92678	ck: 1109	len: 45	1	Aaw92678 Human tachykinin agonist beta-a	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPRKQOFF	PLM
1	35: THERS			1		1		
1	AAW92679	ck: 254	len: 45	1	Aaw92679 Human tachykinin agonist beta-a	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPRKQOFF	GLM
1	35: THERS			1		1		
1	AAW92680	ck: 722	len: 45	1	Aaw92680 Human tachykinin agonist beta-a	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPRKQOFF	GLM
1	35: THERS			1		1		
1	AAW92681	ck: 722	len: 45	1	Aaw92681 Human tachykinin agonist beta-a	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPRKQOFF	GLM
1	35: THERS			1		1		
1	AAW92682	ck: 4	len: 45	1	Aaw92682 Human tachykinin agonist beta-a	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPRKQOFF	GLM
1	35: THERS			1		1		
1	AAW92683	ck: 1726	len: 45	1	Aaw92683 Human tachykinin agonist beta-a	1	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPRKQOFF	GLM
1	35: THERS			1		1		

1	35: THERS	RPKPXQFF	GLM	
1	<u>AAW92684</u>	ck: 1523 len: 45	1 Aaw92684 Human tachykinin agonist beta-amy1	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPXQFF		GLM	
1	35: THERS			
1	<u>AAW92685</u>	ck: 9726 len: 45	1 Aaw92685 Human tachykinin agonist beta-amy1	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		GLC	
1	35: THERS			
1	<u>AAW92688</u>	ck: 1490 len: 45	1 Aaw92688 Human tachykinin agonist beta-amy1	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPXQFF		GLX	
1	35: THERS			
1	<u>AAW92689</u>	ck: 3913 len: 43	1 Aaw92689 Human tachykinin agonist beta-amy1	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		G	
1	35: THERS			
1	<u>AAW92665</u>	ck: 1501 len: 45	1 Aaw92665 Human tachykinin agonist beta-amy1	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		GLM	
1	35: THERS			
1	<u>AAW92667</u>	ck: 1217 len: 45	1 Aaw92667 Human tachykinin agonist beta-amy1	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		GLX	
1	35: THERS			
1	<u>AAW92668</u>	ck: 1217 len: 45	1 Aaw92668 Human tachykinin agonist beta-amy1	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		GLX	
1	35: THERS			
1	<u>AAW92674</u>	ck: 464 len: 45	1 Aaw92674 Human tachykinin agonist beta-amy1	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		ALM	
1	35: THERS			
1	<u>AAW92675</u>	ck: 464 len: 45	1 Aaw92675 Human tachykinin agonist beta-amy1	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		ALM	
1	35: THERS			
1	<u>AAW92676</u>	ck: 722 len: 45	1 Aaw92676 Human tachykinin agonist beta-amy1	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		GLM	
1	35: THERS			
1	<u>AAW92731</u>	ck: 722 len: 45	1 Aaw92731 Human tachykinin agonist beta-a	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		GLM	
1	35: THERS			
1	<u>AAW92656</u>	ck: 2107 len: 45	1 Aaw92656 Human tachykinin agonist beta-a	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		WLM	
1	35: THERS			
1	<u>AAW92657</u>	ck: 2062 len: 45	1 Aaw92657 Human tachykinin agonist beta-a	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		WLL	
1	35: THERS			
1	<u>AAW94412</u>	ck: 4310 len: 46	1 Aaw94412 Cancer protease-sensitive amino	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		GLMN	
1	35: THERS			
1	<u>AAW79662</u>	ck: 722 len: 45	1 Aaw79662 Substance P derivative having c	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		GLM	
1	35: THERS			
1	<u>AAW79663</u>	ck: 722 len: 45	1 Aaw79663 Substance P derivative having c	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		GLM	
1	35: THERS			
1	<u>AAW18483</u>	ck: 722 len: 45	1 Aaw18483 Peptide substrate used to test	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		GLM	
1	35: THERS			
1	<u>AAW23027</u>	ck: 722 len: 45	1 Aaw23027 Human/rat tachykinin Substance	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		GLM	
1	35: THERS			
1	<u>AAW08303</u>	ck: 1633 len: 45	1 Aaw08303 Amino acid sequence of Substance	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		WLL	
1	35: THERS			
1	<u>AAW08313</u>	ck: 2863 len: 45	1 Aaw08313 Amino acid sequence of an antia	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			
	(R)P(K)P-D-P(E)(F)			
	RPKPQQFF		WXL	
1	35: THERS			
1	<u>AAW06257</u>	ck: 1860 len: 51	1 Aaw06257 Substance P analogue #1. 10/200	1
	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W)			

44: GGGGG	(R)P(K)P-P-P(F)(F) RPPQQEFF				
<u>AAAB06258</u>	ck: 3738 len: 54 1 Aab06258 Substance P analogue #2. 10/2000	1			
44: GGGGG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPPQQEFF				
GLM					
<u>AAAB06260</u>	ck: 1196 len: 45 1 Aab06260 Substance P. 10/2000	1			
35: THERS	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPPQWFF				
GLM					
<u>AAAG05042</u>	ck: 1234 len: 348 1 Aag05042 Arabidopsis thaliana protein fragm	1			
157: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
RCFPD					
<u>AAAG05043</u>	ck: 69 len: 333 1 Aag05043 Arabidopsis thaliana protein fragm	1			
142: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
RCFPD					
<u>AAAG05044</u>	ck: 3694 len: 326 1 Aag05044 Arabidopsis thaliana protein fragm	1			
135: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
RCFPD					
<u>AAAG06751</u>	ck: 8736 len: 342 1 Aag06751 Arabidopsis thaliana protein fragm	1			
157: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPPNFFY				
RCFPN					
<u>AAAG06752</u>	ck: 9625 len: 338 1 Aag06752 Arabidopsis thaliana protein fragm	1			
153: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPPNFFY				
RCFPN					
<u>AAAG06753</u>	ck: 4240 len: 290 1 Aag06753 Arabidopsis thaliana protein fragm	1			
105: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y) RPPNFFY				
RCFPN					
<u>AAAG10034</u>	ck: 5300 len: 361 1 Aag10034 Arabidopsis thaliana protein fragm	1			
182: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(W) RPPNFFY				
RCFPD					
<u>AAAG10035</u>	ck: 8399 len: 336 1 Aag10035 Arabidopsis thaliana protein fragm	1			
157: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(W) RPPNFFY				
RCFPD					
<u>AAAG10036</u>	ck: 2931 len: 284 1 Aag10036 Arabidopsis thaliana protein fr	1			
105: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(W) RPPNFFY				
RCFPD					
<u>AAAG13023</u>	ck: 717 len: 336 1 Aag13023 Arabidopsis thaliana protein fr	1			
157: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
RCFPD					
<u>AAAG13024</u>	ck: 6784 len: 321 1 Aag13024 Arabidopsis thaliana protein fr	1			
142: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
RCFPD					
<u>AAAG13025</u>	ck: 5563 len: 314 1 Aag13025 Arabidopsis thaliana protein fr	1			
135: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
RCFPD					
<u>AAAG13500</u>	ck: 957 len: 367 1 Aag13500 Arabidopsis thaliana protein fr	1			
176: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
RCFPD					
<u>AAAG13501</u>	ck: 1234 len: 348 1 Aag13501 Arabidopsis thaliana protein fr	1			
157: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
RCFPD					
<u>AAAG13502</u>	ck: 69 len: 333 1 Aag13502 Arabidopsis thaliana protein fr	1			
142: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
RCFPD					
<u>AAAG13842</u>	ck: 1234 len: 348 1 Aag13842 Arabidopsis thaliana protein fr	1			
157: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
RCFPD					
<u>AAAG13843</u>	ck: 69 len: 333 1 Aag13843 Arabidopsis thaliana protein fr	1			
142: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
RCFPD					
<u>AAAG13844</u>	ck: 3694 len: 326 1 Aag13844 Arabidopsis thaliana protein fr	1			
135: KNAV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W) RPPDFFW				
RCFPD					
<u>AAAG14936</u>	ck: 1234 len: 348 1 Aag14936 Arabidopsis thaliana protein fr	1			

1	(H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RPRPDFFW	RCFPD	
157: KNAV			
1	<u>AAG14937</u> ck: 69 len: 333 i Aag14937 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RPRPDFFW	RCFPD	1
142: KNAV			
1	<u>AAG14938</u> ck: 3694 len: 326 i Aag14938 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RPRPDFFW	RCFPD	1
135: KNAV			
1	<u>AAG17706</u> ck: 1234 len: 348 i Aag17706 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RPRPDFFW	RCFPD	1
157: KNAV			
1	<u>AAG17707</u> ck: 69 len: 333 i Aag17707 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RPRPDFFW	RCFPD	1
142: KNAV			
1	<u>AAG17708</u> ck: 3694 len: 326 i Aag17708 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RPRPDFFW	RCFPD	1
135: KNAV			
1	<u>AAG21999</u> ck: 386 len: 398 i Aag21999 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RPRPDFFW	RCFPD	1
207: KNAV			
1	<u>AAG22000</u> ck: 1234 len: 348 i Aag22000 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RPRPDFFW	RCFPD	1
157: KNAV			
1	<u>AAG22001</u> ck: 69 len: 333 i Aag22001 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RPRPDFFW	RCFPD	1
142: KNAV			
1	<u>AAG30400</u> ck: 2030 len: 324 i Aag30400 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RPRPDFFW	RCFPD	1
137: KDAVG			
1	<u>AAG30401</u> ck: 3697 len: 302 i Aag30401 Arabidopsis thaliana protein fragm (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RPRPDFFW	RCFPD	1
135: KDAVG			
1	<u>AAG30402</u> ck: 2710 len: 272 i Aag30402 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(W) RPRPDFFW	RCFPD	1
105: KDAVG			
1	<u>AAG30526</u> ck: 3692 len: 119 i Aag30526 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(H)P-D-P(Y)(F) RPHPMLYF	F	1
111: TALGA			
1	<u>AAG30528</u> ck: 9507 len: 93 i Aag30528 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(H)P-D-P(Y)(F) RPHPMLYF	F	1
85: TALGA			
1	<u>AAG38754</u> ck: 8835 len: 342 i Aag38754 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(Y) RPRPNFYF	RCFPN	1
157: KDAVG			
1	<u>AAG38755</u> ck: 9712 len: 338 i Aag38755 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(Y) RPRPNFYF	RCFPN	1
153: KDAVG			
1	<u>AAG38756</u> ck: 4354 len: 290 i Aag38756 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(F)(Y) RPRPNFYF	RCFPN	1
105: KDAVG			
1	<u>AAG42826</u> ck: 4761 len: 361 i Aag42826 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(Y)(W) RPRPNFYW	RCFPD	1
182: KVATG			
1	<u>AAG42827</u> ck: 7060 len: 336 i Aag42827 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(Y)(W) RPRPNFYW	RCFPD	1
157: KVATG			
1	<u>AAG42828</u> ck: 2550 len: 284 i Aag42828 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(R)P-D-P(Y)(W) RPRPNFYW	RCFPD	1
105: KVATG			
1	<u>AAG50469</u> ck: 9507 len: 93 i Aag50469 Arabidopsis thaliana protein fr (H,K,R)P(H,K,R)P-D-P(E,Y,W)(F,Y,W) (R)P(H)P-D-P(Y)(F) RPHPMLYF	F	1
85: TALGA			
1	<u>AAY96513</u> ck: 8290 len: 860 i Aay96513 Human zslg43 polypeptide. 9/200		

1	682: LELGV	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(H)P-P-P(W)(F)	VSLDG	
1	AAV58787	ck: 2030 len: 324 i Aay58787 Arabidopsis phosphatidic acid phos		
1	157: KDAVG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W)	RCFPD	
1	AAV58788	ck: 1560 len: 382 i Aay58788 Arabidopsis phosphatidic acid phos		
1	203: KVATG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(W)	RCFPD	
1	AAV58789	ck: 1234 len: 348 i Aay58789 Arabidopsis phosphatidic acid phos		
1	157: KNAVg	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W)	RCFPD	
1	AAV58790	ck: 5033 len: 344 i Aay58790 Corn phosphatidic acid phosphatase		
1	156: KDCVG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W)	RCFPD	
1	AAV58791	ck: 9121 len: 377 i Aay58791 Soybean phosphatidic acid phosphat		
1	181: KNAVg	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W)	RCFPD	
1	AAV58792	ck: 5772 len: 356 i Aay58792 soybean phosphatidic acid phosphat		
1	157: KDAVG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(W)	RCFPD	
1	AAV54319	ck: 165 len: 2,108 i Aay54319 Amino acid sequence of a murine PC		
1	1,672: YHTHL	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(Y)	LEPLP	
1	AAV54320	ck: 8484 len: 2,057 i Aay54320 Amino acid sequence of a human PC		
1	1,612: YHTHL	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(Y)(Y)	LEPLP	
1	AAV66557	ck: 668 len: 1,218 i Aay66557 Membrane-bound protein PRO1188, 4/		
1	369: CKATG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(Y)(F)	WYHND	
1	AAV76061	ck: 24 len: 162 i Aay76061 Rat skin cell transmembrane protei		
		(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y)		
1	152: KLIVG		RPRDFFV	RCF
1	AAV32382	ck: 722 len: 45 i Aay32382 Cell differentiation, prolifera		
1	35: THERS	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	RPKPOGF	GLMG
1	AAV53610	ck: 4816 len: 248 i Aay53610 rbe nitrile hydratase alpha sub		
1	52: RFRHH	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(F)(W)	HPRQSEW	EARAK
1	AAV3571	ck: 7240 len: 191 i Aam3571 Arabidopsis EST encoded protein		
1	88: KLIVG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(Y)	RPRDFFV	RCFPD
1	AAV40285	ck: 2082 len: 600 i Aam40285 Human polypeptide SEQ ID NO 343		
1	585: VLQAP	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(R)P-P-P(F)(F)	RPRPRTF	SWLAS
1	AAV42450	ck: 7719 len: 119 i Aam42450 Human kidney related polypeptid		
1	110: FTSVG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (H)P(R)P-P-P(Y)(F)	HPRPGTYF	VX
1	AAU12377	ck: 668 len: 1,218 i Aau12377 Human PRO1188 polypeptide seque		
1	369: CKATG	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (K)P(R)P-P-P(Y)(F)	KPRPDXYF	WYHND
1	AAV62768	ck: 722 len: 45 i Aag62768 Amino acid sequence of substanc		
1	35: THERS	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	RPKPOOFF	GLMG
1	AAV62769	ck: 3988 len: 46 i Aag62769 Amino acid sequence of substanc		
1	35: THERS	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	RPKPOOFF	GLMG
1	AAV62770	ck: 7513 len: 47 i Aag62770 Amino acid sequence of substanc		
1	35: THERS	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	RPKPOOFF	GLMG
1	AAV62771	ck: 1449 len: 48 i Aag62771 Amino acid sequence of substanc		
1	35: THERS	(H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F)	RPKPOOFF	GLMG

[illegible]

1	<u>AAB98874</u> ck: 7513 len: 47 Aab98874 Chimeric analgesic peptide #30. 8/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF GLMGK	1	<u>AAB91414</u> ck: 765 len: 45 Aab91411 Tachykinins peptide SEQ ID NO:5 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF HLM
1	<u>AAB98875</u> ck: 1449 len: 48 Aab98875 Chimeric analgesic peptide #31. 8/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF GLMGK	1	<u>AAB91412</u> ck: 1410 len: 45 Aab91412 Tachykinins peptide SEQ ID NO:5 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF WLM
1	<u>AAB98878</u> ck: 3913 len: 43 Aab98878 Chimeric analgesic peptide #34. 8/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF G	1	<u>AAB91413</u> ck: 2107 len: 45 Aab91413 Tachykinins peptide SEQ ID NO:5 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF WLM
1	<u>AAB98879</u> ck: 1410 len: 45 Aab98879 Chimeric analgesic peptide #35. 8/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF WLM	1	<u>AAB91414</u> ck: 1633 len: 45 Aab91414 Tachykinins peptide SEQ ID NO:5 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F) RPKPQOWF WLM
1	<u>AAB98880</u> ck: 4676 len: 46 Aab98880 Chimeric analgesic peptide #36. 8/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF WLMG	1	<u>AAB91415</u> ck: 1109 len: 45 Aab91415 Tachykinins peptide SEQ ID NO:5 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F) RPKPQOWF WLL
1	<u>AAB98881</u> ck: 2107 len: 45 Aab98881 Chimeric analgesic peptide #37. 8/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F) RPKPQOWF WLM	1	<u>AAB91422</u> ck: 7516 len: 44 Aab91422 Tachykinins peptide SEQ ID NO:5 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF PLM
1	<u>AAB98882</u> ck: 5373 len: 46 Aab98882 Chimeric analgesic peptide #38. 8/ (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(W)(F) RPKPQOWF WLMG	1	<u>AAB91423</u> ck: 7257 len: 44 Aab91423 Tachykinins peptide SEQ ID NO:5 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF GL
1	<u>AAB92070</u> ck: 722 len: 45 Aab92070 Substance P. 6/2001 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF GLM	1	<u>AAB91427</u> ck: 7257 len: 44 Aab91427 Tachykinins peptide SEQ ID NO:6 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF GL
1	<u>AAB91402</u> ck: 981 len: 45 Aab91402 Tachykinins peptide SEQ ID NO:578. (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF GLM	1	<u>AAB91429</u> ck: 1109 len: 45 Aab91429 Tachykinins peptide SEQ ID NO:6 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF PLM
1	<u>AAB91409</u> ck: 1520 len: 45 Aab91409 Tachykinins peptide SEQ ID NO:585. (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF GLM	1	<u>AAB91432</u> ck: 7516 len: 44 Aab91432 Tachykinins peptide SEQ ID NO:6 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF LM
1	<u>AAB91410</u> ck: 7516 len: 44 Aab91410 Tachykinins peptide SEQ ID NO:586. (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF LM	1	<u>AAB91432</u> ck: 7516 len: 44 Aab91432 Tachykinins peptide SEQ ID NO:6 (H,K,R)P(H,K,R)P-P-P(F,Y,W)(F,Y,W) (R)P(K)P-P-P(F)(F) RPKPQOFF LM

1 AAB91434 > ck: 2062 len: 45 | Aab91434 Tachykinins peptide SEQ ID NO:610.
(H,K,R)P(H,K,R)P-P(E,Y,W)(F,Y,W)
(R)P(K)P-P-P(W)(F)
35: THERS RPKPQOWF WLL

1 AAB91436 > ck: 722 len: 45 | Aab91436 Tachykinins peptide SEQ ID NO:612.
(H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
35: THERS RPKPQOWF GLM

1 AAB91438 > ck: 385 len: 45 | Aab91438 Tachykinins peptide SEQ ID NO:614.
(H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(K)P(R)P-P-P(F)(F)
35: THERS KPRPHQWF GLM

1 AAB91440 > ck: 1449 len: 48 | Aab91440 Tachykinins peptide SEQ ID NO:616.
(H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
35: THERS RPKPQOWF GLMGK

1 AAB91444 > ck: 3913 len: 43 | Aab91444 Tachykinins peptide SEQ ID NO:620.
(H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
35: THERS RPKPQOWF G

1 AAB91449 > ck: 722 len: 45 | Aab91449 Tachykinins peptide SEQ ID NO:625.
(H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
35: THERS RPKPQOWF GLM

1 AAB91450 > ck: 722 len: 45 | Aab91450 Tachykinins peptide SEQ ID NO:626.
(H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
35: THERS RPKPQOWF GLM

1 AAB91451 > ck: 8055 len: 44 | Aab91451 Tachykinins peptide SEQ ID NO:627.
(H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
35: THERS RPKPQOWF GL

1 AAB92023 > ck: 344 len: 58 | Aab92023 Galanin peptide SEQ ID NO:1199. 6/
(H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(R)P(K)P-P-P(W)(F)
48: YLLGP RPKPQOWF WLL

1 AAB92031 > ck: 344 len: 58 | Aab92031 Galanin peptide SEQ ID NO:1207. 6/
(H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(R)P(K)P-P-P(W)(F)
48: YLLGP RPKPQOWF WLL

1 AAB70690 > ck: 4219 len: 209 | Aab70690 Human hDPP protein sequence SEQ ID

1 (H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
106: KLIWG RRPDPDFY RCEPD

1 AAB49755 > ck: 736 len: 45 | Aab49755 Complex sugar bound peptide (SB)
(H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(K)P(R)P-P-P(F)(F)
35: THERS KPRPQOWF GLM

1 AAB65180 > ck: 668 len: 1,218 | Aab65180 Human PRO1188 (UNQ602) protein
(H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(K)P(R)P-P-P(F)(F)
369: CKATG KPRPDKYF WYHND

1 AAB50544 > ck: 722 len: 45 | Aab50544 Prolyl endopeptidase inhibitor
(H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
35: THERS RPKPQOWF GLM

1 AAB50306 > ck: 722 len: 45 | Aab50306 Substance P. 3/2001
(H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(R)P(K)P-P-P(F)(F)
35: THERS RPKPQOWF GLM

1 AAB56000 > ck: 24 len: 162 | Aab56000 Skin cell protein, SEQ ID NO: 3
(H,K,R)P(H,K,R)P-P-P(E,Y,W)(F,Y,W)
(R)P(R)P-P-P(F)(F)
152: KLIWG RRPDPDFY RCF

Databases searched: *A-Gene*
2500, Release 25.0, Released on 25Oct2001, Formatted on 13Dec2001

Total finds: 245
Total length: 91,837,149
Total sequences: 522,463
CPU time: 09:07.03

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 1, 2002, 16:17:29 ; Search time 38.86 Seconds
(Without alignments)
20.968 Million cell updates/sec

Title: US-09-988-792-1

Perfect score: 61

Sequence: 1 RPKPQGFGLM 11

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

(Total number of hits satisfying chosen parameters: 517

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 50%

Maximum Match 100%

Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	11	7 AAP61480	Sequence of undeca
2	61	100.0	11	9 AAP80312	Sequence of neupoc
3	61	100.0	11	12 AAR13162	Static acid-bonded
4	61	100.0	11	12 AAR11854	Undecapeptide subs
5	61	100.0	11	13 AAR21938	Substance P [Me-Ile
6	61	100.0	11	13 AAR21942	Substance P [MeMet
7	61	100.0	11	13 AAR21946	Substance P [Me-Phe
8	61	100.0	11	13 AAR21954	Substance P [Me-Glu
9	61	100.0	11	13 AAR21962	Substance P [Me-Glu
10	61	100.0	11	13 AAR21963	Substance P [p-Chl
11	61	100.0	11	13 AAR28442	Substance P. Synt

12	61	100.0	11	14 AAR42646	Neurokinin 1 recep
13	61	100.0	11	16 AAR85243	Substance P peptid
14	61	100.0	11	16 AAR77310	Substance P. Synt
15	61	100.0	11	18 AAW33180	Mono-DTPA-Arg1 Sub
16	61	100.0	11	18 AAW04616	Substance P peptid
17	61	100.0	11	19 AAW42973	Substrate P report
18	61	100.0	11	20 AAY30985	Non-crosslinked pr
19	61	100.0	11	20 AAY03156	Substance P. Synt
20	61	100.0	11	20 AAW92715	Human tachykinin a
21	61	100.0	11	20 AAW92719	Human tachykinin a
22	61	100.0	11	20 AAW92720	Human tachykinin a
23	61	100.0	11	20 AAW92708	Human tachykinin a
24	61	100.0	11	20 AAW92680	Human tachykinin a
25	61	100.0	11	20 AAW92681	Human tachykinin a
26	61	100.0	11	20 AAW92676	Human tachykinin a
27	61	100.0	11	20 AAW92731	Human tachykinin a
28	61	100.0	11	20 AAW79662	Substance P deriva
29	61	100.0	11	20 AAW79663	Substance P deriva
30	61	100.0	11	21 AAB18483	Peptide substrate
31	61	100.0	11	21 AAB23027	Human/rat tachykin
32	61	100.0	11	21 AAR32382	Cell differentiatl
33	61	100.0	11	22 AAG62768	Amino acid sequenc
34	61	100.0	11	22 AAG62768	Substance P peptid
35	61	100.0	11	22 AAB84527	Amino acid sequenc
36	61	100.0	11	22 AAB98866	Chimeric analgesic
37	61	100.0	11	22 AAB82070	Substance P. Unid
38	61	100.0	11	22 AAB81436	Tachykinins peptid
39	61	100.0	11	22 AAB91449	Tachykinins peptid
40	61	100.0	11	22 AAB91450	Prolyl endopeptida
41	61	100.0	11	22 AAB50544	Substance P. Unid
42	61	100.0	11	22 AAB50306	Tyr-1 substance P
43	61	100.0	12	16 AAR85244	Substance P analog
44	61	100.0	12	20 AAY03157	Substance P-Glycin
45	61	100.0	12	20 AAW94412	Cancer protease-se
46	61	100.0	12	22 AAG62769	Amino acid sequenc
47	61	100.0	12	22 AAG62772	Amino acid sequenc
48	61	100.0	12	22 AAG62772	Amino acid sequenc
49	61	100.0	12	22 AAB84528	Amino acid sequenc
50	61	100.0	12	22 AAB98867	Chimeric analgesic
51	61	100.0	12	22 AAB98870	Chimeric analgesic
52	61	100.0	12	22 AAB98873	Chimeric analgesic
53	61	100.0	13	20 AAB98871	Substance P-Glycin
54	61	100.0	13	20 AAG62770	Amino acid sequenc
55	61	100.0	13	22 AAG62773	Amino acid sequenc
56	61	100.0	13	22 AAG62776	Amino acid sequenc
57	61	100.0	13	22 AAB98868	Chimeric analgesic
58	61	100.0	13	22 AAB98871	Chimeric analgesic
59	61	100.0	13	22 AAB98874	Chimeric analgesic
60	61	100.0	14	20 AAY03159	Substance P-Glycin
61	61	100.0	14	22 AAG62771	Amino acid sequenc
62	61	100.0	14	22 AAG62774	Amino acid sequenc
63	61	100.0	14	22 AAG62777	Amino acid sequenc
64	61	100.0	14	22 AAB98869	Chimeric analgesic
65	61	100.0	14	22 AAB98872	Chimeric analgesic
66	61	100.0	14	22 AAB98875	Chimeric analgesic
67	61	100.0	14	22 AAB91440	Tachykinins peptid
68	61	100.0	14	22 AAB91440	Substance P analog
69	61	100.0	20	21 AAB06258	Human beta-preprot
70	61	100.0	8	8 AAP70431	Human atypical tac
71	61	100.0	129	22 AAG93533	DAB389-SP-Gly fusi
72	61	100.0	401	18 AAW16339	Amyloid precursor
73	61	100.0	487	18 AAW26510	Amyloid precursor
74	61	100.0	487	18 AAW26394	Amyloid precursor
75	61	100.0	487	19 AAW44745	Amyloid precursor
76	61	100.0	487	19 AAW42979	Amyloid precursor
77	61	100.0	492	14 AAR45229	APP-REP 751 amylo
78	61	100.0	492	18 AAW6509	Amyloid precursor
79	61	100.0	492	18 AAW6393	Amyloid precursor
80	61	100.0	492	19 AAW44744	APP-REP 751 protei
81	61	100.0	492	19 AAW42978	Amyloid precursor
82	61	100.0	492	19 AAW42978	Substance P [Tyr7]
83	58	95.1	11	13 AAR21937	Substance P or (7-
84	58	95.1	11	13 AAR21951	Substance P [Glu 3

85	58	95.1	11	13	AA828445	Neurokinine 1 lig	158	49	80.3	9	6	AA850634	Substance P-like p
86	58	95.1	11	14	AA842649	Neurokinin 1 recep	159	49	80.3	9	20	AAW92714	Human tachykinin a
87	58	95.1	11	16	AAW09003	Substance p analog	160	49	80.3	9	22	AA891446	Tachykinins peptid
88	58	95.1	11	18	AAW33181	Mono-DHPA-Lys1 Sub	161	49	80.3	11	22	AA891437	Tachykinins peptid
89	58	95.1	11	19	AAW79775	Substance P. Mamm	162	49	80.3	13	13	AA829593	Vertebrate Stromel
90	58	95.1	11	20	AAW99689	Substance p analog	163	48	78.7	13	4	AA830142	Sequence of peptid
91	58	95.1	11	20	AAW92679	Human tachykinin a	164	48	78.7	11	9	AA880317	Sequence of neurop
92	58	95.1	11	20	AAW92666	Human tachykinin a	165	48	78.7	11	13	AA821966	Cyclic substance p
93	58	95.1	11	20	AAW92666	Human tachykinin a	166	48	78.7	11	13	AA821967	Cyclic substance p
94	58	95.1	11	22	AA891402	Tachykinins peptid	167	48	78.7	11	13	AA821960	Cyclic substance p
95	56	91.8	10	22	AA891409	Tachykinins peptid	168	48	78.7	11	19	AAW50969	Substance p analog
96	56	91.8	10	6	AA850633	Substance P-like p	169	48	78.7	11	19	AAW50969	Human tachykinin a
97	56	91.8	10	13	AA821933	Substance P (2-11)	170	48	78.7	11	20	AAW92683	Human tachykinin a
98	56	91.8	10	20	AAW92663	Human tachykinin a	171	48	78.7	11	20	AAW92685	Human tachykinin a
99	56	91.8	10	22	AA891423	Tachykinins peptid	172	48	78.7	11	20	AAW92656	Human tachykinin a
100	56	91.8	10	22	AA891427	Tachykinins peptid	173	48	78.7	11	22	AAW98881	Chimeric analgesic
101	56	91.8	10	22	AA891445	Tachykinins peptid	174	48	78.7	11	22	AA891413	Tachykinins peptid
102	56	91.8	11	13	AA821945	Substance P (Pro 1	175	47	77.0	11	22	AA898882	Chimeric analgesic
103	56	91.8	11	13	AA821936	Substance P or (7-	176	46	75.4	11	21	AA806260	Substance P. unid
104	56	91.8	11	13	AA821941	Substance P (pGlu	177	46	75.4	8	20	AAW92711	Human tachykinin a
105	56	91.8	11	20	AAW92709	Human tachykinin a	178	46	75.4	10	22	AA891410	Tachykinins peptid
106	56	91.8	11	20	AAW92717	Human tachykinin a	179	46	75.4	10	22	AA891422	Tachykinins peptid
107	56	91.8	11	20	AAW92718	Human tachykinin a	180	46	75.4	17	21	AA806257	Substance p analog
108	56	91.8	11	20	AAW92667	Human tachykinin a	181	45.5	74.6	10	20	AA806329	Substance p from B
109	56	91.8	11	20	AAW92668	Human tachykinin a	182	45.5	74.6	10	22	AA864746	Substance p amino
110	56	91.8	11	20	AAW92670	Human tachykinin a	183	45	73.8	11	5	AA864746	Substance p analog
111	56	91.8	11	20	AAW92672	Human tachykinin a	184	45	73.8	11	9	AA860313	Sequence of neurop
112	56	91.8	11	21	AA808614	Peptide identified	185	45	73.8	11	9	AA860314	Sequence of neurop
113	56	91.8	11	22	AA899350	Substance P tachyk	186	45	73.8	11	11	AA808316	D-arginine 1, D-pr
114	56	90.2	11	13	AA821939	Substance P (Ile 8	187	45	73.8	11	12	AA811144	Substance P analog
115	56	90.2	11	13	AA821943	Substance P (Met 7	188	45	73.8	11	13	AA821968	Cyclic substance p
116	56	90.2	11	13	AA821949	Substance P (Pro 3	189	45	73.8	11	13	AA821969	Cyclic substance p
117	55	90.2	11	13	AA821958	Substance P (Ala 9	190	45	73.8	11	13	AA821970	Cyclic substance p
118	55	90.2	11	20	AAW92669	Human tachykinin a	191	45	73.8	11	19	AAW50966	Substance p analog
119	55	90.2	11	20	AAW92671	Human tachykinin a	192	45	73.8	11	19	AAW50958	Substance p analog
120	55	90.2	11	20	AAW92673	Human tachykinin a	193	45	73.8	11	20	AAW92687	Human tachykinin a
121	55	90.2	11	20	AAW92674	Human tachykinin a	194	45	73.8	11	20	AAW92688	Human tachykinin a
122	55	90.2	11	20	AAW92675	Human tachykinin a	195	45	73.8	11	20	AAW92689	Human tachykinin a
123	55	90.2	11	22	AA849755	Complex sugar bou	196	45	73.8	11	20	AAW92690	Human tachykinin a
124	54	88.5	11	13	AA821940	Substance P (Pro 1	197	45	73.8	11	20	AAW92657	Human tachykinin a
125	54	88.5	11	14	AA842647	Neurokinin 1 recep	198	45	73.8	11	22	AA891434	Tachykinins peptid
126	54	88.5	11	20	AAW92716	Human tachykinin a	199	45	73.8	11	22	AA850312	Galatin(1-12)-Pro-
127	54	88.5	11	20	AAW92721	Human tachykinin a	200	45	73.8	24	13	AA828680	Galatin(1-12)-Pro-
128	53	86.9	10	22	AA891451	Tachykinins peptid	201	45	73.8	24	13	AA892023	Galatin peptide SE
129	53	86.9	11	9	-AA800315	Sequence of neurop	202	45	73.8	20	22	AA892031	Galatin peptide SE
130	53	86.9	11	9	-AA800320	Sequence of neurop	203	44.5	73.0	10	20	AAW99684	Substance p analog
131	53	86.9	11	13	AA821935	Substance P (Pro 9	204	44.5	73.0	10	22	AA866675	Tachykinin peptid
132	53	86.9	11	13	AA821964	Substance P (D-Ala	205	44	72.1	8	3	AA820303	Gastrointestinal m
133	53	86.9	11	19	AAW50978	Substance p analog	206	44	72.1	8	20	AAW92664	Human tachykinin a
134	53	86.9	11	19	AAW50968	Substance p analog	207	44	72.1	8	21	AA867573	p antagonist peptid
135	53	86.9	11	20	AAW92677	Human tachykinin a	208	44	72.1	8	22	AA891416	Tachykinins peptid
136	53	86.9	11	20	AAW92678	Human tachykinin a	209	44	72.1	8	22	AA891424	Tachykinins peptid
137	53	86.9	11	22	AAW98879	Chimeric analgesic	210	44	72.1	11	13	AA821965	Cyclic substance p
138	53	86.9	11	22	AA891411	Tachykinins peptid	211	44	72.1	11	20	AAW92682	Human tachykinin a
139	53	86.9	11	22	AA891412	Tachykinins peptid	212	44	72.1	20	13	AA828679	Galatin(1-12)-Pro-
140	53	86.9	11	22	AA891415	Tachykinins peptid	213	44	72.1	20	22	AA892027	Galatin peptide SE
141	53	86.9	11	22	AA891429	Tachykinins peptid	214	43.5	71.3	10	16	AA865181	S. cerevisiae sske
142	53	86.9	11	22	AA850311	Prevlin peptide #3.	215	43.5	70.5	11	13	AA828392	Bradykinin recepto
143	53	86.9	12	22	AA898880	Chimeric analgesic	216	43	70.5	11	14	AA832183	Ranakinin. Rana r
144	52	85.2	9	13	AA821932	Substance P (1-9)	217	43	70.5	11	16	AAW09004	Substance analogue,
145	52	85.2	9	20	AA821932	Substance P (1-9)	218	43	70.5	11	20	AAW99680	Substance p analog
146	52	85.2	9	20	AAW92665	Human tachykinin a	219	43	70.5	11	20	AAW99691	Substance p analog
147	52	85.2	9	22	AA862780	Amino acid sequenc	220	42	68.9	11	13	AA821971	Cyclic substance p
148	52	85.2	9	22	AA898878	Chimeric analgesic	221	42	68.9	11	20	AAW92691	Human tachykinin a
149	52	85.2	9	22	AA891444	Tachykinins peptid	222	40	65.6	7	20	AA820361	Substance p fragme
150	52	85.2	11	13	AA828443	Neurokinine 1 lig	223	40	65.6	7	20	AAW92658	Human tachykinin a
151	51	83.6	11	19	AAW60208	Peptide NFPI, a su	224	40	65.6	7	22	AA862779	Amino acid sequenc
152	51	83.6	11	21	AA867965	Carboxyfluorescein	225	40	65.6	7	22	AAW98877	Chimeric analgesic
153	50	82.0	11	13	AA821961	Cyclic substance p	226	40	65.6	7	22	AA891443	Tachykinins peptid
154	50	82.0	11	20	AAW92684	Human tachykinin a	227	38	62.3	11	13	AA821972	Cyclic substance p
155	50	82.0	11	20	AAW92686	Human tachykinin a	228	38	62.3	11	20	AAW92692	Human tachykinin a
156	50	82.0	11	22	AA891438	Tachykinins peptid	229	38	62.3	115	21	AA816968	Arabidopsis thalia
157	50	82.0	22	13	AA828681	Galatin(1-12)-Pro-	230	38	62.3	116	21	AA816967	Arabidopsis thalia

231	38	62.3	176	21	AA616966	Arabidopsis thalia	304	34	55.7	6	22	AA691442	Tachykinins peptid
232	38	62.3	249	21	AA621479	Arabidopsis thalia	305	34	55.7	7	13	AA621956	Substance P (5-11)
233	38	62.3	249	21	AA652793	Arabidopsis thalia	306	34	55.7	11	13	AA621974	Cyclic substance P
234	38	62.3	255	21	AA621478	Arabidopsis thalia	307	34	55.7	11	13	AA628446	Neurokinine 1 11ga
235	38	62.3	255	21	AA652792	Arabidopsis thalia	308	34	55.7	11	14	AA642650	Neurokinin 1 recep
236	38	62.3	257	21	AA621477	Arabidopsis thalia	309	34	55.7	11	20	AA692694	Human tachykinin a
237	38	62.3	257	21	AA652791	Arabidopsis thalia	310	34	55.7	162	22	AA672892	Human tachykinin a
238	38	62.3	475	22	AA684839	p73 gamma protein	311	34	55.7	162	22	AA673046	Human olfactory re
239	38	62.3	3722	12	AA610145	Cephalosporin anti	312	34	55.7	467	21	AA630869	Olfactory receptor
240	37	60.7	7	20	AA650324	Neutrophil-activat	313	34	55.7	572	22	AA603506	Arabidopsis thalia
241	37	60.7	7	20	AA692662	Human tachykinin a	314	34	55.7	582	14	AA639556	Human protein kina
242	37	60.7	7	21	AA675574	P antagonist peptid	315	34	55.7	583	22	AA630869	Deduced amino acid
243	37	60.7	7	22	AA691420	Tachykinins peptid	316	34	55.7	587	14	AA639553	Amino acid sequenc
244	37	60.7	7	22	AA691431	Tachykinins peptid	317	34	55.7	587	22	AA630861	Deduced amino acid
245	37	60.7	8	13	AA628444	Neurokinine 1 11ga	318	34	55.7	588	22	AA639555	Amino acid sequenc
246	37	60.7	8	10	AA692710	Human tachykinin a	319	34	55.7	588	22	AA630868	Sequence encoded b
247	37	60.7	8	22	AA691407	Tachykinins peptid	320	34	55.7	598	21	AA630868	Arabidopsis thalia
248	37	60.7	11	5	AA640481	Substance P analog	321	34	55.7	628	21	AA630867	Arabidopsis thalia
249	37	60.7	11	9	AA680316	Sequence of neurop	322	34	55.7	666	21	AA697010	S. cerevisiae esse
250	37	60.7	11	19	AA650979	Substance P analog	323	33	54.1	11	22	AA650314	Previn peptide #6
251	37	60.7	11	19	AA650972	Substance P analog	324	33	54.1	62	20	AA619487	Amino acid sequenc
252	37	60.7	11	19	AA650942	Substance P antago	325	33	54.1	77	21	AA616060	Arabidopsis thalia
253	37	60.7	11	19	AA608303	Amino acid sequenc	326	33	54.1	85	21	AA616059	Arabidopsis thalia
254	37	60.7	11	22	AA691414	Tachykinins peptid	327	33	54.1	138	15	AA662881	Murine anti-human
255	37	60.7	138	21	AA670578	Salmonella pathoge	328	33	54.1	171	18	AA623689	Potato polyphenol
256	36	59.0	9	22	AA699348	Atypical tachykin	329	33	54.1	324	17	AA692786	Canola palmitoyl-A
257	36	59.0	10	22	AA699347	Atypical tachykin	330	33	54.1	328	17	AA692789	Soybean palmitoyl-
258	36	59.0	10	22	AA691383	Tachykinins peptid	331	33	54.1	404	16	AA678621	Chicken GalInAc-a1p
259	36	59.0	11	13	AA621973	Cyclic substance P	332	33	54.1	505	14	AA641941	p17 gene LpTK-2 pr
260	36	59.0	11	22	AA692693	Human tachykinin a	333	33	54.1	505	16	AA685929	Protein tyrosine-k
261	36	59.0	11	22	AA699337	Human atypical tac	334	33	54.1	505	22	AA696304	Escherichia coli P
262	36	59.0	11	22	AA699358	ATT-short peptide.	335	33	54.1	566	22	AA640285	Human polyptide
263	36	59.0	12	6	AA650357	Hyalambtin dodecap	336	33	54.1	711	19	AA644842	Staphylococcus aur
264	36	59.0	12	18	AA604615	Kasasin peptide f	337	32	52.5	6	20	AA650694	Sequence of pharma
265	36	59.0	12	20	AA692730	Human tachykinin a	338	32	52.5	6	26	AA692659	Human tachykinin a
266	36	59.0	45	22	AA699335	Human atypical tac	339	32	52.5	6	21	AA677575	P antagonist peptid
267	36	59.0	45	22	AA699357	ATT peptide. Unid	340	32	52.5	6	22	AA699351	Atypical tachykin
268	36	59.0	56	22	AA618187	Peptide #4621 enco	341	32	52.5	6	22	AA691419	Tachykinins peptid
269	36	59.0	56	22	AA630684	Peptide #4491 enco	342	32	52.5	6	22	AA691421	Tachykinins peptid
270	36	59.0	56	22	AA605809	Peptide #4491 enco	343	32	52.5	7	22	AA699350	Tachykinins peptid
271	36	59.0	68	22	AA699333	Human atypical tac	344	32	52.5	8	22	AA699349	Atypical tachykin
272	36	59.0	76	22	AA699336	Human atypical tac	345	32	52.5	11	18	AA604613	Physalaemin peptid
273	36	59.0	107	22	AA699338	Human atypical tac	346	32	52.5	11	19	AA648280	Tyrosylpeptide phy
274	35	57.4	11	13	AA621975	Cyclic substance P	347	32	52.5	11	22	AA691386	Tachykinins peptid
275	35	57.4	11	14	AA632182	Generic neuropepti	348	32	52.5	11	22	AA650316	Previn peptide #8
276	35	57.4	11	16	AA674982	[D-Arg1, D-Phe3, D	349	32	52.5	12	22	AA692032	Galanin peptide SE
277	35	57.4	11	19	AA648950	Tachykinin peptid	350	32	52.5	13	15	AA649131	Sequence of C-term
278	35	57.4	11	20	AA692695	Human tachykinin a	351	32	52.5	13	15	AA649081	Infectious pancrea
279	35	57.4	11	21	AA608313	Amino acid sequenc	352	32	52.5	13	20	AA692700	Human tachykinin a
280	35	57.4	11	22	AA662781	Amino acid sequenc	353	32	52.5	29	21	AA615454	TCR beta V-N-J reg
281	35	57.4	11	22	AA696883	Chimeric analgesic	354	32	52.5	53	22	AA687377	Human gene 36 enco
282	35	57.4	11	22	AA650313	Previn peptide #5.	355	32	52.5	53	22	AA687407	Human gene 36 enco
283	35	57.4	96	19	AA698597	H. pylori GHPO 124	356	32	52.5	53	22	AA687408	Human gene 36 enco
284	35	57.4	128	19	AA648949	Preprotachykinin-C	357	32	52.5	54	21	AA628048	Human secreted pro
285	35	57.4	130	18	AA633902	Streptococcus pneu	358	32	52.5	54	22	AA675548	Human secreted pro
286	35	57.4	130	22	AA663008	Amino acid sequenc	359	32	52.5	112	22	AA623547	Human EST encoded
287	35	57.4	143	21	AA658600	Arabidopsis thalia	360	32	52.5	126	22	AA632312	Peptide #6349 enco
288	35	57.4	185	21	AA658599	Arabidopsis thalia	361	32	52.5	127	21	AA641066	Human OREF ORF830
289	35	57.4	195	21	AA658598	Arabidopsis thalia	362	32	52.5	128	20	AA637334	Protein involved i
290	35	57.4	250	21	AA656820	Arabidopsis thalia	363	32	52.5	136	21	AA625444	Pinus radiata cell
291	35	57.4	250	21	AA659507	Arabidopsis thalia	364	32	52.5	135	20	AA625444	Rat-derived eosino
292	35	57.4	296	21	AA656819	Arabidopsis thalia	365	32	52.5	181	18	AA623657	Tobacco polyphenol
293	35	57.4	296	21	AA659506	Arabidopsis thalia	366	32	52.5	181	20	AA697990	Tobacco polyphenol
294	35	57.4	304	21	AA656818	Arabidopsis thalia	367	32	52.5	209	22	AA699984	Chick limb deforma
295	35	57.4	304	21	AA659505	Arabidopsis thalia	368	32	52.5	232	21	AA638330	Human secreted pro
296	35	57.4	311	22	AA614238	Human novel protei	369	32	52.5	276	18	AA621195	Lipolytic enzyme/E
297	35	57.4	496	18	AA633901	Streptococcus pneu	370	32	52.5	293	21	AA674880	Neisseria meningit
298	35	57.4	496	22	AA663007	Amino acid sequenc	371	32	52.5	294	21	AA674878	Neisseria gonorrhoe
299	35	57.4	1092	21	AA652029	M. thermotautotroph	372	32	52.5	294	21	AA674879	Neisseria meningit
300	35	57.4	1092	21	AA651658	Methanobacter sp.	373	32	52.5	305	21	AA616920	Arabidopsis thalia
301	35	57.4	1279	22	AA639101	Human polyptide	374	32	52.5	305	21	AA623413	Arabidopsis thalia
302	35	57.4	1305	22	AA640887	Human tachykinin a	375	32	52.5	305	21	AA645709	Arabidopsis thalia
303	34	55.7	6	20	AA692712	Human tachykinin a	376	32	52.5	323	21	AA616919	Arabidopsis thalia

377	32	52.5	323	21	AAG23412	Arabidopsis thalia	450	31	50.8	208	22	AAW04463	Peptide #3145 enco
378	32	52.5	323	21	AAG45708	Arabidopsis thalia	451	31	50.8	249	22	AAW40179	Human polypeptide
379	32	52.5	323	21	AAG45713	Arabidopsis thalia	452	31	50.8	249	22	AAW45066	Human polypeptide
380	32	52.5	381	20	AAV33944	Soluble interleukin	453	31	50.8	249	22	AAW44412	Amino acid sequenc
381	32	52.5	381	21	AAG26698	Arabidopsis thalia	454	31	50.8	264	15	AAW60610	Tobamovirus moveme
382	32	52.5	402	22	AAU00427	Caenorhabditis ele	455	31	50.8	264	16	AAW67755	Tomv P30 elictor.
383	32	52.5	418	20	AAV35520	Chlamydia pneumoni	456	31	50.8	266	21	AAW18251	Plasmodium falcipla
384	32	52.5	433	21	AAG29013	Arabidopsis thalia	457	31	50.8	281	22	AAW12198	Human PRO1341 poly
385	32	52.5	452	21	AAG29012	Arabidopsis thalia	458	31	50.8	298	21	AAW07469	A human leucine-ri
386	32	52.5	462	22	AAW45966	Murine macrophage	459	31	50.8	307	21	AAV56059	HTLV-1 Tax/HLA-A2
387	32	52.5	462	22	AAW49983	Murine macrophage	460	31	50.8	307	21	AAV56083	HTLV tax/HLA-A2 re
388	32	52.5	464	20	AAV35231	Protein involved 1	461	31	50.8	307	21	AAV56086	HTLV tax/HLA-A2 re
389	32	52.5	479	21	AAG45712	Arabidopsis thalia	462	31	50.8	307	21	AAV57859	TCR beta chain and
390	32	52.5	484	21	AAG45711	Arabidopsis thalia	463	31	50.8	307	21	AAV57862	TCR beta chain and
391	32	52.5	508	22	AAW82317	Human immunoglobul	464	31	50.8	307	21	AAV57868	TCR beta chain and
392	32	52.5	531	21	AAG29011	Arabidopsis thalia	465	31	50.8	316	17	AAW05517	HCMV Toledo strain
393	32	52.5	614	20	AAV17905	Pseudomonas alpha-	466	31	50.8	349	22	AAU03566	Pseudomonas fluore
394	32	52.5	614	20	AAV17906	Pseudomonas alpha-	467	31	50.8	372	22	AAW84062	Human protein sequ
395	32	52.5	614	20	AAV17907	Pseudomonas alpha-	468	31	50.8	389	22	AAW84732	Human protein sequ
396	32	52.5	614	20	AAV17908	Pseudomonas alpha-	469	31	50.8	393	20	AAV35055	Chlamydia pneumoni
397	32	52.5	614	20	AAV17909	Pseudomonas alpha-	470	31	50.8	399	22	AAW33773	Human protein sequ
398	32	52.5	614	20	AAV17904	Pseudomonas alpha-	471	31	50.8	406	12	AAW11349	Cytochrome enzyme
399	32	52.5	632	12	AAW15470	Maltotetraose synt	472	31	50.8	447	22	AAW85485	Human protein sequ
400	32	52.5	712	22	AAW18088	Peptide #4522 enco	473	31	50.8	466	21	AAW87880	M. tuberculosis an
401	32	52.5	750	21	AAG45696	Arabidopsis thalia	474	31	50.8	477	22	AAW33231	C. glutamicum prote
402	32	52.5	766	20	AAV13457	Amino acid sequenc	475	31	50.8	477	22	AAW79682	Corynebacterium gl
403	32	52.5	768	21	AAG45695	Arabidopsis thalia	476	31	50.8	479	17	AAW04723	Acornatic acyl tran
404	32	52.5	804	21	AAW25515	Pinus radiata cell	477	31	50.8	491	21	AAW08899	Human secreted ox
405	32	52.5	828	21	AAW25559	Pinus radiata cell	478	31	50.8	512	22	AAU02834	Taxus cuspidata pr
406	32	52.5	843	21	AAW25518	Pinus radiata cell	479	31	50.8	530	21	AAW29626	Cat flea HMT synap
407	32	52.5	1197	21	AAV57445	Mouse Eae2 protein	480	31	50.8	547	22	AAW2957	Human protein sequ
408	32	52.5	1291	20	AAV16101	Acetobacter xylinu	481	31	50.8	566	18	AAW11217	Leishmania tropica
409	32	52.5	1658	21	AAV57450	Mouse Eae2L protei	482	31	50.8	566	20	AAW45167	Leishmania tropica
410	32	52.5	2243	22	AAW84884	Murine protein, SE	483	31	50.8	566	20	AAW45167	Leishmania tropica
411	32	52.5	2266	22	AAW84885	Human protein, SEQ	484	31	50.8	593	21	AAW13870	Arabidopsis thalia
412	32	52.5	2502	22	AAW82665	Porcine reproducti	485	31	50.8	593	21	AAW46880	Arabidopsis thalia
413	31	50.8	7	3	AAW20310	Ty78-SP5-11. Synt	486	31	50.8	612	21	AAW13869	Arabidopsis thalia
414	31	50.8	8	19	AAW50970	Substance P analog	487	31	50.8	612	21	AAW13869	Arabidopsis thalia
415	31	50.8	8	19	AAW50970	Tachykinin peptide	488	31	50.8	631	10	AAW91139	Human type IV coll
416	31	50.8	10	19	AAW48951	Leucocyte O2- prod	489	31	50.8	631	10	AAW91139	Human type IV coll
417	31	50.8	16	17	AAW01448	Leucocyte O2- prod	490	31	50.8	631	11	AAW07350	Human type IV matr
418	31	50.8	16	19	AAW57724	Proline/Arginine r	491	31	50.8	631	11	AAW07350	Human type IV matr
419	31	50.8	19	17	AAW01452	Leucocyte O2- prod	492	31	50.8	631	11	AAW07350	Human type IV matr
420	31	50.8	23	17	AAW01451	Leucocyte O2- prod	493	31	50.8	631	11	AAW07350	Human type IV matr
421	31	50.8	26	17	AAW01447	Leucocyte O2- prod	494	31	50.8	644	22	AAW20490	Human matrix metrl
422	31	50.8	26	19	AAW57523	Proline/Arginine r	495	31	50.8	660	11	AAW06420	Amino acid sequenc
423	31	50.8	27	21	AAW84363	Amino acid sequenc	496	31	50.8	663	19	AAW41111	Chicken matrix met
424	31	50.8	39	14	AAW30491	Antibacterial pept	497	31	50.8	663	19	AAW41127	Chicken matrix met
425	31	50.8	39	17	AAW01446	Leucocyte O2- prod	498	31	50.8	778	20	AAV35090	Chlamydia pneumoni
426	31	50.8	39	17	AAW4446	Synducin peptide (499	31	50.8	874	21	AAW41705	Arabidopsis thalia
427	31	50.8	39	17	AAW4446	Magnatin-derived a	500	31	50.8	874	22	AAW22287	Murine ADAMTS-9 am
428	31	50.8	39	19	AAW57722	Proline/Arginine r	501	31	50.8	882	21	AAW41704	Arabidopsis thalia
429	31	50.8	39	21	AAW57722	PR-39 peptide used	502	31	50.8	950	21	AAW41704	Arabidopsis thalia
430	31	50.8	39	22	AAW84690	Amino acid sequenc	503	31	50.8	958	21	AAW21255	Human metalloprote
431	31	50.8	39	22	AAW97280	PR-39 peptide. Un	504	31	50.8	1073	21	AAW21254	Human metalloprote
432	31	50.8	44	22	AAW51194	E. coli AMP gene p	505	31	50.8	1765	20	AAW41668	Rat sensory neuron
433	31	50.8	75	22	AAW21380	Human HMPF-1 mutan	506	31	50.8	1765	20	AAW06596	Rat sodium channel
434	31	50.8	75	22	AAW30829	Peptide #486 enco	507	31	50.8	1765	20	AAW06597	Rat sodium channel
435	31	50.8	80	11	AAV07349	Fragment of human	508	31	50.8	1765	20	AAV16572	Mouse sodium chan
436	31	50.8	85	11	AAV07338	Fragment of human	509	31	50.8	1765	20	AAW20122	Type 5 sodium chan
437	31	50.8	94	21	AAW16399	Arabidopsis thalia	510	31	50.8	1765	22	AAW20123	Rat sodium channel
438	31	50.8	103	21	AAW16398	Arabidopsis thalia	511	31	50.8	1765	22	AAW20124	Mouse sodium chan
439	31	50.8	136	21	AAW33870	Arabidopsis thalia	512	31	50.8	1882	22	AAW22866	Human ADAMTS-9 am
440	31	50.8	136	21	AAW00558	Human secreted pro	513	31	50.8	1934	22	AAW72301	Human ADAMTS-9 alt
441	31	50.8	136	22	AAW16275	Peptide #2709 enco	514	31	50.8	3639	14	AAW40227	ACVSV. Acetomulum
442	31	50.8	136	22	AAW28761	Peptide #2798 enco	515	31	50.8	3712	12	AAW13896	ACV synthetase. A
443	31	50.8	136	22	AAW04008	Peptide #2690 enco	516	31	50.8	4472	17	AAW97245	Virulence gene clu
444	31	50.8	139	21	AAW33868	Arabidopsis thalia	517	31	50.8	543	12	AAW13405	Parvo virus B19 VP
445	31	50.8	143	22	AAW70696	S cerevisiae apopt	30.5	50.0					
446	31	50.8	143	22	AAW70787	S cerevisiae apopt							
447	31	50.8	197	22	AAW33848	Human protein sequ							
448	31	50.8	208	22	AAW16746	Peptide #3180 enco							
449	31	50.8	208	22	AAW29234	Peptide #3271 enco							

ALIGNMENTS

CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage,
 CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.

XX Sequence 11 AA;

Query Match 91.8%; Score 56; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQOFGFL 10
 Db 1 rpkpqgffgl 10

RESULT 107

AAW92718 ID AAW92718 standard; peptide; 11 AA.

AC AAW92718;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #64.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KM Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.

OS Homo sapiens.

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PA Yankner BA;

PI WPI; 1999-189630/16.

DR Screening for neurotoxin inhibitors - by testing compounds for their
 XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PT Screening for neurotoxin inhibitors - by testing compounds for their
 XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PS Disclosure; Column 37-38; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage,
 CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.

XX Sequence 11 AA;

Query Match 91.8%; Score 56; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQOFGFL 10
 Db 1 rpkpqgffgl 10

RESULT 108

AAW92667 ID AAW92667 standard; peptide; 11 AA.

AC AAW92667;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #13.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KM Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenophilic angiodopathy.

OS Homo sapiens.

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PA Yankner BA;

PI WPI; 1999-189630/16.

DR Screening for neurotoxin inhibitors - by testing compounds for their
 XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PT Screening for neurotoxin inhibitors - by testing compounds for their
 XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PS Disclosure; Column 15-16; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage,
 CC with amyloidosis and non-inherited congenophilic angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.

XX Sequence 11 AA;

Query Match 91.8%; Score 56; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQOFGFL 10
 Db 1 rpkpqgffgl 10

RESULT 109

AAW92668 ID AAW92668 standard; peptide; 11 AA.

AC AAW92668;

DT	30-APR-1999	(first entry)				
XX						
DE	Human tachykinin agonist beta-amyloid peptide fragment #14.					
XX						
KW	Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;					
XX	Alzheimer's disease; Down's syndrome; amyloidosis; human;					
KW	hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.					
XX						
OS	Homo sapiens.					
XX						
FT	Key	Location/Qualifiers				
FT	Modified-site	11				
FT		/label=NLE				
XX						
PN	US5876948-A.					
XX						
PD	02-MAR-1999.					
XX						
PF	27-JUL-1991;	91US-0737371.				
XX						
PR	29-JUL-1991;	91US-0737371.				
XX						
PR	27-JUL-1990;	90US-0559173.				
XX						
PA	(CHIL-) CHILDRENS MEDICAL CENT.					
PI						
P1	Yankner BA;					
XX						
DR	WPI; 1999-189630/16.					
XX						
PT	Screening for neurotoxin inhibitors - by testing compounds for their					
PT	effect on beta-amyloid peptide neurotoxic effect on neuronal cells					
XX						
PS	Disclosure: Column 15-16; 28pp; English.					
XX						
CC	This invention describes a method for screening compounds for inhibiting					
CC	a neurotoxin. The method involves incubating tachykinin agonists with					
CC	neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be					
CC	used for identifying compounds for treating diseases characterised by an					
CC	undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,					
CC	Down's syndrome, and the syndromes of hereditary cerebral haemorrhage					
CC	with amyloidosis and non-inherited congenital angiodopathy with cerebral					
CC	haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human					
CC	beta-amyloid peptide fragments.					
XX						
SO	Sequence	11 AA;				
	Query Match.	91.8%; Score 56; DB 20; Length 11;				
	Best Local Similarity	100.0%; Pred. No. 0.0021;				
	Matches	10; Conservative	0; Mismatches	0; Indels	0; Gaps	0.
QY	1 RPKPOQFFGL	10				
	1 rpkpqgffgl	10				
DB						
	RESULT 110					
	AAW92670					
ID	AAW92670	standard; peptide; 11 AA.				
XX						
AC	AAW92670;					
XX						
DT	30-APR-1999	(first entry)				
XX						
DE	Human tachykinin agonist beta-amyloid peptide fragment #16.					
XX						
KW	Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;					
KW	Alzheimer's disease; Down's syndrome; amyloidosis; human;					
KW	hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.					
XX						
OS	Homo sapiens.					
XX						
FT	Key	Location/Qualifiers				

FT	Modified-site	1	/note= "Residue is ethionine"
XX	US5876948-A.		
XX	02-MAR-1999.		
XX	27-JUL-1991;	91US-0737371.	
XX	29-JUL-1991;	91US-0737371.	
XX	27-JUL-1990;	90US-0559173.	
XX	(CHIL-) CHILDRENS MEDICAL CENT.		
XX	Yankner BA;		
XX	WPI: 1999-189630/16.		
XX	Screening for neurotoxin inhibitors - by testing compounds for their		
XX	effect on beta-amyloid peptide neurotoxic effect on neuronal cells		
XX	Disclosure; Column 17-18; 28pp; English.		
XX	This invention describes a method for screening compounds for inhibiting		
XX	a neurotoxin. The method involves incubating tachykinin agonists with		
XX	neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be		
XX	used for identifying compounds for treating diseases characterised by an		
XX	undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,		
XX	Down's syndrome, and the syndromes of hereditary cerebral haemorrhage		
XX	with amyloidosis and non-inherited congenital anglophly with cerebral		
XX	haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human		
XX	beta-amyloid peptide fragments.		
XX	Sequence 11 AA;		
XX	Query Match	91.8%;	Score 56;
XX	Best Local Similarity	100.0%;	Pred. NO. 0.0021;
XX	Matches 10;	Conservative 0;	Mismatches 0;
XX		Indels 0;	Gaps 0.
QY	2 PKPOOFFGLM 11		
DB	2 pkpgqfgfglm 11		
	RESULT 111		
ID	AAW92672		
XX	AAW92672 standard; peptide; 11 AA.		
AC	AAW92672;		
XX	30-APR-1999 (first entry)		
DT	Human tachykinin agonist beta-amyloid peptide fragment #18.		
XX	Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;		
KW	Alzheimer's disease; Down's syndrome; amyloidosis; human;		
KW	hereditary cerebral haemorrhage; non-inherited congenital anglophly.		
XX	Homo sapiens.		
OS	US5876948-A.		
XX	02-MAR-1999.		
PD	27-JUL-1991;	91US-0737371.	
XX	29-JUL-1991;	91US-0737371.	
XX	27-JUL-1990;	90US-0559173.	
PR	(CHIL-) CHILDRENS MEDICAL CENT.		
XX	Yankner BA;		
PI			

XX DR WPI: 1999-189630/16.
XX PT Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX PS Disclosure: Column 17-18; 28pp; English.
XX CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiotrophy with cerebral
CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX CC
SQ Sequence 11 AA;

Query Match 91.8%; Score 56; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PKPOQFFGLM 11
DB 2 PKPQGFfglm 11

RESULT 112
AAB08614
ID AAB08614 standard; Peptide; 11 AA.
XX AC AAB08614;
XX DT 20-DEC-2000 (first entry)
XX DE Peptide identified from a databank of polypeptides and polynucleotides.
XX KM Precursor peptide; polypeptide hormone; peptide identification.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "hydrogen attached"
XX FT Modified-site 11 /note= "amidated residue"
XX FT
XX PN WO200050636-A1.
XX PD 31-AUG-2000.
XX PE 24-FEB-2000; 2000WO-FR00460.
XX PR 25-FEB-1999; 99US-0257525.
XX PA (SCRC) SCRAS SOC CONSEILS RECH & APPL SCI.
XX PA (CNRS) CNRS CENT NAT RECH SCI.
XX PI Camara Ferrer YJA, Thuriereau C, Martinez J, Berge G, Goze C;
XX DR WPI: 2000-572101/53.
XX PT Identifying peptide with selected function, useful particularly for
XX C-amidated hormones, by screening database for combination of nucleic
XX acid and amino acid sequences -
XX PS Disclosure: Page 22; 40pp; French.
XX CC The specification describes a method for identifying a peptide having
CC a particular function. The method comprises preparing a database of

CC polynucleotides and polypeptides of unknown functions, screening the
CC database for a combination of nucleotides or amino acids indicative of
CC the peptide with a particular function, and identifying polynucleotides
CC and proteins which contain the peptide. The method is used to identify
CC precursor peptides with an amidated C-terminus, especially polypeptide
CC hormones, for studying physiologically active substances. The present
CC sequence represents a peptide which was identified using the method of
CC the invention.
XX CC
SQ Sequence 11 AA;

Query Match 91.8%; Score 56; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PKPOQFFGLM 11
DB 2 PKPQGFfglm 11

RESULT 113
AAB99350
ID AAB99350 standard; peptide; 11 AA.
XX AC AAB99350;
XX DT 24-AUG-2001 (first entry)
XX DE Substance P tachykinin-related peptide SEQ ID NO:3.
XX KM Tachykinin-related peptide; substance P; neurokinin A; neurokinin B;
XX KM physiologically active; tachykinin; drug; veterinary medicine;
XX KM agrochemical.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 11 /note= "amidated"
XX FT
XX PN WO200134637-A1.
XX PD 17-MAY-2001.
XX PE 07-NOV-2000; 2000WO-JP07789.
XX PR 08-NOV-1999; 99JP-0317535.
XX PA (SUNR) SUNTORY LTD.
XX PI Ikeda T, Nomoto K, Minakata H;
XX DR WPI: 2001-329069/34.
XX PT Synthesis of new physiologically-active peptide analogs of tachykinin,
XX useful as drugs, veterinary medicines and agrochemicals, comprises
XX modifying C-terminal amino-acid residues -
XX PS Claim 13; Page 23; 36pp; Japanese.
XX CC The present invention describes a method for producing physiologically
CC active substances. The method comprises converting the amino-acid
CC residue at a specific position in a peptide into another amino-acid
CC residue to provide activity against (in)vertebrates. Also described are:
CC (1) converted unnatural tachykinin-related peptide with tachykinin-like
CC physiological activity against (in)vertebrates which is an amino-acid
CC sequence with the 5 amino-acids at C-terminal as in
CC -Phe-Ala-Gly-Ala-Met-NH₂ (1) where Ala = Val, Ile, Phe, Tyr, His, Met,
CC (Thr, Leu, Gly or Gln and Ala = Ser, Ala, Val, Met, Thr, Pro or Leu; and
CC (2) drugs, veterinary medicines or agrochemicals containing the new
CC tachykinin-related peptide as the active ingredient. The peptide
CC analogues are for use as drugs, veterinary medicines and agrochemicals

CC With activity on vertebrates or invertebrates. By modifying C-terminal
CC amino-acid residues of tachykinin, the activity of tachykinin and its
CC related derivative can therefore be changed from that against
CC vertebrates to that on invertebrates or vice versa. The present sequence
CC represents a specifically claimed tachykinin-related peptide from the
CC present invention.

XX Sequence 11 AA;

Query Match 91.8%; Score 56; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQPFGL 10
|||||

Db 1 rpkpqpfgl 10

RESULT 114

AAR21939
ID AAR21939 standard; Protein: 11 AA.

XX AAR21939;

XX 25-JUN-1992 (first entry)

XX Substance P [1le 8].

DE Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;

XX syndrome; hereditary cerebral haemorrhage.

KW Synthetic.

XX MO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI: 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using

XX tachykinin agonists e.g. substance P, physalaemin and neurokinin

XX B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 10; Page 21; 35pp; English.

XX The peptide is the tachykinin agonist substance P with an

XX isoleucine residue substituted at position 8. The peptide was

XX synthesised by standard solid phase synthesis. Neuronal

XX accumulation of beta-amyloid may be treated by administration of

XX tachykinin agonists. The peptide can reduce the neurotoxic effects

XX of a beta-amyloid related polypeptide on cultured neurons. The

XX peptide and its analogues are useful for controlling diseases

XX characterised by beta amyloid accumulation in the brain such as

XX Alzheimer's disease and Down's syndrome.

XX See also AAR21932-75.

XX Sequence 11 AA;

XX Query Match 90.2%; Score 55; DB 13; Length 11;

XX Best Local Similarity 90.9%; Pred. No. 0.0031;

XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQPFGLM 11
|||||

Db 1 rpkpqpfglm 11

RESULT 115
AAR21943
ID AAR21943 standard; Protein: 11 AA.
XX AAR21943;
XX 25-JUN-1992 (first entry)
XX Substance P [Met 7].
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
KW Synthetic.
XX MO9202248-A.
XX 20-FEB-1992.
XX 29-JUL-1991; 91WO-US05323.
XX 27-JUL-1990; 90US-0559173.
XX (CHIL-) CHILDRENS MED CENT.
XX Yankner BA;
XX WPI: 1992-079804/10.
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX Claim 10; Page 21; 35pp; English.
XX The peptide is the tachykinin agonist substance P with a
XX methionine residue substituted at position 7. The peptide was
XX synthesised by standard solid phase synthesis. Neuronal
XX accumulation of beta-amyloid may be treated by administration of
XX tachykinin agonists. The peptide can reduce the neurotoxic effects
XX of a beta-amyloid related polypeptide on cultured neurons. The
XX peptide and its analogues are useful for controlling diseases
XX characterised by beta amyloid accumulation in the brain such as
XX Alzheimer's disease and Down's syndrome.
XX See also AAR21932-75.

XX Sequence 11 AA;

XX Query Match 90.2%; Score 55; DB 13; Length 11;

XX Best Local Similarity 90.9%; Pred. No. 0.0031;

XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQPFGLM 11
|||||

Db 1 rpkpqpfglm 11

RESULT 116
AAR21949
ID AAR21949 standard; Protein: 11 AA.
XX AAR21949;
XX 25-JUN-1992 (first entry)
XX Substance P [Pro 3].
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;

KW syndrome; hereditary cerebral haemorrhage.
XX Synthetic.
OS
XX W09202248-A.
PN
XX 20-FEB-1992.
PD
XX 29-JUL-1991; 91WO-US05323.
PE
XX 27-JUL-1990; 90US-0559173.
PR
XX (CHIL-) CHILDRENS MED CENT.
PA
XX Yankner BA;
PI
XX WPI: 1992-079804/10.
DR
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Down's syndrome, etc.
PS
XX Claim 10; Page 21; 35pp; English.
PS
XX The peptide is the tachykinin agonist substance P with a Proline
CC residue substituted at position 3. The peptide was
CC synthesised by standard solid phase synthesis. Neuronal
CC accumulation of beta-amyloid may be treated by administration of
CC tachykinin agonists. The peptide can reduce the neurotoxic effects
CC of a beta-amyloid related polypeptide on cultured neurons. The
CC peptide and its analogues are useful for controlling diseases
CC characterised by beta amyloid accumulation in the brain such as
CC Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
CC
CC
SQ Sequence 11 AA:

Query Match 90.2%; Score 55; DB 13; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
DB 11
1 rpppqffglm 11

RESULT 117
AAR21958
ID AAR21958 standard; Peptide: 11 AA.
XX
AC AAR21958;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [Ala 9] or [D-Ala 9].
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
OS
XX
XX Key Location/Qualifiers
FT Modified-site 9 /note= "either L or D form"
FT
XX
XX W09202248-A.
PN
XX 20-FEB-1992.
PD
XX 29-JUL-1991; 91WO-US05323.
PE
XX 27-JUL-1990; 90US-0559173.
PR

XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
DR WPI: 1992-079804/10.
XX
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Down's syndrome, etc.
PS
XX Claim 10; Page 21; 35pp; English.
PS
XX The peptide is the tachykinin agonist substance P with an Ala (D/L)
CC residue substituted at position 9. The peptide was synthesised
CC by standard solid phase synthesis. Neuronal accumulation of
CC beta-amyloid may be treated by administration of tachykinin
CC agonists. The peptide can reduce the neurotoxic effects of a beta-
CC amyloid related polypeptide on cultured neurons. The peptide and
CC its analogues are useful for controlling diseases characterised by
CC beta amyloid accumulation in the brain such as Alzheimer's disease
CC and Down's syndrome.
CC See also AAR21932-75.
CC
CC
SQ Sequence 11 AA:

Query Match 90.2%; Score 55; DB 13; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
DB 11
1 rpkpqffglm 11

RESULT 118
AAW92669
ID AAW92669 standard; peptide: 11 AA.
XX
AC AAW92669;
XX
XX 30-APR-1999 (first entry)
DT
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #15.
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.
OS
XX
XX US5876948-A.
PN
XX 02-MAR-1999.
XX
XX 27-JUL-1991; 91US-0737371.
PE
XX 29-JUL-1991; 91US-0737371.
PR
XX 27-JUL-1990; 90US-0559173.
PR
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX
XX Yankner BA;
PI
XX
XX WPI: 1999-189630/16.
DR
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
PT
XX
XX Disclosure; Column 17-18; 28pp; English.
PS
XX
CC This invention describes a method for screening compounds for inhibiting

CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX
SQ Sequence 11 AA;

Query Match

Best Local Similarity 90.2%; Score 55; DB 20; Length 11;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
1111111111
Db 1 rpkpqgffglm 11

RESULT 119

AAW92671
ID AAW92671 standard; peptide; 11 AA.

XX
AC AAW92671;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #17.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.

XX Homo sapiens.

OS
XX US5876948-A.

XX PD 02-MAR-1999.

XX PF 27-JUL-1991; 91US-0737371.

XX PR 29-JUL-1991; 91US-0737371.

XX PR 27-JUL-1990; 90US-0559173.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.

XX PI Yankner BA;

XX DR WPI; 1999-189630/16.

PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX
PS Disclosure; Column 17-18; 28pp; English.

CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX
SQ Sequence 11 AA;

Query Match

Best Local Similarity 90.2%; Score 55; DB 20; Length 11;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
1111111111
Db 1 rpkpqgffglm 11

RESULT 120

AAW92673
ID AAW92673 standard; peptide; 11 AA.

XX
AC AAW92673;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #19.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;

KM hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.

XX Homo sapiens.

OS
XX US5876948-A.

XX PD 02-MAR-1999.

XX PF 27-JUL-1991; 91US-0737371.

XX PR 29-JUL-1991; 91US-0737371.

XX PR 27-JUL-1990; 90US-0559173.

XX PA (CHIL-) CHILDRENS MEDICAL CENT.

XX PI Yankner BA;

XX DR WPI; 1999-189630/16.

PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX
PS Disclosure; Column 17-18; 28pp; English.

CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

XX
SQ Sequence 11 AA;

Query Match 90.2%; Score 55; DB 20; Length 11;
Best Local Similarity 90.2%; Pred. No. 0.0031;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
1111111111
Db 1 rpkpqgffglm 11

RESULT 121

AAW92674
ID AAW92674 standard; peptide; 11 AA.

XX
AC AAW92674;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #20.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KM hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
 XX
 OS Homo sapiens.
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 PI WPI; 1999-189630/16.
 DR
 XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS Disclosure; Column 19-20; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis, and non-inherited congenital angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 CC
 SQ Sequence 11 AA;

Query Match 90.2%; Score 55; DB 20; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0031;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFGLM 11
 |||||
 DB 1 rpkpqgfalm 11

RESULT 122
 AAW92675
 ID AAW92675 standard; peptide; 11 AA.
 XX
 AC AAW92675;
 XX
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #21.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
 XX
 OS Homo sapiens.
 XX
 PI Key Location/Qualifiers
 FT Misc-difference 9
 FT /note="D-form residue"
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX

PF 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 PI WPI; 1999-189630/16.
 DR
 XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS Disclosure; Column 19-20; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis, and non-inherited congenital angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 CC
 SQ Sequence 11 AA;

Query Match 90.2%; Score 55; DB 20; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0031;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFGLM 11
 |||||
 DB 1 rpkpqgfalm 11

RESULT 123
 AAB49755
 ID AAB49755 standard; peptide; 11 AA.
 XX
 AC AAB49755;
 XX
 DT 17-APR-2001 (first entry)
 XX
 DE Complex sugar bound peptide (SBP) amino acid sequence.
 XX
 KW Sugar peptide complex; SBP; sugar bound peptide; enzymatically stable.
 XX
 OS Synthetic.
 XX
 PN JP2000319297-A.
 XX
 PD 21-NOV-2000.
 XX
 PF 30-MAR-1999; 99JP-0088030.
 XX
 PR 30-MAR-1999; 99JP-0088030.
 XX
 PA (NOGK) 2H NOGUCHI KENKYUSHO.
 XX
 DR WPI; 2001-184996/19.
 XX
 PT A process for preparation of enzymically stable sugar peptide complex
 PT
 PT
 XX
 PS Example 2; Page 3; App; Japanese.
 XX
 CC This invention relates to a process for the preparation of an
 CC enzymatically stable sugar peptide complex, and includes an in vivo
 CC stable inhibitor of peptide-N-glycanase (EC. 3.5.1.52). The process can
 CC be used for the investigation of in vivo reciprocal recognition of

CC cell-cell and substrate-receptor interaction, and their metabolism. The
 CC present sequence represents a complex sugar bound peptide (SBP) amino
 CC acid sequence prepared by the process of the invention.
 XX

SO Sequence 11 AA;

Query Match 90.2%; Score 55; DB 22; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.0031;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
 :|:|||||
 Db 1 krpqgffglm 11

RESULT 124

AAR21940
 ID AAR21940 standard; Protein; 11 AA.

XX AAR21940;

AC AAR21940;

XX 25-JUN-1992 (first entry)

XX Substance P [Pro 10].

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
 KW syndrome; hereditary cerebral haemorrhage.

XX Synthetic.

XX WO9202248-A.

XX 20-FEB-1992.

XX 29-JUL-1991; 91WO-US05323.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MED CENT.

XX Yankner BA;

XX WPI: 1992-079804/10.

XX Treatment of neuronal accumulation of beta-amyloid - using
 PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
 PT B, for treating Alzheimer's disease, Downs syndrome, etc.

XX Claim 10; Page 21; 35pp; English.

XX The peptide is the tachykinin agonist substance P with a proline
 CC residue substituted at position 10. The peptide was
 CC synthesised by standard solid phase synthesis. Neuronal
 CC accumulation of beta-amyloid may be treated by administration of
 CC tachykinin agonists. The peptide can reduce the neurotoxic effects
 CC of a beta-amyloid related polypeptide on cultured neurons. The
 CC peptide and its analogues are useful for controlling diseases
 CC characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome.
 CC See also AAR21932-75.

XX Sequence 11 AA;

Query Match 88.5%; Score 54; DB 13; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0046;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
 |||||
 Db 1 rpkpqgffglm 11

RESULT 125
 AAR42647
 ID AAR42647 standard; peptide; 11 AA.

XX AAR42647;

XX 19-APR-1994 (first entry)

XX Neurokinin 1 receptor affinity-contg. peptide.

XX Neurokinin 1; somatostatin; receptor; cytokine; growth factor;
 KW hormone; intra-operativ; tumour; low energy gamma photon;
 KW radionuclide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 9 /label= Megly

FT Modified-site 11 /note= "Met is Met(O2); the C-terminal is amidated"

XX WO9318797-A.

XX 30-SEP-1993.

XX 24-MAR-1993; 93WO-US02772.

XX 25-MAR-1992; 92EP-0200848.

XX (MLCW) MALINCRODT MEDICAL INC.

XX Doedens BJ, Ensing GJ, Panek KJ;

XX WPI: 1993-320461/40.

XX Intra-operatively detecting and locating tumour tissues - using
 PT specific peptide(s) labelled with low energy gamma photon
 PT emitting radionuclide

XX Disclosure; Page 5; 31pp; English.

XX The method of intraoperatively detecting and locating tumoral
 CC tissues makes use of peptides having selective neurokinin 1
 CC receptor affinity (AAR42644: generic formula: AAR42646-R42650:
 CC specific examples), peptides having selective somatostatin
 CC receptor affinity (AAR42645: generic formula: AAR42651-R42660:
 CC specific examples), and peptides selected from cytokines,
 CC growth factors and hormones.

XX Sequence 11 AA;

Query Match 88.5%; Score 54; DB 14; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0046;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
 |||||
 Db 1 rpkpqgffglm 11

RESULT 126

AAM92716
 ID AAM92716 standard; peptide; 11 AA.

XX AAM92716;

XX 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #62.
 DE
 XX

KM Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenital angiodysplasia.
XX Homo sapiens.
XX US5876948-A.
XX 02-MAR-1999.
XX 27-JUL-1991; 91US-0737371.
XX 29-JUL-1991; 91US-0737371.
XX 27-JUL-1990; 90US-0559173.
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX Yankner BA;
XX WPI: 1999-189630/16.
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX Disclosure: Column 37-38; 28pp; English.
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodysplasia with cerebral
CC haemorrhage. AAW2655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX Sequence 11 AA;
SQ

Query Match 88.5%; Score 54; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPQGFGLM 11
|||||
DT 1 rpkpqgffgpm 11
Db

RESULT 127
AAW92721
ID AAW92721 standard; peptide; 11 AA.
XX AAW92721;
XX 30-APR-1999 (first entry)
XX Human tachykinin agonist beta-amyloid peptide fragment #67.
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodysplasia.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Modified-site 11
FT /label= Memet
FT /note= "N-methyl-methionine"
PN US5876948-A.
PD 02-MAR-1999.
XX

PF 27-JUL-1991; 91US-0737371.
XX 29-JUL-1991; 91US-0737371.
XX 27-JUL-1990; 90US-0559173.
XX (CHIL-) CHILDRENS MEDICAL CENT.
XX Yankner BA;
XX WPI: 1999-189630/16.
XX Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX Disclosure: Column 39-40; 28pp; English.
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodysplasia with cerebral
CC haemorrhage. AAW2655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX Sequence 11 AA;
SQ

Query Match 88.5%; Score 54; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPQGFGLM 11
|||||
DT 1 rpkpqgffgpm 11
Db

RESULT 128
AAB91451
ID AAB91451 standard; Peptide; 10 AA.
XX AAB91451;
XX 22-JUN-2001 (first entry)
XX Tachykinins peptide SEQ ID NO:627.
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX Homo sapiens.
XX Synthetic.
XX WO200069900-A2.
XX 23-NOV-2000.
XX 17-MAY-2000; 2000WO-US13576.
XX 17-MAY-1999; 99US-0134406.
XX 10-SEP-1999; 99US-0153406.
XX 15-OCT-1999; 99US-0159783.
XX (CONR-) CONJUCHEM INC.
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX WPI: 2001-112059/12.
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

PT -
XX
PS Disclosure: Page 403; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide) and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases.
CC Intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
S0 Sequence 10 AA:

Query Match 86.9%; Score 53; DB 22; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQQFFGL 10
 |||||:|
Db 1 rpkpqfgy1 10

RESULT 129
AAB80315
ID AAB80315 standard; protein: 11 AA.
XX
AC AAB80315;
XX
DT 14-SEP-1990 (first entry)
XX
DE Sequence of neuropeptide antagonist C which binds with polypeptide
DE receptor for bombesin type polypeptides.
XX
KW Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist C.
XX
OS Swiss 3T3 cells.
XX
XX
FH Key Location/Qualifiers
FT MISC-difference 2 /label=OTHER
FT /note="DPro"
FT MISC-difference 7 /label=OTHER
FT /note="DPhe"
FT MISC-difference 1 /label=OTHER
FT /note="DTrp"
FT MISC-difference 11 /label=OTHER
FT /note="Met-NH2"
XX
XX
PN W08807551-A.
XX
PD 06-OCT-1988.
XX
PF 31-MAR-1988; 88WO-GB00255.
XX
PR 25-NOV-1987; 87GB-0027638.
XX

PA (IMCR) IMPERIAL CANCER RES.
XX
PI Rosengurt E, Zachary I, Woll P;
XX
DR WPI: 1988-292842/41.
XX
PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
XX
PS Disclosure: Table 2; 42pp; English.
XX
XX
CC The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAB80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX
S0 Sequence 11 AA:

Query Match 86.9%; Score 53; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQQFFGLM 11
 |||||:|
Db 1 rpkpqffwlm 11

RESULT 130
AAB80320
ID AAB80320 standard; protein: 11 AA.
XX
AC AAB80320;
XX
DT 14-SEP-1990 (first entry)
XX
DE Sequence of neuropeptide antagonist H which binds with polypeptide
DE receptor for bombesin type polypeptides.
XX
KW Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist H.
XX
OS Swiss 3T3 cells.
XX
XX
FH Key Location/Qualifiers
FT MISC-difference 1 /label=OTHER
FT /note="DArg"
FT MISC-difference 2 /label=OTHER
FT /note="DPro"
FT MISC-difference 7 /label=OTHER
FT /note="DPhe"
FT MISC-difference 9 /label=OTHER
FT /note="DHis"
FT MISC-difference 11 /label=OTHER
FT

/note="Met-NH2"

FT XX
PN XX WO8807551-A.
XX
PD XX 06-OCT-1988.
XX
PF XX 31-MAR-1988; 88WO-GB00255.
XX
PR XX 25-NOV-1987; 87GB-0027638.
XX
PA (IMCR) IMPERIAL CANCER RES.
XX
PI Rosengurt E, Zachary I, Woll P;
XX WPI; 1988-292842/41.
DR XX
XX
PT New polypeptide receptor for bombesin type polypeptide(s) -
PT is isolated from surface of Swiss 3T3 cells, and antibodies and
PT antagonists are useful for treating uncontrolled cell proliferation
XX
PS Disclosure; Table 2; 42pp; English.
XX
XX The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC cells which binds selectively with polypeptides of the bombesin type and
CC binds with antagonist A and antagonist D. Antagonist A is a
CC commercially available structural variant of substance P, known as
CC [D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as
CC [D-Pro2] spantide. Antagonist B is also commercially available structural
CC variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC 11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC substance P antagonists (see AAP80313-80322) were tested for their
CC ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC potent than either A or D. Spantide (B) had no antagonist activity even
CC at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC growth is associated with disorders of proteins of the bombesin family.
XX
SQ Sequence 11 AA:

Query Match 86.9%; Score 53; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPQGFGLM 11
|||
Db 1 rpkpqgffhlm 11

RESULT 131
AAR21935
ID AAR21935 standard; Protein; 11 AA.
XX
AC AAR21935;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [Pro 9] or [D-Pro 9].
XX
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 9 /note="either L or D form"
XX
XX WO9202248-A.
XX
PD 20-FEB-1992.

XX
PF 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX WPI; 1992-079804/10.
DR XX
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX Claim 10; Page 21; 35pp; English.
XX
XX The peptide is the tachykinin agonist substance P with a Pro (D/L)
CC residue substituted at position 9. The peptide was synthesised
CC by standard solid phase synthesis. Neuronal accumulation of
CC beta-amyloid may be treated by administration of tachykinin
CC agonists. The peptide can reduce the neurotoxic effects of a beta-
CC amyloid related polypeptide on cultured neurons. The peptide and
CC its analogues are useful for controlling diseases characterised by
CC beta amyloid accumulation in the brain such as Alzheimer's disease
CC and Down's syndrome.
XX See also AAR21932-75.
XX
SQ Sequence 11 AA:

Query Match 86.9%; Score 53; DB 13; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPQGFGLM 11
|||
Db 1 rpkpqgffhlm 11

RESULT 132
AAR21964
ID AAR21964 standard; Peptide; 11 AA.
XX
AC AAR21964;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [D-Ala 4].
XX
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4 /note="D form"
XX
XX WO9202248-A.
XX
PD 20-FEB-1992.
XX
PF 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
XX WPI; 1992-079804/10.
XX

PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.

PS Claim 13; Page 22; 35pp; English.

XX The peptide is the tachykinin agonist substance P with a D-Ala
CC residue substituted at position 4. The peptide was synthesised
CC by standard solid phase synthesis. Neuronal accumulation of
CC beta-amyloid may be treated by administration of tachykinin
CC agonists. The peptide can reduce the neurotoxic effects of a beta-
CC amyloid related polypeptide on cultured neurons. The peptide and
CC its analogues are useful for controlling diseases characterised by
CC beta amyloid accumulation in the brain such as Alzheimer's disease
CC and Down's syndrome.
CC See also AAR21932-75.

XX Sequence 11 AA;

SO Query Match 86.9%; Score 53; DB 13; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 rpkpqffglm 11

RESULT 133

AAW50978 AAW50978 standard; peptide; 11 AA.

AAW50978;

31-JUL-1998 (first entry)

Substance P analogue [D-Arg1,D-Pro2,D-Phe7,D-His9].

Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;

Substance P; cancer; inhibition; growth hormone releasing factor;

spantide.

Synthetic.

Key

Misc-difference 1 Location/Qualifiers

Misc-difference 2 /note= "D-form residue"

Misc-difference 7 /note= "D-form residue"

Misc-difference 9 /note= "D-form residue"

Modified-site 11 /note= "C-terminal amide"

EP835662-A2.

15-APR-1998.

11-DEC-1996; 96EP-0309012.

08-OCT-1996; 96US-0727679.

16-AUG-1996; 96IN-0001822.

(NAIM-) NAT INST IMMUNOLOGY.

Jaggi M, Mukherjee R;

WPI: 1998-208959/19.

Composition containing analogues of vasoactive intestinal peptide,

PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)

PS Disclosure; Page 13; 49pp; English.

XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 ACCKNFEDWKTRSC (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.

XX Sequence 11 AA;

SO Query Match 86.9%; Score 53; DB 19; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPOQFFGLM 11
Db 1 rpkpqffglm 11

RESULT 134

AAW50968 AAW50968 standard; peptide; 11 AA.

AAW50968;

31-JUL-1998 (first entry)

Substance P analogue, [D-Pro2,D-Phe7,D-Tip9].

Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;

Substance P; cancer; inhibition; growth hormone releasing factor;

spantide.

Synthetic.

Key

Misc-difference 2 Location/Qualifiers

Misc-difference 7 /note= "D-form residue"

Misc-difference 9 /note= "D-form residue"

Modified-site 11 /note= "C-terminal amide"

EP835662-A2.

15-APR-1998.

11-DEC-1996; 96EP-0309012.

08-OCT-1996; 96US-0727679.

16-AUG-1996; 96IN-0001822.

(NAIM-) NAT INST IMMUNOLOGY.

Jaggi M, Mukherjee R;

WPI: 1998-208959/19.

XX Composition containing analogues of vasoactive intestinal peptide,
 PT somatostatin - bombesin and substance P, for treatment of tumours
 PT and for inhibiting over-expression of these peptide(s)
 PS
 XX Disclosure; Page 13; 49pp; English.

CC The invention relates to a new composition which comprises: (1) the
 CC somatostatin analogue SOM2 AGCKNFRDKMTPTSdc (3-14 disulphide bridge),
 CC and (11) at least 4 of the peptides: antagonist of vasoactive
 CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
 CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
 CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
 CC more general compositions containing peptide analogues of somatostatin,
 CC VIP, bombesin and substance P. The compositions are used in human or
 CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
 CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
 CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
 CC breast, kidney or particularly rectum and colon, and (b) to prevent,
 CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
 CC cells express receptors for VIP, somatostatin, bombesin and/or substance
 CC P. The present sequence represents a substance P analogue.

SQ Sequence 11 AA;

Query Match 86.9%; Score 53; DB 19; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0069;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
 |||||
 Db 1 rpkpqgfflwm 11

RESULT 135
 AAM92677

ID AAM92677 standard; peptide; 11 AA.

XX AAM92677;

DT 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #23.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.

XX Homo sapiens.

XX US5876948-A.

XX 02-MAR-1999.

XX 27-JUL-1991; 91US-0737371.

XX 29-JUL-1991; 91US-0737371.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Yankner BA.

XX WPI; 1999-189630/16.

XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX Disclosure; Column 19-20; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with

CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
 CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.

SQ Sequence 11 AA;

Query Match 86.9%; Score 53; DB 20; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0069;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
 |||||
 Db 1 rpkpqgfflwm 11

RESULT 136
 AAM92678

ID AAM92678 standard; peptide; 11 AA.

XX AAM92678;

DT 30-APR-1999 (first entry)

XX Human tachykinin agonist beta-amyloid peptide fragment #24.

XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;

KW Alzheimer's disease; Down's syndrome; amyloidosis; human;

KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.

XX Homo sapiens.

XX US5876948-A.

XX 02-MAR-1999.

XX 27-JUL-1991; 91US-0737371.

XX 29-JUL-1991; 91US-0737371.

XX 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Yankner BA.

XX WPI; 1999-189630/16.

XX Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells

XX Disclosure; Column 19-20; 28pp; English.

XX This invention describes a method for screening compounds for inhibiting

CC a neurotoxin. The method involves incubating tachykinin agonists with

CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be

CC used for identifying compounds for treating diseases characterised by an

CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,

CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage

CC with amyloidosis and non-inherited congenital angiodopathy with cerebral

CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human

CC beta-amyloid peptide fragments.

XX Sequence 11 AA;

SQ

Query Match 86.9%; Score 53; DB 20; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
| | | | | | | | | | | |
DB 1 rpkpqgffwlm 11

RESULT 137

AAB98879
ID AAB98879 standard; Peptide; 11 AA.

AC AAB98879;

DT 14-AUG-2001 (first entry)

DE Chimeric analgesic peptide #35.

KW Opioid receptor binding; nociceptive receptor binding; analgesic;
pain; chimeric peptide.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 2 /note- "D-form residue"

FT Misc-difference 7 /note- "D-form residue"

FT Misc-difference 9 /note- "D-form residue"

FT Modified-site 11 /label= OTHER

FT /note= "C-terminal amide"

PN WO200136371-A2.

XX 03-MAY-2001.

PF 27-OCT-2000; 2000WO-US29789.

PR 28-OCT-1999; 99US-0428692.

PA (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.

PI Carr DB, Lipkowski AW, Kream R, Misicka-Kesik A;

DR WPI; 2001-397593/42.

XX New chimeric peptides used for treating pain comprise opioid receptor

PS binding group and nociceptive receptor binding group

CC Claim 10; Page 15; 34pp; English.

CC The present invention describes a number of chimeric peptides comprising

CC an opioid receptor binding moiety and a nociceptive receptor binding

CC moiety. These can be used as analgesics for the treatment of pain. Unlike

CC opioid receptor based peptides alone, tolerance does not result from

CC their long-term use. The present sequence is one of the peptides of the

CC invention.

XX Sequence 11 AA;

OY 1 RPKPOFFGLM 11
| | | | | | | | | | | |
DB 1 rpkpqgffwlm 11

RESULT 138
AAB91411
ID AAB91411 standard; Peptide; 11 AA.

AC AAB91411;

DT 22-JUN-2001 (first entry)

DE Tachykinins peptide SEQ ID NO:587.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;

KW blood component; modification; succinimidyl; maleimido group; amino;

KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

DR WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents

XX peptidase degradation, useful for increasing length of in vivo activity

XX disclosure; Page 392; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)

CC comprising a therapeutically active amino acid region (III) and a

CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to

CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptide stabilized therapeutic peptide composed of 3-50 amino acids.

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

CC factors and neurotransmitters, to protect them from peptidase activity

CC in vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent

CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half

CC life) and specificity as bonding to large molecules decreases.

CC Intercellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the

CC exemplification of the present invention.

XX Sequence 11 AA;

Query Match 86.9%; Score 53; DB 22; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
| | | | | | | | | | | |
DB 1 rpkpqgffwlm 11

RESULT 139

AAB91412
ID AAB91412 standard; Peptide; 11 AA.

AC AAB91412;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:588.
XX
KM Protection: endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0135406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 392; 733pp; English.
XX
SS The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;
XX

Query Match 86.9%; Score 53; DB 22; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOFFGLM 11
Db 1 rpkpqgffwlm 11

RESULT 140;
AAB91415
ID AAB91415 standard; Peptide; 11 AA.
XX
AC AAB91415;
XX
DT 22-JUN-2001 (first entry)
XX

DE Tachykinins peptide SEQ ID NO:591.
XX
KM Protection: endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure; Page 393; 733pp; English.
XX
SS The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 11 AA;
XX

Query Match 86.9%; Score 53; DB 22; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOOFFGLM 11
Db 1 rpkpqgffwlm 11

RESULT 141
AAB91429
ID AAB91429 standard; Peptide; 11 AA.
XX
AC AAB91429;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:605.
XX
KM Protection: endogenous therapeutic peptide; peptidase; conjugation;
KM blood component; modification; succinimidyl; maleimido group; amino;

KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US13576.
 XX
 PR 17-MAY-1999; 99US-0134446.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT
 PS Disclosure: Page 397; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptide stabilized therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specifically as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 CC
 XX
 SQ Sequence: 11 AA;

Query Match 86.9%; Score 53; DB 22; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0069;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
 |||||
 Db 1 rpkpqgffglm 11

RESULT 142
 AAB50311
 ID AAB50311 standard; peptide: 11 AA.
 XX
 AC AAB50311;
 XX
 DT 08-MAR-2001 (first entry)
 XX
 DE Previn peptide #3.
 XX
 KW Asian tcd; antibacterial; Botulinum toxin inhibitor; BtxB;
 KW previn; tetanus neurotoxin; buforin.
 XX
 OS Bufo bufo gargarizans.
 OS Synthetic.
 XX

PN WO200069891-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 15-MAY-2000; 2000WO-US13215.
 XX
 PR 17-MAY-1999; 99US-0134446.
 XX
 PA (USSA) US DEPT OF THE ARMY.
 XX
 PI Gordon RK, Moorad DR, Doctor BP, Garcia GE;
 XX
 DR WPI; 2001-025001/03.
 XX
 PT Novel Previn compounds useful for inhibiting the protease activity of
 PT Botulinum B and tetanus toxins -
 XX
 PS Claim 7; Page 29; 47pp; English.
 XX
 CC The present sequence is a previn compound which inhibits the enzymatic
 CC activity of BtxB and tetanus neurotoxins. Previn
 CC may be used to construct compounds such as buforinins.
 CC
 XX
 SQ Sequence: 11 AA;

Query Match 86.9%; Score 53; DB 22; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0069;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
 |||||
 Db 1 rakpqgffglm 11

RESULT 143
 AAB98880
 ID AAB98880 standard; peptide: 12 AA.
 XX
 AC AAB98880;
 XX
 DT 14-AUG-2001 (first entry)
 XX
 DE Chimeric analgesic peptide #36.
 XX
 KW Opioid receptor binding; nociceptive receptor binding; analgesic;
 KW pain; chimeric peptide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH MISC-difference 2
 FT MISC-difference 2 /note- "D-form residue"
 FT MISC-difference 7 /note- "D-form residue"
 FT MISC-difference 9 /note- "D-form residue"
 FT Modified-site 12
 FT /label= OTHER
 FT /note= "C-terminal amide"
 XX
 PN WO200130371-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 27-OCT-2000; 2000WO-US29789.
 XX
 PR 28-OCT-1999; 99US-0428692.
 XX
 PA (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
 XX
 PI Carr DB, Lipkowski AM, Kream R, Misicka-Kesik A;
 XX

DR WPI; 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
binding group and nociceptive receptor binding group
XX
PS Claim 10; Page 15-16; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 12 AA:

Query Match 86.9%; Score 53; DB 22; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.0075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQGFGLM 11
1111111111
Db 1 rpkpqgffwlm 11

RESULT 144
AAR21932
ID AAR21932 standard; peptide; 9 AA.
XX
AC AAR21932;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P (1-9) fragment.
XX
KM Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
PN WO9202248-A.
XX
PD 20-FEB-1992.
XX
PF 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
DR WPI; 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalamin and neurokinin
PT B. for treating Alzheimer's disease, Down's syndrome, etc.
XX
PS Claim 9; Page 21; 35pp; English.
XX
CC The peptide is a tachykinin agonist consisting of residues 1-9 of
CC substance P. The peptide was synthesised by standard solid phase
CC synthesis. Analogues of the peptide, with C-terminal deletions down
CC to substance P (1-4) were also synthesised. Neuronal accumulation of
CC beta-amyloid may be treated by administration of these tachykinin
CC agonists. The peptides reduce the neurotoxic effects of a beta-
CC amyloid related polypeptide on cultured neurons. The peptide and
CC its analogues are useful for controlling diseases characterised by
CC beta amyloid accumulation in the brain such as Alzheimer's disease
CC and Down's syndrome.
XX See also AAR21933-75.
XX

SQ Sequence 9 AA:

Query Match 85.2%; Score 52; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQGFGLM 9
1111111111
Db 1 rpkpqgffg 9

RESULT 145
AAY03162
ID AAY03162 standard; peptide; 9 AA.
XX
AC AAY03162;
XX
DT 10-JUN-1999 (first entry)
XX
DE Substance P fragment P/1-9#.
XX
KM Opioid peptide; opioid analgesia; enhancer; opioid anaesthesia;
KM substance P.
XX
OS Synthetic.
XX
PN US5891842-A.
XX
PD 06-APR-1999.
XX
PF 12-APR-1996; 96US-0631434.
XX
PR 09-APR-1993; 93US-0044954.
XX
PR 12-APR-1996; 96US-0631434.
XX
PA (TUFT) TUFTS COLLEGE.
XX
PI Kream RM;
XX
DR WPI; 1999-253906/21.
XX
PT Synergistic method for enhancing opioid analgesia and anaesthesia
PT within a human
XX
PS Disclosure; Column 14; 20pp; English.
XX
CC This sequence is a fragment of substance P used in the method of the
CC invention. The method is for enhancing opioid analgesia within a human
CC subject for a duration of 15 minutes comprises concurrent administration
CC of substance P, or one of its precursors. The method is used to elicit
CC opioid analgesia and anaesthesia, either prior to or after the occurrence
CC of a nociceptive event. The components have a synergistic effect. The
CC method allows use of low doses of opioid that produce little or no
CC physiological effect reducing conventional risks of toxicity and
CC addiction, and allows the use of low doses of substance P and its related
CC analogs that limit their in vivo physiological consequences. The
CC analgesia is naloxone reversible allowing diminishment or complete
CC elimination of opioid analgesia if desired and on demand. The treatment
CC provides a durable analgesic effect, but only minimally disturbs and
CC interrupts the normal metabolic processes of the body.
XX
SQ Sequence 9 AA:

Query Match 85.2%; Score 52; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQGFGLM 9
1111111111
Db 1 rpkpqgffg 9

RESULT 146
AAW92665
ID AAW92665 standard; peptide; 9 AA.
XX
AC AAW92665;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #11.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI; 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 15-16; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 9 AA:

Query Match 85.2%; Score 52; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQGFPG 9
Db 1 rpkpqgffg 9

RESULT 147
AAG62780
ID AAG62780 standard; peptide; 9 AA.
XX
AC AAG62780;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of a substance P fragment.
XX
KW Clostridial neurotoxin; pain; botulinum toxin; Substance P.
XX
OS Unidentified.
XX

PN W0200153336-A1.
XX
PD 26-JUL-2001.
XX
XX 17-JAN-2001; 2001WO-US01529.
XX
XX 19-JAN-2000; 2000US-0489667.
XX
XX (ALLR) ALLERGAN SALES INC.
XX
PA Donovan S;
XX
DR WPI; 2001-451900/48.
XX
PT Agent useful for treating pain comprises a clostridial neurotoxin (or
PT component) attached to a targeting moiety
XX
PS Disclosure; Page 72; 77pp; English.
XX
XX The specification describes an agent, comprising a clostridial neurotoxin
CC attached to a targeting moiety, where the targeting moiety is selected
CC from transmission compounds, and compounds substantially similar to the
CC transmission compounds. The agent may be used for treating pain, where
CC the clostridial neurotoxin component is derived from botulinum toxin
CC selected from botulinum types A, B, C, D, E, F, G and mixtures of these.
CC The targeting moiety comprises a light chain and an amine end segment of
CC a heavy chain and comprises Substance P as the targeting moiety. The pain
CC alleviating effects persist for 2-6 months. The present sequence
CC represents a substance P fragment, and is used in the course of the
CC invention.
XX
SQ Sequence 9 AA:

Query Match 85.2%; Score 52; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPQGFPG 9
Db 1 rpkpqgffg 9

RESULT 148
AAB98878
ID AAB98878 standard; Peptide; 9 AA.
XX
AC AAB98878;
XX
DT 14-AUG-2001 (first entry)
XX
DE Chimeric analgesic peptide #34.
XX
KW Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
XX Synthetic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 9 /label=OTHER
FT /note="C-terminal amide"
XX
XX W0200130371-A2.
XX
PD 03-MAY-2001.
XX
XX 27-OCT-2000; 2000WO-US29789.
XX
XX 28-OCT-1999; 99US-0428692.
XX
PA (NEME-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX

PI Carr DB, Lipkowski AM, Kream R, Misicka-Kesik A;
XX
DR WPI: 2001-397593/42.
XX
PT New chimeric peptides used for treating pain comprise opioid receptor
XX binding group and nociceptive receptor binding group
PS Claim 10; Page 15; 34pp; English.
XX
CC The present invention describes a number of chimeric peptides comprising
CC an opioid receptor binding moiety and a nociceptive receptor binding
CC moiety. These can be used as analgesics for the treatment of pain. Unlike
CC opioid receptor based peptides alone, tolerance does not result from
CC their long-term use. The present sequence is one of the peptides of the
CC invention.
XX
SQ Sequence 9 AA;
XX
Query Match 85.2%; Score 52; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RPKPQGF 9
DB 1 rpkpqgffg 9
RESULT 149
AAB91444
ID AAB91444 standard; Peptide; 9 AA.
XX
AC AAB91444;
XX
DT 22-JUN-2001 (first entry)
XX
DE Tachykinins peptide SEQ ID NO:620.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimide group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 9905-0134406.
PR 10-SEP-1999; 9905-0153406.
PR 15-OCT-1999; 9905-0159783.
XX
PA (CONT-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudreau K;
XX
DR WPI: 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
XX
PS Disclosure; Page 401; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 9 AA;
XX
Query Match 85.2%; Score 52; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RPKPQGF 9
DB 1 rpkpqgffg 9
RESULT 150
AAR28443
ID AAR28443 standard; peptide; 11 AA.
XX
AC AAR28443;
XX
DT 22-MAR-1993 (first entry)
XX
DE Neurokinine 1 ligand #1.
XX
KW NK1 receptor; tumour; malignant glioma; pheochromocytoma;
KW paraganglia; small cell lung cancer; nerve regeneration; lymphoma;
KW granuloma; Crohn's disease.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 9
FT /label= MeGly
FT Modified-site 11
FT /label= OTHER
FT /note= "Met(O)2-NH2"
XX
PN WO9218536-A.
XX
PD 29-OCT-1992.
XX
PF 22-APR-1992; 92WO-US03307.
XX
PR 22-APR-1991; 91EP-0200955.
XX
PA (MLCW) MALLINCKRODT MEDICAL INC.
XX
PI Bakker WH, Hagen PM, Krenning EP, Lamberts SWJ, Visser TJ;
XX
DR WPI: 1992-382047/46.
XX
PT Detection and localisation of tissues with neurokinine-1 receptors
PT - for detecting and treating tumours having neurokinine-1
PT receptors e.g. malignant glioma, small cell lung cancer etc.
XX
XX
PS Disclosure; Page 4; 22pp; English.
XX
CC This peptide or its tyro deriv. is a preferred peptide having a
CC selective affinity to neurokinine-1 receptors which (when
CC labelled with a radioactive isotope) can be used in imaging methods.
CC A generic formula for preferred peptides is AAR28441. Such peptides
CC are thus useful in diagnosis and treatment of conditions that are
CC related to NK1 receptors and in visualising NK1 receptors on certain

RESULT 153
AAR21961
ID AAR21961 standard; peptide: 11 AA.
XX
AC AAR21961;
XX
DT 25-JUN-1992 (first entry)
XX
DE Cyclic substance P [Hcys 5,11].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 5
FT /label= OTHER
FT /note= "OTHER = homocysteine"
FT Misc-difference 11
FT /label= OTHER
FT /note= "OTHER = homocysteine"
XX
PN MO9202248-A.
XX
PD 20-FEB-1992.
XX
PE 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;
XX
DR WPI: 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
PS Claim 11; Page 22; 35pp; English.
XX
CC The peptide is the tachykinin agonist, substance P with
CC homocysteine substituted at positions 5 and 11, with a disulphide
CC bond formed between them making the peptide cyclic. The
CC peptide was synthesised by standard solid phase synthesis.
CC Neuronal accumulation of beta-amyloid may be treated by administ-
CC ration of tachykinin agonists. The peptide can reduce the neuro-
CC toxic effects of a beta-amyloid related polypeptide on cultured
CC neurons. The peptide and its analogues are useful for controlling
CC diseases characterised by beta amyloid accumulation in the brain
CC such as Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA;

Query Match 82.0%; Score 50; DB 13; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPODFGL 10
DB 1 rpkpxqfifgl 10

RESULT 154
AAW92684
ID AAW92684 standard; peptide: 11 AA.
XX
AC AAW92684;
XX

DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #30.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 5
FT /note= "Residue is homocysteine"
FT Modified-site 10
FT /note= "Residue is homocysteine"
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PE 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI: 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 23-24; 28pp; English.
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA;

Query Match 82.0%; Score 50; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RPKPODFGLM 11
DB 1 rpkpxqfifgxm 11

RESULT 155
AAW92686
ID AAW92686 standard; peptide: 11 AA.
XX
AC AAW92686;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #32.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.

XX	Key	Location/Qualifiers
XX	Modified-site	5
FT	Modified-site	/note- "Residue is homocysteine"
FT	Modified-site	11
XX	Modified-site	/note- "Residue is homocysteine"
PN	US5876948-A.	
XX	02-MAR-1999.	
PD		
PE	27-JUL-1991;	91US-0737371.
XX		
PE	29-JUL-1991;	91US-0737371.
PR	27-JUL-1990;	90US-0559173.
XX		
PA	(CHIL-) CHILDRENS MEDICAL CENT.	
PI	Yankner BA;	
PI		
DR	WPI, 1999-189630/16.	
XX		
PT	Screening for neurotoxin inhibitors - by testing compounds for their effect on beta-amyloid peptide neurotoxic effect on neuronal cells	
PT		
PS	Disclosure; Column 23-24; 28pp; English.	
XX		
CC	<p>This invention describes a method for screening compounds for inhibiting a neurotoxin. The method involves incubating tachykinin agonists with neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be used for identifying compounds for treating diseases characterised by an undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease, Down's syndrome, and the syndromes of hereditary cerebral haemorrhage with amyloidosis and non-inherited congenital angiodopathy with cerebral haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human beta-amyloid peptide fragments.</p>	
CC		
XX		
XX	Sequence	11 AA;
XX		

PR 10-SEP-1999: 99US-0153406.
PR 15-OCT-1999: 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K:
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX -
PS Disclosure: Page 399; 733pp: English.

XX
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90839 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention.

Sequence 11 AA:

PF 14-MAY-1992; 92EP-0850108.
 XX
 PR 15-MAY-1991; 91SE-0001472.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PI Ahren B, Bartfai T, Consolo S, Hoekfelt T, Land T;
 PI Langel U, Lindskog S, Wiesenfeld-Hallin Z;
 XX
 DR WPI: 1992-384184/47.
 XX
 PR New galanin antagonist peptide(s) - used for treating
 PT Alzheimer's-type senile dementia, schizophrenia, analgesia and
 PT intestinal diseases
 XX
 PS Disclosure: Page 7; 21pp; English.
 XX
 CC The C-terminal of this peptide is amidated. MW-2392; IC50= 40nM.
 CC The peptides given in AAR26679-90 are used to treat disorders in
 CC mammals caused by the function of galanin at its receptor. The
 CC peptides may be useful in the regulation of insulin release, growth
 CC hormone release, acetylcholine release, dopamine release, substance
 CC P release, somatostatin release and noradrenaline release. They are
 CC useful in endocrinology, food intake, neurology and psychiatry, and
 CC to treat Alzheimer-type senile dementia, schizophrenia, intestinal
 CC diseases, and in analgesia. Dosage is 0.01-1000, pref. 0.1-1000
 CC microg/kg body wt.
 XX
 SQ Sequence 22 AA;

Query Match 82.0%; Score 50; DB 13; Length 22;
 Best Local Similarity 90.0%; Pred. No. 0.044; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PKQOQFFGLM 11
 I | | | | | | | |
 DB 13 pppqgffglm 22

RESULT 158
 AAP50634
 ID AAP50634 standard; Peptide; 9 AA.
 XX
 AC AAP50634;
 XX
 DT 09-MAR-1992 (first entry)
 XX
 DE Substance P-like peptide.
 XX
 KW Hair tonic; growth; regeneration.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /label- pyroglutamic acid
 XX
 PN JP6020807-A.
 XX
 PD 14-OCT-1985.
 XX
 PF 28-MAR-1984; 84JP-0058390.
 XX
 PR 28-MAR-1984; 84JP-0058390.
 XX
 PA (MEIJ) MEIJI SEIKA KAISHA.
 XX
 DR WPI: 1985-293619/47.
 XX
 PT Hair tonic compsn. - comprises peptide contg. pyroglutamic acid
 PT or other aminoacid(s) residue
 XX

PS Disclosure: Page 2; 3pp; Japanese.
 XX
 CC The C-terminal is amidated. Substance P (H-RPKPEERFGLM-NH2) or
 CC this peptide derived from it can be used in aq. soln. or suspension
 CC to promote hair growth and regeneration.
 CC See also AAP50632 and AAP50633.
 XX
 SQ Sequence 9 AA;

Query Match 80.3%; Score 49; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPQOQFFGLM 11
 I | | | | | | | |
 DB 1 kpqgffglm 9

RESULT 159
 AAW92714
 ID AAW92714 standard; peptide; 9 AA.
 XX
 AC AAW92714;
 XX
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #60.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
 XX
 OS Homo sapiens.
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI: 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS Disclosure: Column 37-38; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SQ Sequence 9 AA;

Query Match 80.3%; Score 49; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KPQOQFFGLM 11

AC	AA029593;
XX	
DT	22-APR-1993 (first entry)
XX	
DE	vertebrate Stromelysin artificial substrate.
XX	
KW	Enzyme inhibitors; diagnosis; screening; testing; enzyme stimulators; hydrolytic enzymes; HIV protease; glycosidases; nucleases.
XX	
PN	EP518557-A.
XX	
PD	16-DEC-1992.
XX	
PF	03-JUN-1992; 92EP-0305109.
XX	
PR	10-JUN-1991; 91US-0712828.
XX	
PA	(ELIL) LILLY & CO ELI.
XX	
PI	Heath WF, Lai MT, Manetta JV, Sportsman JR, Yan SCB; Lai MHT;
XX	
DR	WPI; 1992-417420/51.
XX	
PT	Measurement of hydrolytic enzyme activity in large numbers of samples - using resin bound substrate attached to reporter molecule for easy assessment of change rate e.g. of HIV-1 protease
PS	Claim 10; Page 18; 19pp: English.
CC	This sequence represents an artificial substrate for vertebrate stromelysin. The N terminal residue may opt. be biotinylated, and the C terminal opt. conjugated to FITC.
SO	Sequence 13 AA:
OY	1 RPKPOQFFGLM 11 1 : Db 1 rrrpqffglm 11
RESULT 163	
AAP30142	
ID	AAP30142 standard; Protein; 11 AA.
AC	AAP30142;
XX	
DT	14-JUN-1992 (first entry)
XX	
DE	Sequence of peptides with substance P inhibiting activity.
XX	
KW	Substance P antagonist; pain therapy; hypertension.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 2 /label= D-P
FT	Modified-site 7 /label= D-W
FT	Misc-difference 8 /label= F,I
FT	Modified-site 9 /label= D-W
FT	Modified-site 11 /label= M,I
FT	/note= "bonded to NH2"
PN	WO8301251-A.

```

XX 14-APR-1983.
XX PD
XX PF 09-OCT-1981; 81WO-DE00171.
XX PR 09-OCT-1981; 81WO-DE00171.
XX PR 09-OCT-1981; 81EP-0902802.
XX PA (FERR ) FERRING ARZNEIMITTE.
XX PA (HORI/) HORIG J.
XX PI Horig J;
XX DR WPI: 1983-39155K/16 (39155K).
XX PT Undeca:peptide derivs. with substance P inhibiting activity -
XX PT usef. for treating pain and hypertension
XX PS Claim 2; Page 18; 25pp; German.
XX CC The peptides of the invention are powerful antagonists of Substance
XX CC P and so are useful in human and veterinary medicine, for treating
XX CC pain and hypertension (esp.) chronic conditions. A 10 microm concn.
XX CC of the peptide produced about 50% inhibition at a Substance P concn. of
XX CC 7.5-20 nanom.
XX SQ Sequence 11 AA;

Query Match 78.7%; Score 48; DB 4; Length 11;
Best Local Similarity 81.8%; Pred. NO. 0.049; 1; Indels 0; Gaps 0;
Matches 9; Conservative 1; Mismatches 1;

OY 1 RPKPOQFFGLM 11
   |||||:| 11
Db 1 rpkpqgwfvlm 11

RESULT 164
AAP80317
ID AAP80317 standard; protein; 11 AA.
XX AC AAP80317;
XX DT 14-SEP-1990 (first entry)
XX DE Sequence of neuropeptide antagonist E which binds with polypeptide
XX DE receptor for bombesin type polypeptides.
XX KW Spantide; neuropeptide; polypeptide receptor; cancer diagnosis;
XX KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
XX KW antagonist E.
XX SS Swiss 3T3 cells.
XX FH Key Location/Qualifiers
XX FT Misc-difference 2 /label=OTHER
XX FT /note="DPro"
XX FT Misc-difference 7 /label=OTHER
XX FT /note="DTrp"
XX FT Misc-difference 9 /label=OTHER
XX FT /note="DTrp"
XX FT Misc-difference 11 /label=OTHER
XX FT /note="Met-NH2"
XX EN W08807551-A.
XX PD 06-OCT-1988.

```

PF 31-MAR-1988; 88WO-GB00255.
XX
XX 25-NOV-1987; 87GB-0027638.
XX
XX (IMCR) IMPERIAL CANCER RES.
XX
XX Rosengurt E, Zachary I, Woll P;
XX WPI; 1988-292842/41.
XX
XX
XX New polypeptide receptor for bombesin type polypeptide(s) -
XX is isolated from surface of Swiss 3T3 cells; and antibodies and
XX antagonists are useful for treating uncontrolled cell proliferation
XX
XX
XX Disclosure; Table 2; 42pp; English.
XX
XX The patent claims a polypeptide isolated from the surface of Swiss 3T3
XX cells which binds selectively with polypeptides of the bombesin type and
XX binds with antagonist A and antagonist D. Antagonist A is a
XX commercially available structural variant of substance P. It is also known as
XX [D-Arg1, D-Pic2, D-Trp7,9, Leu11] substance P. It is also known as
XX [D-Pro2] spantide. Antagonist B is also commercially available structural
XX variant of substance P known as [D-Phe5] spantide. Substance P is an
XX 11-mer neuropeptide, of interest in studies in pain transmission. Ten
XX substance P antagonists (see AAP80313-80322) were tested for their
XX ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
XX of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
XX potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
XX potent than either A or D. Spantide (B) had no antagonist activity even
XX at 100 uM. Polypeptide antagonists A and D and novel variants are useful
XX for diagnosis and therapy, esp. of cancers where uncontrolled cell
XX growth is associated with disorders of proteins of the bombesin family.
XX
SQ Sequence 11 AA:

Query Match 78.7%; Score 48; DB 9; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.049;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
||| ||| |
Db 1 rpkpqgfwlm 11

RESULT 165
AAR21966
ID AAR21966 standard; Peptide; 11 AA.
XX
XX AAR21966;
XX
XX 25-JUN-1992 (first entry)
XX
XX Cyclic substance P (D Cys 5, hCys 10).
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX key Location/Qualifiers
XX Disulfide-bond 5..10
XX Misc-difference 10
XX /Label= homocysteine
XX Modified-site 5
XX /note="D form"
XX
XX W09202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX

PR 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX
XX
XX Claim 11; Page 22; 35pp; English.
XX
XX The peptide is the tachykinin agonist substance P with a D Cys
XX residue substituted at position 5 and a homocys at position 9,
XX with a disulphide bond formed between them making the peptide
XX cyclic. The peptide was synthesised by standard solid phase
XX synthesis. Neuronal accumulation of beta-amyloid may be treated
XX by administration of tachykinin agonists. The peptide can reduce
XX the neurotoxic effects of a beta-amyloid related polypeptide on
XX cultured neurons. The peptide and its analogues are useful for
XX controlling diseases characterised by beta amyloid accumulation
XX in the brain such as Alzheimer's disease and Down's syndrome.
XX See also AAR21932-75.
XX
SQ Sequence 11 AA:

Query Match 78.7%; Score 48; DB 13; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
||| ||| |
Db 1 rpkpcqffgxm 11

RESULT 166
AAR21967
ID AAR21967 standard; Peptide; 11 AA.
XX
XX AAR21967;
XX
XX 25-JUN-1992 (first entry)
XX
XX Cyclic substance P [Cys 5, 11].
XX
XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
XX syndrome; hereditary cerebral haemorrhage.
XX
XX Synthetic.
XX
XX key Location/Qualifiers
XX Disulfide-bond 5..11
XX
XX W09202248-A.
XX
XX 20-FEB-1992.
XX
XX 29-JUL-1991; 91WO-US05323.
XX
XX 27-JUL-1990; 90US-0559173.
XX
XX (CHIL-) CHILDRENS MED CENT.
XX
XX Yankner BA;
XX
XX WPI; 1992-079804/10.
XX
XX
XX Treatment of neuronal accumulation of beta-amyloid - using
XX tachykinin agonists e.g. substance P, physalaemin and neurokinin
XX B, for treating Alzheimer's disease, Downs syndrome, etc.
XX

XX PS Claim 11; Page 22; 35pp; English.

CC The peptide is the tachykinin agonist substance P with Cys

CC residues substituted at positions 5 and 11, with a disulphide bond

CC formed between them, making the peptide cyclic. The peptide was

CC synthesised by standard solid phase synthesis. Neuronal accumu-

CC lation of beta-amyloid may be treated by administration of tachykinin

CC agonists. The peptide can reduce the neurotoxic effects of a beta-

CC amyloid related polypeptide on cultured neurons. The peptide and

CC its analogues are useful for controlling diseases characterised by

CC beta amyloid accumulation in the brain such as Alzheimer's disease

CC and Down's syndrome.

CC See also AAR21932-75.

XX SQ Sequence 11 AA;

QY Query Match 78.7%; Score 48; DB 13; Length 11;

Best Local Similarity 90.0%; Pred. No. 0.049; 1; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPQGFGL 10

|||||

Db 1 rpkpqgffgl 10

RESULT 167

AAR21960

ID AAR21960 standard; Peptide; 11 AA.

XX AAR21960;

AC AAR21960;

XX 25-JUN-1992 (first entry)

DT

XX Cyclic substance P [Hcys 5,9].

DE

XX Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;

KW syndrome; hereditary cerebral haemorrhage.

KX

OS Synthetic.

OS

XX Key Location/Qualifiers

FT Misc-difference 5

FT /label= OTHER

FT /note= "OTHER = homocysteine"

FT Misc-difference 9

FT /label= OTHER

FT /note= "OTHER = homocysteine"

XX WO9202248-A.

PN

XX 20-FEB-1992.

PD

XX 29-JUL-1991; 91WO-US05323.

PF

XX 27-JUL-1990; 90US-0559173.

PR

XX (CHIL-) CHILDRENS MED CENT.

PA

XX Yankner BA.

PI

XX WPI; 1992-079804/10.

DR

XX Treatment of neuronal accumulation of beta-amyloid - using

PT tachykinin agonists e.g. substance P, physalaemin and neurokinin

PT B, for treating Alzheimer's disease, Down's syndrome, etc.

PT

XX Claim 11; Page 22; 35pp; English.

PS

XX The peptide is the tachykinin agonist, substance P with

CC homocysteine substituted at positions 5 and 9, with a disulphide

CC bond formed between them making the peptide cyclic. The

CC peptide was synthesised by standard solid phase synthesis.

CC Neuronal accumulation of beta-amyloid may be treated by administ-

CC ration of tachykinin agonists. The peptide can reduce the neuro-

CC toxic effects of a beta-amyloid related polypeptide on cultured

CC neurons. The peptide and its analogues are useful for controlling

CC diseases characterised by beta amyloid accumulation in the brain

CC such as Alzheimer's disease and Down's syndrome.

CC See also AAR21932-75.

XX SQ Sequence 11 AA;

QY Query Match 78.7%; Score 48; DB 13; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.049; 2; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPQGFGL 11

|||||

Db 1 rpkpxgffxlm 11

RESULT 168

AAW50969

ID AAW50969 standard; peptide; 11 AA.

XX AAW50969;

AC AAW50969;

XX 31-JUL-1998 (first entry)

DT

XX Substance P analogue, [D-Pro2,D-Trp7,9].

DE

XX Vasoactive intestinal peptide; VIP; antagonist; somatostatin; bombesin;

KW Substance P; cancer; inhibition; growth hormone releasing factor;

KX spantide.

XX

OS Synthetic.

OS

XX Key Location/Qualifiers

FT Misc-difference 2

FT /note= "D-form residue"

FT Misc-difference 7

FT /note= "D-form residue"

FT Misc-difference 9

FT /note= "D-form residue"

FT Modified-site 11

FT /note= "C-terminal amide"

XX EP835662-A2.

PN

XX 15-APR-1998.

PD

XX 11-DEC-1996; 96EP-0309012.

PF

XX 08-OCT-1996; 96US-0727679.

PR

XX 16-AUG-1996; 96IN-0001822.

PR

XX (NAIM-) NAT INST IMMUNOLOGY.

PA

XX Jaggi M, Mukherjee R;

PI

XX WPI; 1998-208959/19.

DR

XX Composition containing analogues of vasoactive intestinal peptide,

PT somatostatin - bombesin and substance P, for treatment of tumours

PT and for inhibiting over-expression of these peptide(s)

PT

XX Disclosure; Page 13; 49pp; English.

PS

XX The invention relates to a new composition which comprises: (i) the

CC somatostatin analogue SOM2 AGCKNFRDWRPSDC (3-14 disulphide bridge),

CC and (ii) at least 4 of the peptides: antagonist of vasoactive

CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP

CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin

CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.
XX
SQ Sequence 11 AA:

Query Match 78.7%; Score 48; DB 19; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.049;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 RPKPOFFGLM 11
| | | | | | | | | | | |
Db 1 rpkpqwfwlm 11

RESULT 169
AAW92683
ID AAW92683 standard; peptide; 11 AA.
XX
AC AAW92683;
XX
DT 30-APR-1999 (first entry)
XX
DE Human tachykinin agonist beta-amyloid peptide fragment #29.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 5 /note= "Residue is homocysteine"
FT Modified-site 9 /note= "Residue is homocysteine"
FT FT
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI: 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 23-24; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human

CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA:

Query Match 78.7%; Score 48; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 RPKPOFFGLM 11
| | | | | | | | | | | |
Db 1 rpkpqffxlm 11

RESULT 170
AAW92685
ID AAW92685 standard; peptide; 11 AA.
XX
AC AAW92685;
XX
DT 30-APR-1999 (first entry)
XX

DE Human tachykinin agonist beta-amyloid peptide fragment #31.
XX
KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
OS Homo sapiens.
XX
PN US5876948-A.
XX
PD 02-MAR-1999.
XX
PF 27-JUL-1991; 91US-0737371.
XX
PR 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI Yankner BA;
XX
DR WPI: 1999-189630/16.
XX
PT Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
PS Disclosure; Column 23-24; 28pp; English.
XX
XX This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX
SQ Sequence 11 AA:

Query Match 78.7%; Score 48; DB 20; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOFFGL 10
| | | | | | | | | | | |
Db 1 rpkpcqffgl 10

RESULT 171

AAW92656
 ID AAW92656 standard; peptide; 11 AA.
 XX
 AC AAW92656;
 XX
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #2.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 27-JUL-1991; 91US-0737371.
 XX
 PR 29-JUL-1991; 91US-0737371.
 PR 27-JUL-1990; 90US-0559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;
 XX
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
 XX
 PS Disclosure; Column 11-12; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments.
 XX
 SQ Sequence 11 AA;
 XX

Query Match 78.7%; Score 48; DB 20; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.049;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
 DB 1 rpkpqgfwlm 11

RESULT 172
 AAB98881
 ID AAB98881 standard; Peptide; 11 AA.
 XX
 AC AAB98881;
 XX
 DT 14-AUG-2001 (first entry)
 XX

DE Chimeric analgesic peptide #37.
 XX
 KW Opioid receptor binding; nociceptive receptor binding; analgesic;
 KW pain; chimeric peptide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2 /note= "D-form residue"
 FT Misc-difference 7 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /label= OTHER
 FT /note= "C-terminal amide"
 XX
 PN WO200130371-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 27-OCT-2000; 2000WO-US29789.
 XX
 PR 28-OCT-1999; 99US-0428692.
 XX
 PA (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
 XX
 PI Carr DB, Lipkowski AW, Kream R, Misicka-Keslk A;
 XX
 DR WPI; 2001-397593/42.
 XX
 PT New chimeric peptides used for treating pain comprise opioid receptor
 PT binding group and nociceptive receptor binding group
 XX
 PS Claim 10; Page 16; 34pp; English.
 XX
 CC The present invention describes a number of chimeric peptides comprising
 CC an opioid receptor binding moiety and a nociceptive receptor binding
 CC moiety. These can be used as analgesics for the treatment of pain. Unlike
 CC opioid receptor based peptides alone, tolerance does not result from
 CC their long-term use. The present sequence is one of the peptides of the
 CC invention.
 XX
 SQ Sequence 11 AA;
 XX

Query Match 78.7%; Score 48; DB 22; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.049;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOQFFGLM 11
 DB 1 rpkpqgfwlm 11

RESULT 173
 AAB91413
 ID AAB91413 standard; Peptide; 11 AA.
 XX
 AC AAB91413;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Tachykinins peptide SEQ ID NO:589.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimideyl; maleimide group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX

PN WO200069900-A2.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US13576.
XX
XX 17-MAY-1999; 99US-0134406.
XX 10-SEP-1999; 99US-0134406.
XX 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K,
XX
XX WPI; 2001-112059/12.
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
XX peptide degradation, useful for increasing length of in vivo activity
XX
XX
XX Disclosure; Page 392; 733pp; English.
XX
XX The present invention describes a modified therapeutic peptide (I)
XX comprising a therapeutically active amino acid region (III) and a
XX reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
XX a less therapeutically active amino acid region (IV), which covalently
XX bonds with amino/hydroxyl/thiol groups on blood components to form a
XX peptide stabilized therapeutic peptide composed of 3-50 amino acids.
XX (I) are useful for modifying therapeutic peptides e.g. hormones, growth
XX factors and neurotransmitters, to protect them from peptidase activity
XX in vivo for the treatment of various disorders. Endogenous therapeutic
XX peptides are not suitable as drug candidates as they require frequent
XX administration due to rapid degradation by peptidases in the body.
XX Modifying and attaching therapeutic peptides to albumin prevents or
XX reduces the action of peptidases to increase length of activity (half
XX life) and specificity as bonding to large molecules decreases.
XX Intracellular uptake and interference with physiological processes.
XX AAB90829 to AAB92441 represent peptides which can be used in the
XX exemplification of the present invention.
XX
XX Sequence 11 AA:
SQ

Query Match 78.7%; Score 48; DB 22; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.049;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQGFGLM 11
DB 1 rpkpqgfwlm 11

RESULT 174
AAB98882
ID AAB98882 standard; Peptide: 12 AA.
XX
XX AAB98882;
AC
XX 14-AUG-2001 (first entry)
DT
XX
XX Chimeric analgesic peptide #38.
DE
XX
XX Opioid receptor binding; nociceptive receptor binding; analgesic;
KW pain; chimeric peptide.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 2
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 7 /note= "D-form residue"
FT Misc-difference 9

FT /note= "D-form residue"
FT Modified-site 12
FT /label= OTHER
FT /note= "C-terminal amide"
XX
XX WO200130371-A2.
XX
XX 03-MAY-2001.
XX
XX 27-OCT-2000; 2000WO-US29789.
XX
XX 28-OCT-1999; 99US-0428692.
XX
XX (NEW-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
XX
XX Carr DB, Lipkowski AM, Kream R, Misicka-Kesik A;
XX
XX WPI; 2001-397593/42.
XX
XX New chimeric peptides used for treating pain comprise opioid receptor
XX binding group and nociceptive receptor binding group
XX
XX
XX Claim 10; Page 16; 34pp; English.
XX
XX The present invention describes a number of chimeric peptides comprising
XX an opioid receptor binding moiety and a nociceptive receptor binding
XX moiety. These can be used as analgesics for the treatment of pain. Unlike
XX opioid receptor based peptides alone, tolerance does not result from
XX their long-term use. The present sequence is one of the peptides of the
XX invention.
XX
XX Sequence 12 AA:
SQ

Query Match 78.7%; Score 48; DB 22; Length 12;
Best Local Similarity 81.8%; Pred. No. 0.054;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPKPQGFGLM 11
DB 1 rpkpqgfwlm 11

RESULT 175
AAB06260
ID AAB06260 standard; peptide: 11 AA.
XX
XX AAB06260;
AC
XX 16-OCT-2000 (first entry)
DT
XX
XX Substance P.
DE
XX
XX Substance P; SP; neurokinin-1 receptor; NK-1R; nociception; saporin; SAP;
KW analgesic; anti-inflammatory; neuroprotective; anti-asthmatic;
KW anti-allergic; dermatological; anti-ulcer; tranquiliser;
KW immunosuppressive; anti-migraine; cytostatic; substance P antagonist;
KW cytotoxic; ribosome inactivator; prostaglandin antagonist; cancer;
KW respiratory disease; asthma; allergic rhinitis; ophthalmic disease;
KW conjunctivitis; allergic dermatitis; psoriasis; ulcerative colitis;
KW Crohn's disease; gastrointestinal disorder; anxiety; psychosis;
KW rheumatoid arthritis; carcinoma; lupus erythematosus conjunctivitis.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 11
FT /note= "C-terminal amide"
XX
XX US6063758-A.
XX
XX 16-MAY-2000.

PF 09-JUL-1997; 97US-0890157.
XX
XX 09-JUL-1997; 97US-0890157.
XX
PA (ADTA-) ADVANCED TARGETING SYSTEMS INC.
XX
PI Lappi DA, Wiley RG;
XX
DR WPI: 2000-430049/37.
XX
XX New conjugates comprising substance P or its analog, and a
XX ribosome-inactivating protein (for example saporin), for alleviating
XX pain and treating disorders associated with neurokinin-1 receptor -
PS
XX Disclosure: Column 14; 21pp; English.
XX
XX The present sequence is substance P (SP), which binds to the neurokinin-1
XX receptor (NK-1R). SP is secreted by small unmyelinated C-fibres of the
XX peripheral nervous system that are thought to be primary nociceptive
XX neurons. The present sequence may be conjugated to Saporin (SAP), a
XX ribosome-inactivating protein, to produce SP-SAP. The conjugate may be
XX used to control chronic pain by specifically targeting cells having NK1
XX receptors, and inhibiting proliferation of or causing death of these
XX cells. It may also be used to treat NK-1R-associated disorders
XX including respiratory conditions (e.g. asthma, allergic rhinitis),
XX ophthalmic conditions (e.g. conjunctivitis), cutaneous conditions (e.g.
XX allergic dermatitis, psoriasis), intestinal conditions (e.g. ulcerative
XX colitis, Crohn's disease), gastrointestinal disorders, central nervous
XX system disorders (e.g. anxiety, psychosis), inflammatory diseases (e.g.
XX rheumatoid arthritis), proliferative conditions (e.g. carcinoma),
XX disorders related to immune enhancement or suppression (e.g. lupus
XX erythematosus conjunctivitis), and especially migraine.
SQ
XX Sequence 11 AA:

Query Match 77.0%; Score 47; DB 21; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOQFGSLM 11
IIII IIIII
DB 1 rpkpwffglm 11

RESULT 176
AAW92711
ID AAW92711 standard; peptide; 8 AA.
XX
AC AAW92711;
XX
XX 30-APR-1999 (first entry)
XX
XX Human tachykinin agonist beta-amyloid peptide fragment #57.
DE
XX
XX Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
KW hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX
XX Homo sapiens.
OS
XX
XX US5876948-A.
PN
XX
XX 02-MAR-1999.
PD
XX
XX 27-JUL-1991; 91US-0737371.
PF
XX
XX 29-JUL-1991; 91US-0737371.
PR
XX 27-JUL-1990; 90US-0539173.
XX
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA
XX
XX Yankner BA;

XX
XX WPI: 1999-189630/16.
DR
XX
XX Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX
XX
XX Disclosure: Column 35-36; 28pp; English.
PS
XX
XX This invention describes a method for screening compounds for inhibiting
XX a neurotoxin. The method involves incubating tachykinin agonists with
XX neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
XX used for identifying compounds for treating diseases characterised by an
XX undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
XX Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
XX with amyloidosis and non-inherited congenital angiodopathy with cerebral
XX haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
XX beta-amyloid peptide fragments.
CC
XX
SQ Sequence 8 AA:

Query Match 75.4%; Score 46; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RPKPOQFP 8
IIII IIIII
DB 1 rpkpqgff 8

RESULT 177
AAB91410
ID AAB91410 standard; peptide; 10 AA.
XX
XX AAB91410;
AC
XX
XX 22-JUN-2001 (first entry)
DT
XX
XX Tachykinins peptide SEQ ID NO:586.
DE
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
OS
XX
XX WO200069900-A2.
PN
XX
XX 23-NOV-2000.
PD
XX
XX 17-MAY-2000; 2000WO-US13576.
PF
XX
XX 17-MAY-1999; 99US-0134406.
PR
XX 10-SEP-1999; 99US-0153406.
PR
XX 15-OCT-1999; 99US-0159783.
XX
XX (CONJ-) CONJUCHEM INC.
PA
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
PI
XX
XX WPI: 2001-112059/12.
DR
XX
XX Modifying and attaching therapeutic peptides to albumin prevents
XX peptidase degradation, useful for increasing length of in vivo activity
XX
XX
XX Disclosure: Page 391; 733pp; English.
PS
XX
XX The present invention describes a modified therapeutic peptide (I)
XX comprising a therapeutically active amino acid region (III) and a
XX reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
XX a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

SO Sequence 10 AA;

Query Match 75.4%; Score 46; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQGF 8
|||||||
Db 1 rpkpqqff 8

RESULT 178

AAB91422
ID AAB91422 standard; Peptide: 10 AA.

AC AAB91422;

DT 22-JUN-2001 (first entry)

DE Tachykinins peptide SEQ ID NO:598.

KW Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI: 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

XX -

PS Disclosure: Page 395; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)

CC comprising a therapeutically active amino acid region (III) and a

CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to

CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity

CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

SO Sequence 10 AA;

Query Match 75.4%; Score 46; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKPQGF 8
|||||||
Db 1 rpkpqqff 8

RESULT 179

AAB91432
ID AAB91432 standard; Peptide: 10 AA.

AC AAB91432;

DT 22-JUN-2001 (first entry)

DE Tachykinins peptide SEQ ID NO:608.

KW Protection: endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.
OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI: 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity

XX -

PS Disclosure: Page 398; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)

CC comprising a therapeutically active amino acid region (III) and a

CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to

CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.

XX Sequence 10 AA;

Query Match 75.4%; Score 46; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOOF 8
| | | | | | | |
Db 1 rpkpqgf 8

RESULT 180

AAB06257

ID AAB06257 standard; peptide; 17 AA.

AC AAB06257;

DT 16-OCT-2000 (first entry)

DE Substance P analogue #1.

XX Substane P; SP; neurokinin-1 receptor; NK-1R; nociception; SSP-SAP;
KW Saporin; SAP; analgesic; anti-inflammatory; neuroprotective;
KW anti-asthmatic; anti-allergic; dermatological; anti-ulcer;
KW tranquilliser; immunosuppressive; anti-migraine; cyostatic;
KW substance P antagonist; cytotoxic; ribosome inactivator;
KW prostaglandin antagonist; cancer; respiratory disease; asthma;
KW allergic rhinitis; ophthalmic disease; conjunctivitis;
KW allergic dermatitis; psoriasis; ulcerative colitis; Crohn's disease;
KW gastrointestinal disorder; anxiety; psychosis; rheumatoid arthritis;
KW carcinoma; lupus erythematosus conjunctivitis.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 17 /note="linked to SarlMet(O2)-amide"

FT US6063758-A.

PN 16-MAY-2000.

PD 09-JUL-1997; 97US-0890157.

PF 09-JUL-1997; 97US-0890157.

PR 09-JUL-1997; 97US-0890157.

PA (ADVA-) ADVANCED TARGETING SYSTEMS INC.

XX Lappl DA, Wiley RG;

XX WPI; 2000-430049/37.

XX New conjugates comprising substance P or its analog, and a
PT ribosome-inactivating protein (for example saporin), for alleviating
PT pain and treating disorders associated with neurokinin-1 receptor

XX Claim 1; Column 2; 21pp; English.

XX The present sequence is an analogue of substance P (SP). SP, which binds
CC to the neurokinin-1 receptor (NK-1R), is best known for its role in
CC nociception. It is secreted by small unmyelinated C-fibres of the
CC peripheral nervous system that are thought to be primary nociceptive
CC neurons. The present sequence may be conjugated to Saporin (SAP), a
CC ribosome-inactivating protein, to produce SSP-SAP. The conjugate may be
CC used to control chronic pain by specifically targeting cells having NK1
CC receptors, and inhibiting proliferation of or causing death of these

CC cells. It may also be used to treat NK-1R-associated disorders
CC including respiratory conditions (e.g. asthma, allergic rhinitis),
CC ophthalmic conditions (e.g. conjunctivitis), cutaneous conditions (e.g.
CC allergic dermatitis, psoriasis), intestinal conditions (e.g. ulcerative
CC colitis, Crohn's disease), gastrointestinal disorders, central nervous
CC system disorders (e.g. anxiety, psychosis), inflammatory diseases (e.g.
CC rheumatoid arthritis), proliferative conditions (e.g. carcinoma),
CC disorders related to immune enhancement or suppression (e.g. lupus
CC erythematosus conjunctivitis), and especially migraine.

XX Sequence 17 AA;

Query Match 75.4%; Score 46; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPKQOOF 8
| | | | | | | |
Db 10 rpkpqgf 17

RESULT 181

AAV06939

ID AAV06939 standard; peptide; 10 AA.

AC AAV06939;

DT 02-JUL-1999 (first entry)

DE Substance P from Bradykinin.

XX Peptide purification; hexylene glycol; biopharmaceutical; bradykinin;
KW protein separation; reversed-phase liquid chromatography.

XX Synthetic.

PN W09921889-A1.

PD 06-MAY-1999.

PF 08-OCT-1998; 98WO-US21238.

PR 24-OCT-1997; 97US-0957760.

PA (GETH) GENENTECH INC.

XX Fahrner RL, Reifsnnyder D;

XX WPI; 1999-302984/25.

XX Purification of molecules, e.g. peptides

XX Example 2; Page 26; 47pp; English.

XX The invention relates to a process for purifying a molecule selected
CC from a peptide, a polypeptide, and a biologically active non-peptidyl
CC compound. The process comprises the elution of the molecule from the
CC column with a buffer containing hexylene glycol. The method is
CC specifically used for purifying biopharmaceuticals. While ethanol,
CC methanol, isopropanol, and, in particular, acetonitrile, used in prior
CC art purification, often provide good protein separations using reversed
CC phase liquid chromatography, they are flammable solvents, and using them
CC at large scale requires expensive non-flammable-capable equipment and
CC facilities. Further, acetonitrile is a denaturant and is toxic to the
CC environment. The new method purifies molecules by reversed-phase liquid
CC chromatography using the non-flammable eluent hexylene glycol rather
CC than a flammable eluent.

XX Sequence 10 AA;

Query Match 74.6%; Score 45.5; DB 20; Length 10;

Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 RPXPOQFFGLM 11
|||||
Db 1 rpkp-qffglm 10

RESULT 182

AAG64746 standard; peptide: 10 AA.

AAG64746;

25-SEP-2001 (first entry)

Substance P amino acid sequence used in reversed-phase chromatography.

Protein purification; hexylene glycol; reversed-phase chromatography;

Insulin-like growth factor-I; IGF-I; thrombopoietin; hormone;

substance P.

Unidentified.

US6265542-B1.

24-JUL-2001.

08-OCT-1998; 98US-0168548.

24-OCT-1997; 97US-0063119.

(GENH) GENENTECH INC.

Fahrner RL, Relfnyder D;

WPI; 2001-463942/50.

Purifying polypeptides, e.g. insulin-like growth factor, by
reversed-phase liquid chromatography using hexylene glycol as eluate -

Example 2; Column 21-22; 27pp; English.

This invention relates to a process for purifying a polypeptide. The process comprises loading a mixture containing the polypeptide onto a reversed-phase liquid chromatography column and eluting the polypeptide from the column with a buffer containing hexylene glycol. The process is used for purifying a peptide from hydrophobic peptides, where the peptide to be purified is e.g. a growth factor (especially insulin-like growth factor-I IGF-I), thrombopoietin, a hormone, a chicken egg protein, a peptide of between 5 and 25 amino acids, an antibody and/or a hormone binding protein. The present sequence represents a peptide termed substance P which is used in an example illustrating the use of hexylene glycol as a reversed-phase eluent.

Sequence 10 AA:

Query Match 74.6%; Score 45.5; DB 22; Length 10;
Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 RPXPOQFFGLM 11
|||||
Db 1 rpkp-qffglm 10

RESULT 183

AAP40479 standard; peptide: 11 AA.

AAP40479;

DT 27-NOV-1991 (first entry)
XX Substance P analogue.
DE Substance P analogue; antiinflammatory agent; analgesic.

XX US4481139-A.
XX
PN
XX
PD 06-NOV-1984.

PF 13-APR-1983; 83US-0484646.

PR 13-APR-1983; 83US-0484646.

PA (UYTE-) UNIVERSITY OF TEXAS SYSTEM.

PI Folkers K, Ji-cheng X;

DR WPI; 1984-294258/47.

XX Peptide analogues of substance P - useful as antagonists, e.g. as
PT antiinflammatory agents and analgesics.

PS Claim 1; page 5; 5pp; English.

XX The peptide is a D-Arg1, D-Trp7, D-Trp9, Leu11 analogue of substance
CC P. The peptide is a substance P antagonist with higher activity than
CC known substance P analogues. It may be used as a biological
CC research tool, ophthalmological antiinflammatory agent and analgesic.

Sequence 11 AA:

Query Match 73.8%; Score 45; DB 5; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPXPOQFFGLM 11
|||||
Db 1 rpkpqwfwll 11

RESULT 184

AAP80313 standard; protein: 11 AA.

AAP80313;

DT 14-SEP-1990 (first entry)

XX Sequence of neuropeptide antagonist A which binds with polypeptide
DE receptor for bombesin type polypeptides.

XX Spantide; neuropeptide; polypeptide receptor; bombesin; cancer diagnosis;
KW cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW antagonist A.

XX Swiss 3T3 cells.

XX Key Location/Qualifiers

FT Misc-difference 1 /label-OTHER

FT /note="DArg"

FT Misc-difference 2 /label-OTHER

FT /note="DPro"

FT Misc-difference 7 /label-OTHER

FT /note="DTrp"

FT Misc-difference 9 /label-OTHER

FT /note="Dtrp"

FT Misc-difference 11

FT	/label=OTHER
FT	/note="Leu-NH2"
XX	
PN	WO8807551-A.
PD	06-OCT-1988.
XX	
PF	31-MAR-1988; 88WO-GB00255.
XX	
PR	25-NOV-1987; 87GB-0027638.
XX	
PA	(IMCR) IMPERIAL CANCER RES.
PI	Rosengurt E, Zachary I, Woll P;
DR	WPI; 1988-292842/41.
XX	
PT	New polypeptide receptor for bombesin type polypeptide(s) -
PT	antagonists are useful for treating uncontrolled cell proliferation
XX	
PS	Disclosure; Table 2; 42pp; English.
XX	
CC	The patent claims a polypeptide isolated from the surface of Swiss 3T3
CC	cells which binds selectively with polypeptides of the bombesin type and
CC	binds with antagonist A and antagonist D. Antagonist A is a
CC	commercially available structural variant of substance P, known as
CC	[D-Arg1, D-Pro2, D-Trp1,9, Leu11] substance P. It is also known as
CC	[D-Pro2] spantide. Antagonist B is also commercially available structural
CC	variant of substance P, known as [D-Phe5] spantide. Substance P is an
CC	11-mer neuropeptide, of interest in studies in pain transmission. Ten
CC	substance P antagonists (see AAP80313-80322) were tested for their
CC	ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue
CC	of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most
CC	potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less
CC	potent than either A or D. Spantide (B) had no antagonist activity even
CC	at 100 uM. Polypeptide antagonists A and D and novel variants are useful
CC	for diagnosis and therapy, esp. of cancers where uncontrolled cell
CC	growth is associated with disorders of proteins of the bombesin family.
XX	
SO	Sequence 11 AA:
XX	
QY	1 RPKPQGFGLM 11
	: :
Db	1 rpkpqgfwll 11
RESULT 185	
ID	AAP80314
XX	AAP80314 standard; protein; 11 AA.
AC	AAP80314:
XX	
DT	14-SEP-1990 (first entry)
XX	
DE	Sequence of neuropeptide antagonist B which binds with polypeptide
XX	receptor for bombesin type polypeptides.
XX	
KW	Spantide; neuropeptide; polypeptide receptor; bombesin; cancer diagnosis;
KW	cancer therapy; Swiss 3T3 cells; bombesin type polypeptides;
KW	antagonist B.
XX	
OS	Swiss 3T3 cells.
XX	
FH	Key
FT	Misc-difference 1
FT	/label=OTHER
FT	/note="DArg"

FT	Misc-difference	7	/label=OTHER
FT			/note="Dtrp"
FT	Misc-difference	1	
FT			/label=OTHER
FT			/note="Dtrp"
FT	Misc-difference	14	
FT			/label=OTHER
FT			/note="Leu-NH2"
PN			
PN	W08807551-A.		
PD			
PD	06-OCT-1988.		
XX			
XX	31-MAR-1988;	88WO-GB00255.	
XX			
XX	25-NOV-1987;	87GB-0027638.	
XX			
PA	(IMCR) IMPERIAL CANCER RES.		
XX			
XX	Rosengurt E, Zachary I, Woll P;		
XX			
XX	WPI; 1988-292842/41.		
XX			
PT	New polypeptide receptor for bombesin type polypeptide(s) -		
PT	is isolated from surface of Swiss 3T3 cells, and antibodies and		
PT	antagonists are useful for treating uncontrolled cell proliferation		
PS			
PS	Disclosure; Table 2; 42pp; English.		
XX			
XX	The patent claims a polypeptide isolated from the surface of Swiss 3T3		
CC	cells which binds selectively with polypeptides of the bombesin type and		
CC	binds with antagonist A and antagonist D. Antagonist A is a		
CC	commercially available structural variant of substance P, known as		
CC	[D-Arg1, D-Pro2, D-Trp7,9, Leu11] substance P. It is also known as		
CC	[D-Pro2] spantide. Antagonist B is also commercially available structural		
CC	variant of substance P, known as [D-Phe5] spantide. Substance P is an		
CC	11-mer neuropeptide, of interest in studies in pain transmission. Ten		
CC	substance P antagonists (see AAP80313-80322) were tested for their		
CC	ability to inhibit mitogenesis stimulated by GRP (the mammalian homologue		
CC	of bombesin in Swiss 3T3 cells). Antagonist D was clearly the most		
CC	potent GRP antagonist. Peptides B, C, D, E, F, G, H, J and K were less		
CC	potent than either A or D. Spantide (B) had no antagonist activity even		
CC	at 100 uM. Polypeptide antagonists A and D and novel variants are useful		
CC	for diagnosis and therapy, esp. of cancers where uncontrolled cell		
CC	growth is associated with disorders of proteins of the bombesin family.		
XX			
XX	Sequence 11 AA;		
SO			
	Query Match	73.8%;	Score 45; DB 9; Length 11;
	Best Local Similarity	72.7%;	Pred. NO. 0.16;
	Matches 8; Conservative	2;	Mismatches 1; Indels 0; Gaps 0.
QY	1 RPKQOQFGLM 11		
	: :		
DB	1 rpkpqgfwll 11		
	RESULT 186		
	AAR05856		
ID	AAR05856 standard; protein; 11 AA.		
XX			
XX	AAR05856;		
XX			
DT	07-SEP-1990 (first entry)		
XX			
DE	D-arginine 1, D-proline 2, D-tryptophan 7,9, leucine 11,		
DE	-substance P angiotensin antagonist.		
XX			
KW	Angiotensin; ectopic hormone; was oncogene; cancer;		
KW	neuroblastoma; neuroendocrine.		
XX			

OS	Synthetic.
XX	
FH	Key
FT	Modified-site Location/Qualifiers 1 /label=Dextrorotatory form.
FT	Modified-site 2 /label=Dextrorotatory form.
FT	Modified-site 7 /label=Dextrorotatory form.
FT	Modified-site 9 /label=Dextrorotatory form. /label=Dextrorotatory form.
XX	
FN	W09003181-A.
XX	
PD	05-APR-1990.
XX	
PE	22-SEP-1989; 89WO-0001121.
PR	24-SEP-1988; 88GB-0022483.
XX	
PA	(MED-) MED RES COUNCIL.
XX	
PI	Hanley MR, Goedert M;
DR	WPL: 1990-132106/17.
XX	
PT	Use of substances which block the activity of angiotensin - for the treatment or prevention of tumour development or ectopic hormona prodn.
PS	Claim 3; Page 19; 23pp; English.
CC	Peptide blocks biological activity of angiotensin and is active against the mas oncogene, retarding tumour growth, esp neuroendocrine and neuroblastoma tumours.
SO	Sequence 11 AA;
Oy	Query Match 73.8%; Score 45; DB 11; Length 11; Best Local Similarity 72.7%; Pred. No. 0.16; Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0,
Db	1 RRPQOFGGLM 11 1: 1 rpkpqgfwl1 11
RESULT 187	
AAR1144	
ID	AAR1144 standard; Protein; 11 AA.
XX	
AC	AAR1144;
XX	
PT	21-MAY-1991 (first entry)
XX	
DE	Substance P analogue.
XX	
KW	Anti-proliferation agent; neurogenetic inflammation; fibroblasts; agonist.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Modified-site Location/Qualifiers 1 /label= D-Trp
FT	Modified-site 7 /label= D-Trp
FT	Modified-site 9 /label= D-Trp
FT	Modified-site 9.10 /label= non-peptide bond /note= "Trp-L[CH2NH]-Trp"
FT	

FT	Modified-site	11
XX	/label= Nle	
PN	MO9102745-A.	
PD	07-MAR-1991.	
PF	16-AUG-1990;	90WO-US04633.
PR	16-AUG-1989;	89US-0394727.
PA	(TULA) TULANE E FUND ADMINISTRA.	
PI	Coy DH, Moreau JP;	
DR	WPI; 1991-087240/12.	
PT	Modified linear peptide analogue of natural substance P - acts as	
PT	competitive inhibitor of substance P and is used for treating	
PT	neuro genetic inflammation and as anti-proliferative agent.	
PS	Claim 11; Page 34; 40pp; English.	
XX		
CC	The peptide has a non-peptide bond introduced between Trp9 and	
CC	Leu10. This may alternatively be positioned between Leu10 and	
CC	Nle11. For prep., a benzhydrylamine resin was coupled to Boc-Leu.	
CC	Boc-Leu aldehyde was dissolved in 5 ml DMF and added to the resin	
CC	TFA salt suspension followed by addn. of NaCNBH3 and stirring for	
CC	one hour. The remaining amino acids were then coupled successively.	
CC	In tests the peptide inhibited P-stimulated amylase release from	
CC	pancreatic acini.	
CC	See also AAR11143.	
SQ	Sequence 11 AA:	
OY	Query Match	73.8%; Score 45; DB 12; Length 11;
	Best Local Similarity	72.7%; Pred. NO. 0.16;
	Matches 8; Conservative	2; Mismatches 1; Indels 0; Gaps 0.
DB	1 RPKPOQFFGLM 11 : : 1 rpkpqg*fwl 11	
RESULT 188		
ID	AAR21968	
AC	AAR21968 standard; Peptide: 11 AA.	
AC	AAR21968;	
DT	25-JUN-1992 (first entry)	
DE	Cyclic substance P [D-Cys 5, Cys 8].	
KW	Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;	
RW	syndrome; hereditary cerebral haemorrhage.	
OS	Synthetic.	
FH	Key	Location/Qualifiers
FT	Disulfide-bond	5..8
FT	Modified-site	5
FT		\note="D form"
EN	WO9202248-A.	
PD	20-FEB-1992.	
PE	29-JUL-1991;	91WO-US05323.
RR	27-JUL-1990;	90US-0559173.

PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA.
XX
DR WPI; 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Down's syndrome, etc.
XX
PS Claim 11; Page 22; 35pp; English.
XX
CC The peptide is the tachykinin agonist substance P with a D Cys
CC residue substituted at position 5 and a Cys at position 8, with
CC a disulphide bond formed between them, making the peptide cyclic.
CC The peptide was synthesised by standard solid phase synthesis.
CC Neuronal accumulation of beta-amyloid may be treated by administ-
CC ration of tachykinin agonists. The peptide can reduce the neuro-
CC toxic effects of a beta-amyloid related polypeptide on cultured
CC neurons. The peptide and its analogues are useful for controlling
CC diseases characterised by beta amyloid accumulation in the brain
CC such as Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
CC
SQ Sequence 11 AA;
XX
OY 1 RPKPOQFGIM 11
DB 1 rpkpcqcfglm 11
XX
RESULT 189
AAR21969
ID AAR21969 standard; Peptide; 11 AA.
XX
AC AAR21969;
XX
DT 25-JUN-1992 (first entry)
XX
DE Cyclic substance P [D-Cys 5, Cys 7].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 5..7
FT Modified-site \note="D form"
XX
PN WO9202248-A.
XX
PD 20-FEB-1992.
XX
PE 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA.
XX
DR WPI; 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Down's syndrome, etc.

XX
PS Claim 11; Page 22; 35pp; English.
XX
CC The peptide is the tachykinin agonist substance P with a D Cys
CC residue substituted at position 5 and a Cys at position 7, with
CC a disulphide bond formed between them, making the peptide cyclic.
CC The peptide was synthesised by standard solid phase synthesis.
CC Neuronal accumulation of beta-amyloid may be treated by administ-
CC ration of tachykinin agonists. The peptide can reduce the neuro-
CC toxic effects of a beta-amyloid related polypeptide on cultured
CC neurons. The peptide and its analogues are useful for controlling
CC diseases characterised by beta amyloid accumulation in the brain
CC such as Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
CC
SQ Sequence 11 AA;
XX
OY 1 RPKPOQFGIM 11
DB 1 rpkpcqcfglm 11
XX
RESULT 190
AAR21970
ID AAR21970 standard; Peptide; 11 AA.
XX
AC AAR21970;
XX
DT 25-JUN-1992 (first entry)
XX
DE Cyclic substance P [D/L-Cys 3, Cys 6].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's;
KW syndrome; hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 3..6
FT Modified-site /note="D or L form"
XX
PN WO9202248-A.
XX
PD 20-FEB-1992.
XX
PE 29-JUL-1991; 91WO-US05323.
XX
PR 27-JUL-1990; 90US-0559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA.
XX
DR WPI; 1992-079804/10.
XX
PT Treatment of neuronal accumulation of beta-amyloid - using
PT tachykinin agonists e.g. substance P, physalaemin and neurokinin
PT B, for treating Alzheimer's disease, Down's syndrome, etc.
XX
PS Claim 11; Page 22; 35pp; English.
XX
CC The peptide is the tachykinin agonist substance P with a D/L Cys
CC residue substituted at position 3 and a Cys at position 6, with
CC a disulphide bond formed between them, making the peptide cyclic.
CC The peptide was synthesised by standard solid phase synthesis.
CC Neuronal accumulation of beta-amyloid may be treated by administ-
CC ration of tachykinin agonists. The peptide can reduce the neuro-

CC toxic effects of a beta-amyloid related polypeptide on cultured
CC neurons. The peptide and its analogues are useful for controlling
CC diseases characterised by beta amyloid accumulation in the brain
CC such as Alzheimer's disease and Down's syndrome.
CC See also AAR21932-75.
XX
SQ Sequence 11 AA:

Query Match 73.8%; Score 45; DB 13; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
1111111111
Db 1 rpkpqcffglm 11

RESULT 191

AAM50966
ID AAM50966 standard; peptide; 11 AA.

XX AAM50966;

DT 31-JUL-1998 (first entry)

DE Substance P analogue, spantide I.

XX Vasoactive intestinal peptide; VIP; antagonist: somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor;
KM spantide.

XX Synthetic.

OS

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

FT EP835662-A2.

PN 15-APR-1998.

XX 11-DEC-1996; 96EP-0309012.

XX 08-OCT-1996; 96US-0727679.

PR 16-AUG-1996; 96IN-0001822.

XX (NAIM-) NAT INST IMMUNOLOGY.

PA Jaggi M, Mukherjee R;

PI WPI; 1998-208959/19.

XX Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)

XX Disclosure; Page 13; 49pp; English.

XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 ACCKNPFdWKTPSdc (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin
CC antagonist (BOM1) and substance P antagonist (SPI). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or

CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue, spantide I.
XX
SQ Sequence 11 AA:

Query Match 73.8%; Score 45; DB 19; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKPOFFGLM 11
1111111111
Db 1 rpkpqwfvl 11

RESULT 192

AAM50958
ID AAM50958 standard; peptide; 11 AA.

XX AAM50958;

DT 31-JUL-1998 (first entry)

DE Substance P analogue, [D-Arg1,D-Pro2,D-Trp7,9,Leu11]-Substance P.

XX Vasoactive intestinal peptide; VIP; antagonist: somatostatin; bombesin;
KW Substance P; cancer; inhibition; growth hormone releasing factor.

XX Synthetic.

OS

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 2 /note= "D-form residue"

FT Misc-difference 7 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

FT EP835662-A2.

PN 15-APR-1998.

XX 11-DEC-1996; 96EP-0309012.

XX 08-OCT-1996; 96US-0727679.

PR 16-AUG-1996; 96IN-0001822.

XX (NAIM-) NAT INST IMMUNOLOGY.

PA Jaggi M, Mukherjee R;

PI WPI; 1998-208959/19.

XX Composition containing analogues of vasoactive intestinal peptide,
PT somatostatin - bombesin and substance P, for treatment of tumours
PT and for inhibiting over-expression of these peptide(s)

XX Disclosure; Page 12; 49pp; English.

XX The invention relates to a new composition which comprises: (i) the
CC somatostatin analogue SOM2 ACCKNPFdWKTPSdc (3-14 disulphide bridge),
CC and (ii) at least 4 of the peptides: antagonist of vasoactive
CC intestinal peptide (VIP1); VIP receptor-binding inhibitor (VIP2); VIP
CC receptor antagonist (VIP3); somatostatin analogue (SOM1); bombesin

CC antagonist (BOM1) and substance P antagonist (SPI). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or

CC antagonist (BOM1) and substance P antagonist (SP1). Also claimed are
CC more general compositions containing peptide analogues of somatostatin,
CC VIP, bombesin and substance P. The compositions are used in human or
CC veterinary medicine: (a) to kill (or inhibit multiplication of) tumour
CC or cancer cells, particularly for treatment of leukaemia, lymphoma,
CC adenocarcinoma of stomach, pancreas or prostate, or cancer of lung,
CC breast, kidney or particularly rectum and colon, and (b) to prevent,
CC inhibit or modulate over-expression of, e.g. VIP. A wide range of cancer
CC cells express receptors for VIP, somatostatin, bombesin and/or substance
CC P. The present sequence represents a substance P analogue.
XX
SQ Sequence 11 AA;

Query Match 73.8%; Score 45; DB 19; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RPKQOQFGIM 11
|||||:| |
Db 1 rpkpgqgfwll 11

RESULT 193

AAW92687
ID AAW92687 standard; peptide; 11 AA.

XX AAW92687;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #33.

KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX Homo sapiens.

OS
XX
FH Key Location/Qualifiers

FT Misc-difference 5 /note= "D-form residue"

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PA Yankner BA;

PI WPI; 1999-189630/16.

DR Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PT Disclosure; Column 25-26; 28pp; English.

XX
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

SQ Sequence 11 AA;

Query Match 73.8%; Score 45; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKQOQFGIM 11
|||||:| |
Db 1 rpkpgqgfwll 11

RESULT 194

AAW92688
ID AAW92688 standard; peptide; 11 AA.

XX AAW92688;

DT 30-APR-1999 (first entry)

DE Human tachykinin agonist beta-amyloid peptide fragment #34.

KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
XX Homo sapiens.

OS
XX
FH Key Location/Qualifiers

FT Misc-difference 5 /note= "D-form residue"

PN US5876948-A.

PD 02-MAR-1999.

PF 27-JUL-1991; 91US-0737371.

PR 29-JUL-1991; 91US-0737371.

PR 27-JUL-1990; 90US-0559173.

XX (CHIL-) CHILDRENS MEDICAL CENT.

PA Yankner BA;

PI WPI; 1999-189630/16.

DR Screening for neurotoxin inhibitors - by testing compounds for their
XX effect on beta-amyloid peptide neurotoxic effect on neuronal cells

PT Disclosure; Column 25-26; 28pp; English.

XX
XX
CC This invention describes a method for screening compounds for inhibiting
CC a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodopathy with cerebral
CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.

SQ Sequence 11 AA;

Query Match 73.8%; Score 45; DB 20; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 RPKQOQFGIM 11
|||||:| |
Db 1 rpkpgqgfwll 11

RESULT	195
AAM92689	ID AAM92689 standard; peptide; 11 AA.
XX AC	AAM92689;
XX DT	30-APR-1999 (first entry)
DE XX	Human tachykinin agonist beta-amylloid peptide fragment #35.
KX XX	Tachykinin agonist; beta-amylloid; inhibition; neurotoxin; treatment;
KM KM	Alzheimer's disease; Down's syndrome; amyloidosis; human;
XX XX	hereditary cerebral haemorrhage; non-inherited congenital angiodopathy.
OS OS	Homo sapiens.
FH FH	Key Location/Qualifiers
FT FT	Misc-difference 3
Pt Pt	/note= "D-form residue"
PM PM	US5876948-A.
PD PD	02-MAR-1999.
PF PF	27-JUL-1991; 91US-073737L.
PR PR	29-JUL-1991; 91US-073737L.
XX XX	27-JUL-1990; 90US-0559173.
PA PA	(CHIL-) CHILDRENS MEDICAL CENT.
XX XX	Yankner BA:
PI PI	WP1: 1999-189630/16.
DR DR	Screening for neurotoxin inhibitors - by testing compounds for their effect on beta-amylloid peptide neurotoxic effect on neuronal cells
PT PT	Disclosure: Column 25-26; 28pp; English.
PS PS	This invention describes a method for screening compounds for inhibiting a neurotoxin. The method involves incubating tachykinin agonists with neuronal cells and a beta-amylloid peptide neurotoxin. The methods can be used for identifying compounds for treating diseases characterised by an undesirable build up of beta-amylloid protein, e.g. Alzheimer's disease, Down's syndrome, and the syndromes of hereditary cerebral hemorrhage with amyloidosis and non-inherited congenital angiodopathy with cerebral haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human beta-amylloid peptide fragments.
CC CC	Sequence 11 AA;
XX XX	
SQ SQ	
Query Match	73.8%; Score 45; DB 20; Length 11;
Best Local Similarity	81.8%; Pred. No. 0.16;
Matches 9; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
OY 1 RPKPQQFGIM 11	
I I I I I I I I	
Db 1 fpcpqcffgIm 11	
RESULT 196	
AAM92690	ID AAM92690 standard; peptide; 11 AA.
XX AC	AAM92690;
XX DT	30-APR-1999 (first entry)
DE XX	Human tachykinin agonist beta-amylloid peptide fragment #36.

KW	Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM	Alzheimer's disease; Down's syndrome; amyloidosis; human;
KX	hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
OS	Homo sapiens.
PN	US5876948-A.
XX	02-MAR-1999.
PD	
XX	27-JUL-1991; 91US-0737371.
PF	
XX	29-JUL-1991; 91US-0737371.
PR	27-JUL-1990; 90US-0559173.
XX	
PA	(CHIL-) CHILDRENS MEDICAL CENT.
XX	
PI	Yankner BA;
XX	
DR	WPI: 1999-189630/16.
XX	
PT	Screening for neurotoxin inhibitors - by testing compounds for their
PT	effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX	
PS	Disclosure: Column 25-26; 28pp; English.
XX	
CC	This invention describes a method for screening compounds for inhibiting
CC	a neurotoxin. The method involves incubating tachykinin agonists with
CC	neuronal cells and a beta-amyloid peptide neurotoxin. The methods can
CC	be used for identifying compounds for treating diseases characterised by an
CC	undetectable build up of beta-amyloid protein, e.g. Alzheimer's disease,
CC	Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC	with amyloidosis and non-inherited congenital angiodystrophy with cerebral
CC	haemorrhage. AAM92655-M92731 are tachykinin agonists derived from human
CC	beta-amyloid peptide fragments.
XX	
SQ	Sequence 11 AA;
XX	
Query Match	73.8%; Score 45; DB 20; Length 11;
Best Local Similarity	81.8%; Pred. No. 0.16;
Matches	9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	1 RPKPOOFFGLM 11
	1111111111
Db	1 rpkpccffglm 11
XX	
RESULT 197	
AAM92657	
ID	AAM92657 standard; peptide; 11 AA.
XX	
AC	AAM92657;
XX	
DT	30-APR-1999 (first entry)
XX	
DE	Human tachykinin agonist beta-amyloid peptide fragment #3.
XX	
KW	Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
KM	Alzheimer's disease; Down's syndrome; amyloidosis; human;
KX	hereditary cerebral haemorrhage; non-inherited congenital angiodystrophy.
OS	Homo sapiens.
XX	
XX	
PH	Key
FT	Misc-difference 1 Location/Qualifiers
FT	Misc-difference 7 /note= "D-form residue"
FT	Misc-difference 9 /note= "D-form residue"
FT	Misc-difference 9 /note= "D-form residue"
XX	
PN	US5876948-A.

XX 02-MAR-1999.
PD Best Local Similarity 72.7%; Score 45; DB 20; Length 11;
PT Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX 27-JUL-1991; 91US-0737371.
XX 29-JUL-1991; 91US-0737371.
PR 27-JUL-1990; 90US-0559173.
XX (CHIL-) CHILDRENS MEDICAL CENT.
PA Yankner BA;
XX WPI; 1999-189630/16.
DR Screening for neurotoxin inhibitors - by testing compounds for their
PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells
XX Disclosure; Column 11-12; 28pp; English.
PS This invention describes a method for screening compounds for inhibiting
XX a neurotoxin. The method involves incubating tachykinin agonists with
CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
CC used for identifying compounds for treating diseases characterised by an
CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease.
CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
CC with amyloidosis and non-inherited congenital angiodystrophy with cerebral
CC haemorrhage. AAM92655-W92731 are tachykinin agonists derived from human
CC beta-amyloid peptide fragments.
XX Sequence 11 AA;
SQ

Query Match 73.8%; Score 45; DB 20; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPOOFFGLM 11
Db 1 rpkpqgfwl1 11

RESULT 198
AAB91434
ID AAB91434 standard; Peptide: 11 AA.
XX AAB91434;
AC 22-JUN-2001 (first entry)
DT Tachykinins peptide SEQ ID NO:610.
XX DE
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimide; maleimide group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX Homo sapiens.
OS Synthetic.
OS WO200069900-A2.
XX 23-NOV-2000.
PD 17-MAY-2000; 2000WO-US13576.
XX 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX (CONJ-) CONJUCHEM INC.
PA Bridon DP, Errin AM, Milner PG, Holmes DL, Thibaudau K;
XX WPI; 2001-112059/12.
DR

XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT Disclosure; Page 398; 733pp; English.
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX Sequence 11 AA;
SQ

Query Match 73.8%; Score 45; DB 22; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.16;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RPKPOOFFGLM 11
Db 1 rpkpqgfwl1 11

RESULT 199
AAB50312
ID AAB50312 standard; peptide: 11 AA.
XX AAB50312;
AC 08-MAR-2001 (first entry)
DT Previn peptide #4.
XX DE
XX Asian toad; antibacterial; Botulinum toxin inhibitor; BttxB;
KW previn; tetanus neurotoxin; butorfinin.
XX Bufo bufo gargarizans.
OS Synthetic.
OS WO200069891-A2.
XX 23-NOV-2000.
PD 15-MAY-2000; 2000WO-US13215.
XX 17-MAY-1999; 99US-0134446.
XX (USSA) US DEPT OF THE ARMY.
PA Gordon RK, Moorad DR, Doctor BP, Garcia GE;
XX WPI; 2001-025001/03.
DR Novel Previn compounds useful for inhibiting the protease activity of
PT Botulinum B and tetanus toxins -
XX Claim 7; Page 29; 47pp; English.
XX The present sequence is a previn compound which inhibits the enzymatic
CC

CC activity of BtxB and tetanus neurotoxins. Previns
 CC may be used to construct compounds such as butorinins.
 XX
 SQ Sequence 11 AA:

Query Match 73.8%; Score 45; DB 22; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.16;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RPKPQGFGLM 11
 1 1 1 1 1 1 1 1 1 1 1
 Db 1 rkpqgffglm 11

RESULT 200

AAR28680
 ID AAR28680 standard; Protein; 24 AA.

XX
 AC AAR28680:

XX 22-MAR-1993 (first entry)

XX Galanin(1-12)-Pro-Spantide amide (C7).

XX Receptor; Substance P; insulin; growth hormone;
 KW acetylcholine; dopamine; somatostatin; noradrenaline;
 KW endocrinology; food intake; neurology; psychiatry;
 KW Alzheimer-type senile dementia; schizophrenia;
 KW intestinal diseases.

XX Synthetic.

XX Key Location/Qualifiers

FT MISC-difference 14 /note= "D-form residue"

FT MISC-difference 20 /note= "D-form residue"

FT MISC-difference 22 /note= "D-form residue"

FT Peptide 1..12 /label= galanin(1-12)

FT Peptide 14..24 /label= spantide

XX EP514361-A.

XX 19-NOV-1992.

XX 14-MAY-1992; 92EP-0850108.

XX 15-MAY-1991; 91SE-0001472.

XX (ASTR) ASTRA AB.

XX Ahren B, Bartfal T, Consolo S, Hoekfelt T, Land T;
 PI Langel U, Lindskog S, Wiesenfeld-Hallin Z;

XX WPI; 1992-384184/47.

XX New galanin antagonist peptide(s) - used for treating
 PT Alzheimer's-type senile dementia, schizophrenia, analgesia and
 PT intestinal diseases

XX Disclosure; Page 7; 21pp; English.

XX The C-terminal of this peptide is amidated. MW= 2827; IC50= 0.2nM.
 CC The peptides given in AAR28679-90 are used to treat disorders in
 CC mammals caused by the function of galanin at its receptor. The
 CC peptides may be useful in the regulation of insulin release, growth
 CC hormone release, acetylcholine release, dopamine release, substance
 CC P release, somatostatin release and noradrenaline release. They are
 CC useful in endocrinology, food intake, neurology and psychiatry, and

CC to treat Alzheimer-type senile dementia, schizophrenia, intestinal
 CC diseases, and in analgesia. Dosage is 0.01-1000, pref. 0.1-1000
 CC microg/kg body wt.
 XX
 SQ Sequence 24 AA:

Query Match 73.8%; Score 45; DB 13; Length 24;
 Best Local Similarity 72.7%; Pred. No. 0.34;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RPKPQGFGLM 11
 1
 Db 14 rkpqgwfll 24

Search completed: April 1, 2002, 16:18:20
 Job time: 51 sec